



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 12:59 PM GMT

PDB ID : 1F4A
Title : E. COLI (LACZ) BETA-GALACTOSIDASE (NCS CONSTRAINED MONOMER-ORTHORHOMBIC)
Authors : Juers, D.H.; Jacobson, R.H.; Wigley, D.; Zhang, X.J.; Huber, R.E.; Tronrud, D.E.; Matthews, B.W.
Deposited on : 2000-06-07
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

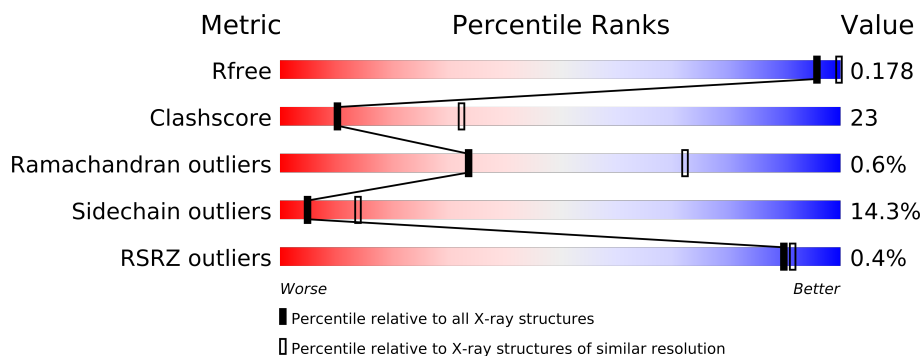
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1021	
1	B	1021	
1	C	1021	
1	D	1021	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34424 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called BETA-GALACTOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1021	Total	C	N	O	S	84	7	0
			8238	5209	1466	1525	38			
1	B	1021	Total	C	N	O	S	84	7	0
			8238	5209	1466	1525	38			
1	C	1021	Total	C	N	O	S	84	7	0
			8238	5209	1466	1525	38			
1	D	1021	Total	C	N	O	S	84	7	0
			8238	5209	1466	1525	38			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		
2	D	2	Total	Mg	0	0
			2	2		
2	C	2	Total	Mg	0	0
			2	2		

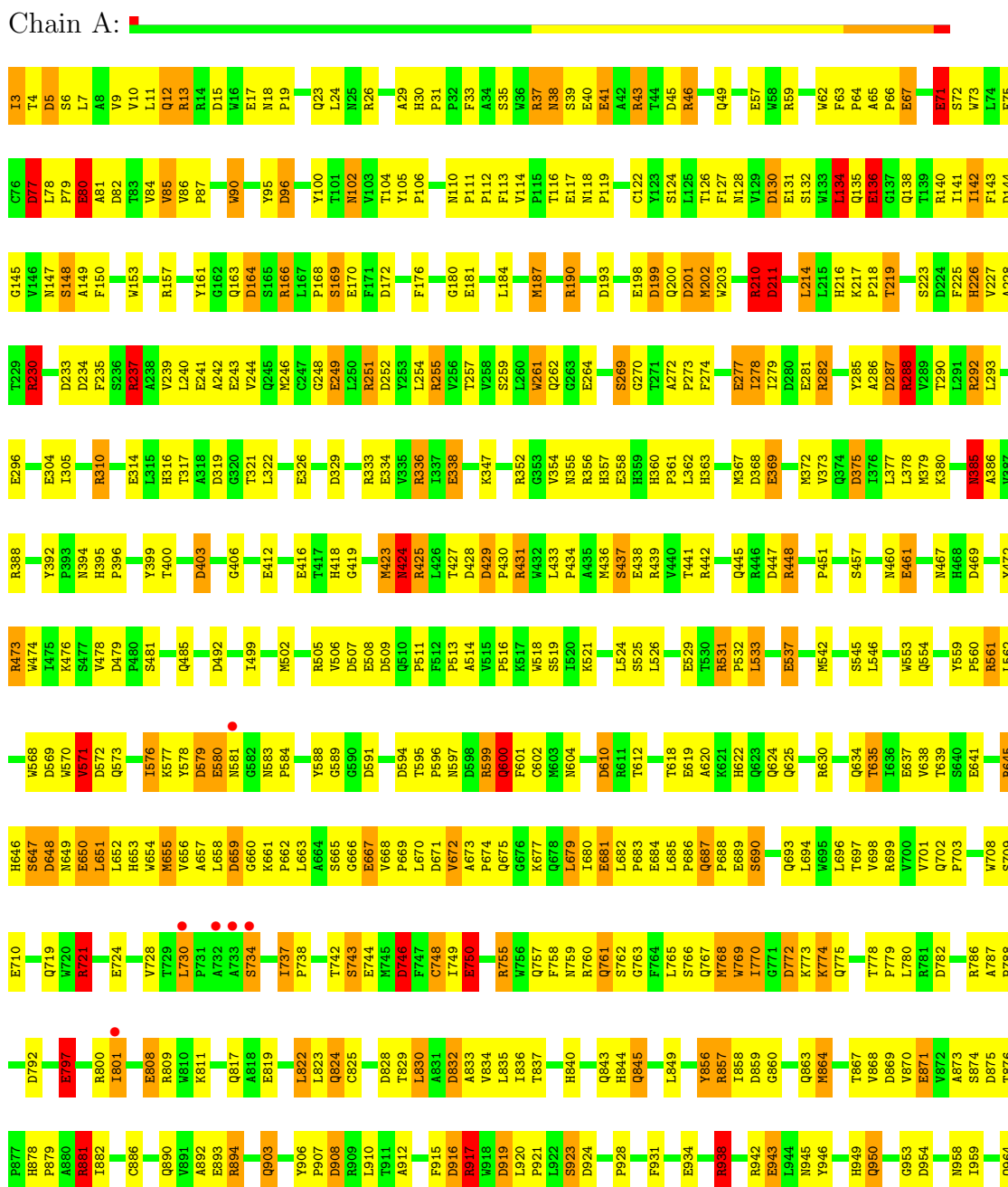
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	365	Total	O	0	0
			365	365		
3	B	366	Total	O	0	0
			366	366		
3	C	367	Total	O	0	0
			367	367		
3	D	366	Total	O	0	0
			366	366		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

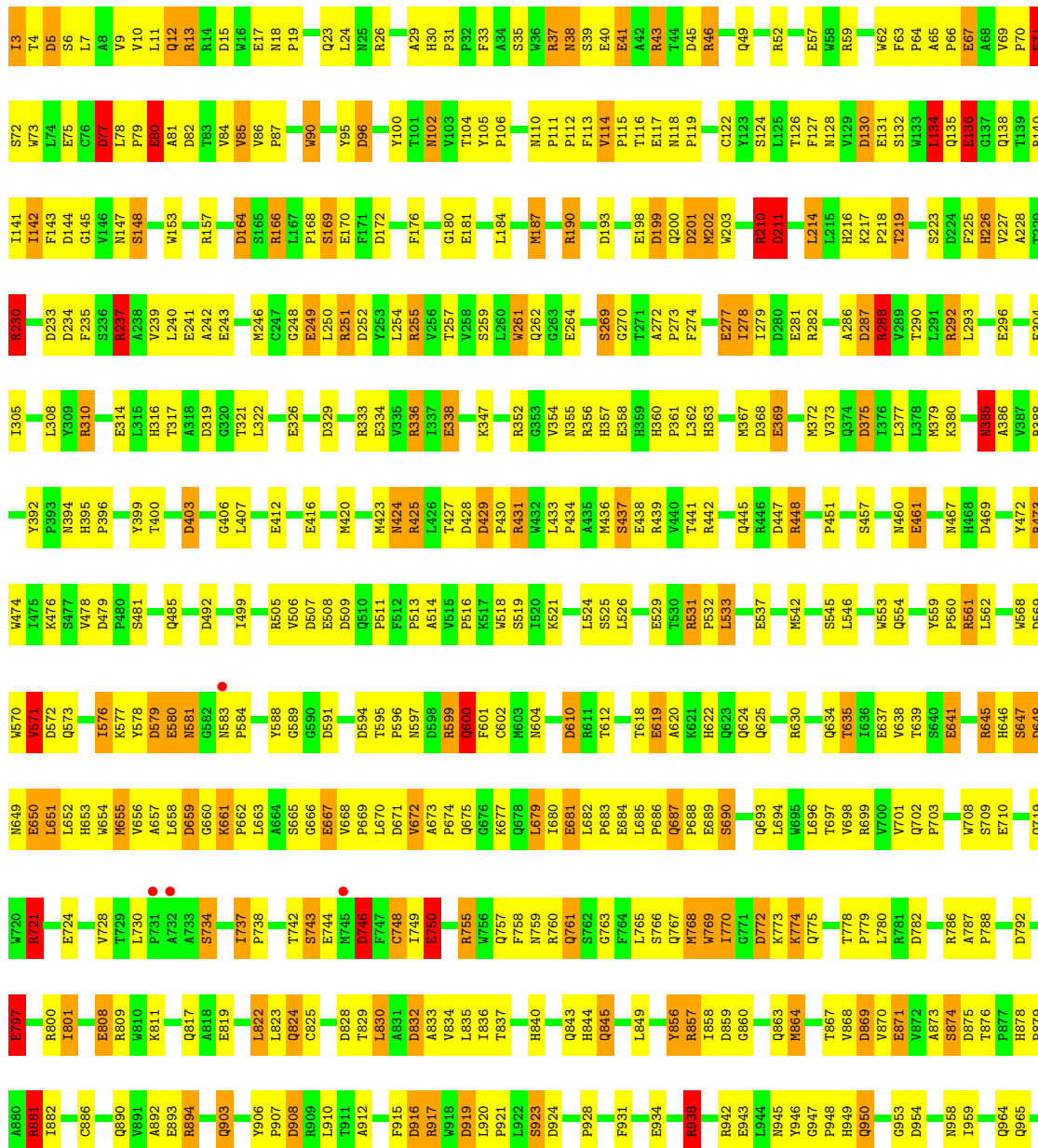
• Molecule 1: BETA-GALACTOSIDASE





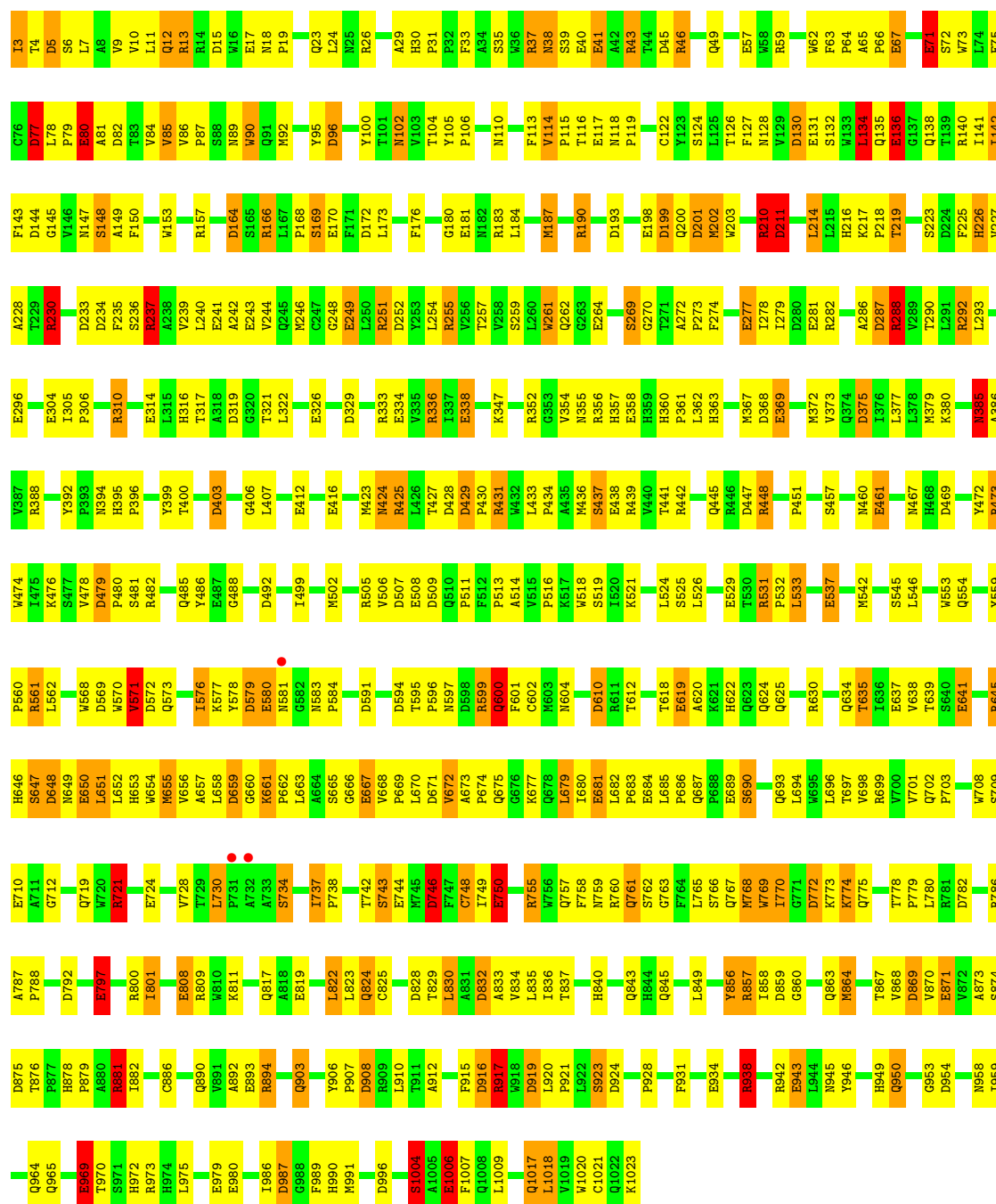
• Molecule 1: BETA-GALACTOSIDASE

Chain B:



• Molecule 1: BETA-GALACTOSIDASE

Chain C:



E369	H878	E792	U720	L651	D569	R473	R388	E304	T229
E370	P879	E793	R721	L652	W570	W474	Y392	I305	R230
S971	A880	R800	E724	H653	V571	I475	Y393	L308	D233
R972	R881	R801	E725	H654	D572	K476	N394	R310	D234
R973	I882	E808	V728	M655	Q573	S477	H395	E314	F235
H974	C886	R809	T729	A657	T576	D479	P396	E315	S236
L975	Q890	R810	L730	L658	K577	P480	Y399	L316	R237
E979	W891	R811	P731	D659	Y578	S481	T400	T317	V239
E980	A892	Q817	A732	G660	D579	Q485	D403	A318	L240
E983	E893	A818	A733	K661	E580	Q485	L407	D319	E241
R894	R894	E819	S734	P662	G581	D492	L407	G320	A242
D987	Q903	E822	I737	L664	N583	D492	E412	E326	E243
G988	L823	R823	P738	S665	P584	I499	E412	L321	M246
F989	L824	Q824	T742	G666	D591	R506	E416	L322	C247
H990	C925	R825	S743	E667	D594	V506	T417	E326	G248
M991	D908	E744	E745	P669	T595	D507	H418	D329	E249
D996	R909	W746	D746	L670	E508	E508	G419	R333	L250
S1004	L910	F747	C748	D671	D509	P511	N423	R334	D252
A1005	T911	F748	F748	A673	Q510	Q510	N423	E334	V253
E1006	A831	C748	C748	P674	D598	P513	R425	V335	L254
F1007	D832	I749	E750	P675	R599	P513	R425	R336	R255
Q1008	A833	E750	E750	G676	Q600	A514	L426	I337	V256
L1009	W834	R755	R755	G677	F601	V515	T427	E338	T257
Q1017	L835	W756	W756	K678	C502	P516	D428	K347	S259
L1018	T837	Q757	Q757	L679	M603	V258	D429	R352	L260
W1019	L920	F758	F758	I680	N604	W518	P430	V352	Q261
C1020	P921	W759	W759	E681	D610	S519	R431	G353	G262
Q1022	L922	R760	R760	L682	R611	L433	N432	V354	G263
K1023	S923	Q761	Q761	P683	T612	K521	L433	N355	E264
P928	H844	S762	S762	E684	T618	L524	A435	R356	
F931	Q845	G763	G763	L685	E619	S525	N436	H357	S269
E934	L849	L765	L765	P686	A620	L526	S437	E358	G270
R938	R854	S766	S766	E688	K621	E438	E438	H359	T271
R942	T855	Q767	Q767	E689	H622	R439	R439	H360	A272
E943	Y856	W768	W768	S690	Q623	T530	Y440	P361	P273
L944	R857	W769	W769		Q624	R531	T441	L362	F274
N945	R857	I770	I770	Q693	Q625	P532	R442	H363	
Y946	R864	G771	G771	L694	L630	L533	Q445	M367	E277
H949	T867	D772	D772	V695	R630	E537	R446	D368	L278
Q950	V868	K773	K773	L696	Q634	M542	D447	E369	L279
G953	D869	Q774	Q774	T697	T635	M542	R448	E281	D280
D954	V870	Q775	Q775	V698	I636	S545	P451	M372	R282
E954	R871	T778	T778	R699	E637	L546	Q451	V373	A286
N958	W872	P779	P779	V700	V638	L546	S457	Q374	D287
I959	A873	L780	L780	W701	T639	W553	N460	D375	R288
Q964	S874	R781	R781	Q702	S840	Q554	E461	L376	V289
Q965	D875	D782	D782	P703	E641	Q554	N461	L377	T290
	T876	R786	R786	W708	R645	Y559	N467	L378	L291
	P877	L788	L788	S709	H646	P560	H468	M379	R292
		W789	W789	E710	S647	R561	D469	K380	L293
		P788	P788	A711	D548	L562	A386	R385	
		D792	D792	G712	N649	W568	Y472	V387	E296

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	153.40Å 173.40Å 204.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.80 24.97 – 2.82	Depositor EDS
% Data completeness (in resolution range)	88.0 (25.00-2.80) 80.5 (24.97-2.82)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.80Å)	Xtriage
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.167 , 0.198 0.148 , 0.178	Depositor DCC
R_{free} test set	1590 reflections (1.53%)	DCC
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 76.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 105768 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	34424	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.86 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.2179e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.08	52/8515 (0.6%)	1.61	173/11615 (1.5%)
1	B	1.08	52/8515 (0.6%)	1.61	175/11615 (1.5%)
1	C	1.08	52/8515 (0.6%)	1.61	174/11615 (1.5%)
1	D	1.08	52/8515 (0.6%)	1.61	176/11615 (1.5%)
All	All	1.08	208/34060 (0.6%)	1.61	698/46460 (1.5%)

All (208) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	75	GLU	CD-OE2	9.53	1.36	1.25
1	C	75	GLU	CD-OE2	9.53	1.36	1.25
1	D	75	GLU	CD-OE2	9.49	1.36	1.25
1	B	75	GLU	CD-OE2	9.46	1.36	1.25
1	D	710	GLU	CD-OE2	7.62	1.34	1.25
1	B	710	GLU	CD-OE2	7.61	1.34	1.25
1	A	710	GLU	CD-OE2	7.61	1.34	1.25
1	C	710	GLU	CD-OE2	7.61	1.34	1.25
1	B	136	GLU	CD-OE2	7.46	1.33	1.25
1	D	136	GLU	CD-OE2	7.44	1.33	1.25
1	A	181	GLU	CD-OE2	7.44	1.33	1.25
1	C	181	GLU	CD-OE2	7.43	1.33	1.25
1	D	181	GLU	CD-OE2	7.43	1.33	1.25
1	D	264	GLU	CD-OE2	7.43	1.33	1.25
1	A	136	GLU	CD-OE2	7.42	1.33	1.25
1	B	181	GLU	CD-OE2	7.41	1.33	1.25
1	B	40	GLU	CD-OE2	7.41	1.33	1.25
1	A	508	GLU	CD-OE2	7.40	1.33	1.25
1	A	264	GLU	CD-OE2	7.39	1.33	1.25
1	A	681	GLU	CD-OE2	7.38	1.33	1.25
1	B	264	GLU	CD-OE2	7.38	1.33	1.25
1	C	264	GLU	CD-OE2	7.38	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	508	GLU	CD-OE2	7.38	1.33	1.25
1	B	508	GLU	CD-OE2	7.37	1.33	1.25
1	C	681	GLU	CD-OE2	7.37	1.33	1.25
1	B	681	GLU	CD-OE2	7.36	1.33	1.25
1	C	40	GLU	CD-OE2	7.36	1.33	1.25
1	C	136	GLU	CD-OE2	7.36	1.33	1.25
1	D	40	GLU	CD-OE2	7.36	1.33	1.25
1	A	40	GLU	CD-OE2	7.35	1.33	1.25
1	C	508	GLU	CD-OE2	7.35	1.33	1.25
1	D	681	GLU	CD-OE2	7.34	1.33	1.25
1	B	314	GLU	CD-OE2	7.32	1.33	1.25
1	C	943	GLU	CD-OE2	7.26	1.33	1.25
1	A	314	GLU	CD-OE2	7.25	1.33	1.25
1	A	943	GLU	CD-OE2	7.24	1.33	1.25
1	C	314	GLU	CD-OE2	7.24	1.33	1.25
1	B	943	GLU	CD-OE2	7.22	1.33	1.25
1	D	314	GLU	CD-OE2	7.21	1.33	1.25
1	D	943	GLU	CD-OE2	7.18	1.33	1.25
1	C	369	GLU	CD-OE2	7.11	1.33	1.25
1	B	369	GLU	CD-OE2	7.07	1.33	1.25
1	A	797	GLU	CD-OE2	7.05	1.33	1.25
1	C	797	GLU	CD-OE2	7.04	1.33	1.25
1	D	369	GLU	CD-OE2	7.04	1.33	1.25
1	B	797	GLU	CD-OE2	7.04	1.33	1.25
1	A	369	GLU	CD-OE2	7.03	1.33	1.25
1	D	797	GLU	CD-OE2	7.02	1.33	1.25
1	C	979	GLU	CD-OE2	6.94	1.33	1.25
1	D	979	GLU	CD-OE2	6.92	1.33	1.25
1	A	650	GLU	CD-OE2	6.88	1.33	1.25
1	A	979	GLU	CD-OE2	6.87	1.33	1.25
1	D	650	GLU	CD-OE2	6.85	1.33	1.25
1	B	650	GLU	CD-OE2	6.85	1.33	1.25
1	C	650	GLU	CD-OE2	6.82	1.33	1.25
1	D	969	GLU	CD-OE2	6.81	1.33	1.25
1	C	750	GLU	CD-OE2	6.79	1.33	1.25
1	A	326	GLU	CD-OE2	6.77	1.33	1.25
1	B	979	GLU	CD-OE2	6.77	1.33	1.25
1	B	326	GLU	CD-OE2	6.76	1.33	1.25
1	A	969	GLU	CD-OE2	6.76	1.33	1.25
1	D	326	GLU	CD-OE2	6.76	1.33	1.25
1	D	724	GLU	CD-OE2	6.76	1.33	1.25
1	C	969	GLU	CD-OE2	6.75	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	750	GLU	CD-OE2	6.75	1.33	1.25
1	C	326	GLU	CD-OE2	6.75	1.33	1.25
1	B	969	GLU	CD-OE2	6.74	1.33	1.25
1	B	724	GLU	CD-OE2	6.73	1.33	1.25
1	C	724	GLU	CD-OE2	6.73	1.33	1.25
1	B	198	GLU	CD-OE2	6.72	1.33	1.25
1	A	724	GLU	CD-OE2	6.72	1.33	1.25
1	B	750	GLU	CD-OE2	6.69	1.33	1.25
1	D	241	GLU	CD-OE2	6.68	1.32	1.25
1	A	198	GLU	CD-OE2	6.67	1.32	1.25
1	C	198	GLU	CD-OE2	6.66	1.32	1.25
1	C	241	GLU	CD-OE2	6.66	1.32	1.25
1	A	241	GLU	CD-OE2	6.66	1.32	1.25
1	D	198	GLU	CD-OE2	6.65	1.32	1.25
1	D	750	GLU	CD-OE2	6.64	1.32	1.25
1	B	241	GLU	CD-OE2	6.61	1.32	1.25
1	C	338	GLU	CD-OE2	6.55	1.32	1.25
1	A	338	GLU	CD-OE2	6.50	1.32	1.25
1	B	338	GLU	CD-OE2	6.50	1.32	1.25
1	D	338	GLU	CD-OE2	6.45	1.32	1.25
1	A	461	GLU	CD-OE2	6.38	1.32	1.25
1	C	438	GLU	CD-OE2	6.37	1.32	1.25
1	B	461	GLU	CD-OE2	6.35	1.32	1.25
1	D	461	GLU	CD-OE2	6.35	1.32	1.25
1	B	438	GLU	CD-OE2	6.34	1.32	1.25
1	A	438	GLU	CD-OE2	6.34	1.32	1.25
1	C	461	GLU	CD-OE2	6.32	1.32	1.25
1	B	296	GLU	CD-OE2	6.32	1.32	1.25
1	D	438	GLU	CD-OE2	6.32	1.32	1.25
1	A	296	GLU	CD-OE2	6.31	1.32	1.25
1	D	296	GLU	CD-OE2	6.30	1.32	1.25
1	C	296	GLU	CD-OE2	6.26	1.32	1.25
1	C	249	GLU	CD-OE2	6.22	1.32	1.25
1	A	249	GLU	CD-OE2	6.21	1.32	1.25
1	D	249	GLU	CD-OE2	6.21	1.32	1.25
1	B	537	GLU	CD-OE2	6.20	1.32	1.25
1	A	744	GLU	CD-OE2	6.20	1.32	1.25
1	D	744	GLU	CD-OE2	6.19	1.32	1.25
1	B	744	GLU	CD-OE2	6.19	1.32	1.25
1	C	637	GLU	CD-OE2	6.17	1.32	1.25
1	C	808	GLU	CD-OE2	6.17	1.32	1.25
1	C	744	GLU	CD-OE2	6.17	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	808	GLU	CD-OE2	6.16	1.32	1.25
1	B	637	GLU	CD-OE2	6.15	1.32	1.25
1	C	537	GLU	CD-OE2	6.15	1.32	1.25
1	A	808	GLU	CD-OE2	6.14	1.32	1.25
1	C	57	GLU	CD-OE2	6.14	1.32	1.25
1	A	637	GLU	CD-OE2	6.14	1.32	1.25
1	D	537	GLU	CD-OE2	6.14	1.32	1.25
1	D	808	GLU	CD-OE2	6.14	1.32	1.25
1	A	537	GLU	CD-OE2	6.14	1.32	1.25
1	B	249	GLU	CD-OE2	6.12	1.32	1.25
1	D	57	GLU	CD-OE2	6.12	1.32	1.25
1	A	57	GLU	CD-OE2	6.10	1.32	1.25
1	B	57	GLU	CD-OE2	6.10	1.32	1.25
1	D	637	GLU	CD-OE2	6.10	1.32	1.25
1	D	667	GLU	CD-OE2	6.08	1.32	1.25
1	D	641	GLU	CD-OE2	6.05	1.32	1.25
1	D	281	GLU	CD-OE2	6.04	1.32	1.25
1	A	667	GLU	CD-OE2	6.03	1.32	1.25
1	C	667	GLU	CD-OE2	6.03	1.32	1.25
1	A	641	GLU	CD-OE2	6.03	1.32	1.25
1	B	641	GLU	CD-OE2	6.00	1.32	1.25
1	B	80	GLU	CD-OE2	6.00	1.32	1.25
1	C	80	GLU	CD-OE2	5.99	1.32	1.25
1	B	667	GLU	CD-OE2	5.99	1.32	1.25
1	D	80	GLU	CD-OE2	5.99	1.32	1.25
1	A	80	GLU	CD-OE2	5.97	1.32	1.25
1	A	281	GLU	CD-OE2	5.97	1.32	1.25
1	C	641	GLU	CD-OE2	5.96	1.32	1.25
1	C	281	GLU	CD-OE2	5.96	1.32	1.25
1	B	281	GLU	CD-OE2	5.94	1.32	1.25
1	C	871	GLU	CD-OE2	5.90	1.32	1.25
1	C	41	GLU	CD-OE2	5.89	1.32	1.25
1	A	871	GLU	CD-OE2	5.88	1.32	1.25
1	D	871	GLU	CD-OE2	5.88	1.32	1.25
1	D	41	GLU	CD-OE2	5.87	1.32	1.25
1	A	41	GLU	CD-OE2	5.84	1.32	1.25
1	B	871	GLU	CD-OE2	5.84	1.32	1.25
1	B	41	GLU	CD-OE2	5.83	1.32	1.25
1	B	334	GLU	CD-OE2	5.77	1.31	1.25
1	A	334	GLU	CD-OE2	5.74	1.31	1.25
1	D	334	GLU	CD-OE2	5.73	1.31	1.25
1	C	334	GLU	CD-OE2	5.68	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	71	GLU	CD-OE2	5.55	1.31	1.25
1	C	71	GLU	CD-OE2	5.52	1.31	1.25
1	A	71	GLU	CD-OE2	5.50	1.31	1.25
1	D	71	GLU	CD-OE2	5.48	1.31	1.25
1	B	619	GLU	CD-OE2	5.45	1.31	1.25
1	B	1006	GLU	CD-OE2	5.42	1.31	1.25
1	A	619	GLU	CD-OE2	5.41	1.31	1.25
1	C	1006	GLU	CD-OE2	5.39	1.31	1.25
1	C	619	GLU	CD-OE2	5.39	1.31	1.25
1	C	412	GLU	CD-OE2	5.39	1.31	1.25
1	D	1006	GLU	CD-OE2	5.38	1.31	1.25
1	D	131	GLU	CD-OE2	5.37	1.31	1.25
1	B	412	GLU	CD-OE2	5.36	1.31	1.25
1	A	1006	GLU	CD-OE2	5.36	1.31	1.25
1	B	131	GLU	CD-OE2	5.36	1.31	1.25
1	D	980	GLU	CD-OE2	5.36	1.31	1.25
1	D	580	GLU	CD-OE2	5.35	1.31	1.25
1	D	619	GLU	CD-OE2	5.35	1.31	1.25
1	A	412	GLU	CD-OE2	5.33	1.31	1.25
1	C	131	GLU	CD-OE2	5.33	1.31	1.25
1	A	17	GLU	CD-OE2	5.32	1.31	1.25
1	D	412	GLU	CD-OE2	5.31	1.31	1.25
1	A	131	GLU	CD-OE2	5.31	1.31	1.25
1	A	277	GLU	CD-OE2	5.31	1.31	1.25
1	B	277	GLU	CD-OE2	5.31	1.31	1.25
1	A	980	GLU	CD-OE2	5.30	1.31	1.25
1	A	580	GLU	CD-OE2	5.30	1.31	1.25
1	D	117	GLU	CD-OE2	5.30	1.31	1.25
1	C	17	GLU	CD-OE2	5.30	1.31	1.25
1	D	17	GLU	CD-OE2	5.29	1.31	1.25
1	B	17	GLU	CD-OE2	5.29	1.31	1.25
1	A	934	GLU	CD-OE2	5.29	1.31	1.25
1	C	580	GLU	CD-OE2	5.28	1.31	1.25
1	C	277	GLU	CD-OE2	5.28	1.31	1.25
1	A	117	GLU	CD-OE2	5.28	1.31	1.25
1	D	277	GLU	CD-OE2	5.28	1.31	1.25
1	B	934	GLU	CD-OE2	5.27	1.31	1.25
1	C	980	GLU	CD-OE2	5.27	1.31	1.25
1	B	893	GLU	CD-OE2	5.27	1.31	1.25
1	B	580	GLU	CD-OE2	5.27	1.31	1.25
1	A	684	GLU	CD-OE2	5.27	1.31	1.25
1	B	980	GLU	CD-OE2	5.27	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	689	GLU	CD-OE2	5.26	1.31	1.25
1	D	934	GLU	CD-OE2	5.26	1.31	1.25
1	A	893	GLU	CD-OE2	5.26	1.31	1.25
1	C	117	GLU	CD-OE2	5.26	1.31	1.25
1	C	934	GLU	CD-OE2	5.26	1.31	1.25
1	B	689	GLU	CD-OE2	5.25	1.31	1.25
1	C	893	GLU	CD-OE2	5.24	1.31	1.25
1	D	684	GLU	CD-OE2	5.23	1.31	1.25
1	D	689	GLU	CD-OE2	5.22	1.31	1.25
1	A	689	GLU	CD-OE2	5.22	1.31	1.25
1	C	819	GLU	CD-OE2	5.21	1.31	1.25
1	B	819	GLU	CD-OE2	5.21	1.31	1.25
1	C	684	GLU	CD-OE2	5.21	1.31	1.25
1	B	684	GLU	CD-OE2	5.20	1.31	1.25
1	D	893	GLU	CD-OE2	5.20	1.31	1.25
1	B	117	GLU	CD-OE2	5.20	1.31	1.25
1	A	819	GLU	CD-OE2	5.19	1.31	1.25
1	D	819	GLU	CD-OE2	5.16	1.31	1.25

All (698) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	809[A]	ARG	NE-CZ-NH1	11.76	126.18	120.30
1	B	809[B]	ARG	NE-CZ-NH1	11.76	126.18	120.30
1	A	809[A]	ARG	NE-CZ-NH1	11.62	126.11	120.30
1	A	809[B]	ARG	NE-CZ-NH1	11.62	126.11	120.30
1	D	809[A]	ARG	NE-CZ-NH1	11.61	126.11	120.30
1	D	809[B]	ARG	NE-CZ-NH1	11.61	126.11	120.30
1	C	809[A]	ARG	NE-CZ-NH1	11.53	126.06	120.30
1	C	809[B]	ARG	NE-CZ-NH1	11.53	126.06	120.30
1	C	881	ARG	NE-CZ-NH1	11.03	125.82	120.30
1	D	881	ARG	NE-CZ-NH1	10.99	125.80	120.30
1	C	881	ARG	NE-CZ-NH2	-10.99	114.80	120.30
1	A	881	ARG	NE-CZ-NH1	10.98	125.79	120.30
1	D	881	ARG	NE-CZ-NH2	-10.98	114.81	120.30
1	A	881	ARG	NE-CZ-NH2	-10.95	114.82	120.30
1	B	881	ARG	NE-CZ-NH1	10.95	125.78	120.30
1	B	881	ARG	NE-CZ-NH2	-10.89	114.86	120.30
1	A	531	ARG	NE-CZ-NH1	10.76	125.68	120.30
1	B	531	ARG	NE-CZ-NH1	10.73	125.67	120.30
1	D	531	ARG	NE-CZ-NH1	10.73	125.66	120.30
1	C	531	ARG	NE-CZ-NH1	10.71	125.65	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	385	ASN	CB-CA-C	-10.44	89.51	110.40
1	A	385	ASN	CB-CA-C	-10.44	89.52	110.40
1	B	385	ASN	CB-CA-C	-10.44	89.53	110.40
1	C	385	ASN	CB-CA-C	-10.43	89.54	110.40
1	D	507	ASP	CB-CG-OD2	-10.36	108.97	118.30
1	C	507	ASP	CB-CG-OD2	-10.34	109.00	118.30
1	A	507	ASP	CB-CG-OD2	-10.32	109.01	118.30
1	B	507	ASP	CB-CG-OD2	-10.26	109.07	118.30
1	C	356	ARG	NE-CZ-NH1	9.72	125.16	120.30
1	A	13	ARG	NE-CZ-NH2	-9.71	115.45	120.30
1	C	13	ARG	NE-CZ-NH2	-9.70	115.45	120.30
1	D	13	ARG	NE-CZ-NH2	-9.69	115.46	120.30
1	A	356	ARG	NE-CZ-NH1	9.69	125.14	120.30
1	B	356	ARG	NE-CZ-NH1	9.67	125.13	120.30
1	B	13	ARG	NE-CZ-NH2	-9.63	115.48	120.30
1	D	356	ARG	NE-CZ-NH1	9.63	125.11	120.30
1	D	237	ARG	NE-CZ-NH1	9.62	125.11	120.30
1	D	591	ASP	CB-CG-OD2	-9.56	109.70	118.30
1	C	591	ASP	CB-CG-OD2	-9.56	109.70	118.30
1	A	237	ARG	NE-CZ-NH1	9.55	125.08	120.30
1	B	237	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	C	237	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	A	591	ASP	CB-CG-OD2	-9.53	109.72	118.30
1	D	439	ARG	NE-CZ-NH1	9.51	125.06	120.30
1	A	439	ARG	NE-CZ-NH1	9.50	125.05	120.30
1	B	439	ARG	NE-CZ-NH1	9.49	125.05	120.30
1	B	591	ASP	CB-CG-OD2	-9.48	109.77	118.30
1	C	439	ARG	NE-CZ-NH1	9.40	125.00	120.30
1	C	249	GLU	N-CA-CB	9.26	127.27	110.60
1	A	249	GLU	N-CA-CB	9.24	127.24	110.60
1	B	249	GLU	N-CA-CB	9.24	127.23	110.60
1	D	249	GLU	N-CA-CB	9.22	127.20	110.60
1	D	509	ASP	CB-CG-OD2	-9.18	110.04	118.30
1	A	509	ASP	CB-CG-OD2	-9.14	110.07	118.30
1	B	509	ASP	CB-CG-OD2	-9.14	110.08	118.30
1	C	509	ASP	CB-CG-OD2	-9.12	110.09	118.30
1	C	424	ASN	CB-CA-C	-9.11	92.18	110.40
1	B	424	ASN	CB-CA-C	-9.11	92.19	110.40
1	A	424	ASN	CB-CA-C	-9.10	92.20	110.40
1	D	424	ASN	CB-CA-C	-9.10	92.20	110.40
1	C	938	ARG	NE-CZ-NH2	-8.88	115.86	120.30
1	A	938	ARG	NE-CZ-NH2	-8.81	115.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	938	ARG	NE-CZ-NH2	-8.81	115.90	120.30
1	B	429	ASP	CB-CG-OD1	8.80	126.22	118.30
1	D	938	ARG	NE-CZ-NH2	-8.79	115.91	120.30
1	A	429	ASP	CB-CG-OD1	8.74	126.17	118.30
1	C	429	ASP	CB-CG-OD1	8.74	126.16	118.30
1	D	429	ASP	CB-CG-OD1	8.71	126.14	118.30
1	B	210	ARG	NE-CZ-NH1	8.68	124.64	120.30
1	A	210	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	C	210	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	D	210	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	C	509	ASP	CB-CG-OD1	8.49	125.94	118.30
1	D	509	ASP	CB-CG-OD1	8.46	125.92	118.30
1	A	509	ASP	CB-CG-OD1	8.43	125.89	118.30
1	B	509	ASP	CB-CG-OD1	8.41	125.87	118.30
1	B	233	ASP	CB-CG-OD1	8.23	125.70	118.30
1	A	233	ASP	CB-CG-OD1	8.22	125.70	118.30
1	D	233	ASP	CB-CG-OD1	8.20	125.68	118.30
1	C	233	ASP	CB-CG-OD1	8.19	125.67	118.30
1	B	130	ASP	CB-CG-OD2	-8.16	110.95	118.30
1	D	226	HIS	CB-CA-C	-8.16	94.08	110.40
1	C	226	HIS	CB-CA-C	-8.16	94.08	110.40
1	A	130	ASP	CB-CG-OD2	-8.15	110.96	118.30
1	B	226	HIS	CB-CA-C	-8.15	94.10	110.40
1	A	226	HIS	CB-CA-C	-8.14	94.11	110.40
1	D	287	ASP	CB-CG-OD2	-8.14	110.97	118.30
1	A	287	ASP	CB-CG-OD2	-8.13	110.98	118.30
1	B	287	ASP	CB-CG-OD2	-8.13	110.98	118.30
1	C	130	ASP	CB-CG-OD2	-8.12	111.00	118.30
1	C	287	ASP	CB-CG-OD2	-8.11	111.00	118.30
1	D	130	ASP	CB-CG-OD2	-8.11	111.00	118.30
1	D	479	ASP	CB-CG-OD2	-8.09	111.02	118.30
1	A	479	ASP	CB-CG-OD2	-8.04	111.07	118.30
1	B	479	ASP	CB-CG-OD2	-8.04	111.07	118.30
1	C	479	ASP	CB-CG-OD2	-8.03	111.07	118.30
1	B	211	ASP	CB-CG-OD1	7.98	125.48	118.30
1	D	211	ASP	CB-CG-OD1	7.97	125.48	118.30
1	A	211	ASP	CB-CG-OD1	7.96	125.47	118.30
1	B	828	ASP	CB-CG-OD2	-7.95	111.15	118.30
1	C	211	ASP	CB-CG-OD1	7.93	125.44	118.30
1	A	828	ASP	CB-CG-OD2	-7.93	111.16	118.30
1	D	792	ASP	CB-CG-OD2	-7.92	111.17	118.30
1	D	828	ASP	CB-CG-OD2	-7.92	111.17	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	828	ASP	CB-CG-OD2	-7.92	111.18	118.30
1	B	792	ASP	CB-CG-OD2	-7.91	111.19	118.30
1	A	792	ASP	CB-CG-OD2	-7.87	111.22	118.30
1	C	792	ASP	CB-CG-OD2	-7.87	111.22	118.30
1	D	13	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	A	13	ARG	NE-CZ-NH1	7.79	124.20	120.30
1	C	13	ARG	NE-CZ-NH1	7.79	124.19	120.30
1	A	385	ASN	N-CA-CB	-7.77	96.62	110.60
1	B	385	ASN	N-CA-CB	-7.77	96.62	110.60
1	D	288	ARG	NE-CZ-NH1	-7.76	116.42	120.30
1	D	385	ASN	N-CA-CB	-7.76	96.63	110.60
1	C	385	ASN	N-CA-CB	-7.76	96.63	110.60
1	C	310	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	D	310	ARG	NE-CZ-NH1	7.73	124.16	120.30
1	C	648	ASP	CB-CG-OD2	-7.72	111.35	118.30
1	B	13	ARG	NE-CZ-NH1	7.72	124.16	120.30
1	A	659	ASP	CB-CG-OD2	-7.71	111.36	118.30
1	A	648	ASP	CB-CG-OD2	-7.70	111.37	118.30
1	C	659	ASP	CB-CG-OD2	-7.70	111.37	118.30
1	B	310	ARG	NE-CZ-NH1	7.70	124.15	120.30
1	B	648	ASP	CB-CG-OD2	-7.69	111.38	118.30
1	D	648	ASP	CB-CG-OD2	-7.69	111.38	118.30
1	A	310	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	C	832	ASP	CB-CG-OD2	-7.67	111.40	118.30
1	B	659	ASP	CB-CG-OD2	-7.66	111.41	118.30
1	A	288	ARG	NE-CZ-NH1	-7.66	116.47	120.30
1	B	288	ARG	NE-CZ-NH1	-7.64	116.48	120.30
1	C	288	ARG	NE-CZ-NH1	-7.64	116.48	120.30
1	D	659	ASP	CB-CG-OD2	-7.64	111.43	118.30
1	D	832	ASP	CB-CG-OD1	7.64	125.17	118.30
1	B	832	ASP	CB-CG-OD1	7.63	125.17	118.30
1	A	832	ASP	CB-CG-OD2	-7.62	111.44	118.30
1	B	832	ASP	CB-CG-OD2	-7.61	111.45	118.30
1	A	832	ASP	CB-CG-OD1	7.61	125.15	118.30
1	D	479	ASP	CB-CG-OD1	7.61	125.15	118.30
1	A	479	ASP	CB-CG-OD1	7.61	125.15	118.30
1	C	479	ASP	CB-CG-OD1	7.60	125.14	118.30
1	C	832	ASP	CB-CG-OD1	7.60	125.14	118.30
1	D	832	ASP	CB-CG-OD2	-7.60	111.46	118.30
1	B	479	ASP	CB-CG-OD1	7.59	125.14	118.30
1	B	639	THR	CA-CB-CG2	-7.47	101.94	112.40
1	C	639	THR	CA-CB-CG2	-7.46	101.95	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	431[A]	ARG	NE-CZ-NH1	7.46	124.03	120.30
1	D	431[B]	ARG	NE-CZ-NH1	7.46	124.03	120.30
1	C	252	ASP	CB-CG-OD2	-7.45	111.59	118.30
1	A	639	THR	CA-CB-CG2	-7.45	101.97	112.40
1	D	639	THR	CA-CB-CG2	-7.44	101.98	112.40
1	B	199	ASP	CB-CG-OD2	-7.42	111.62	118.30
1	D	252	ASP	CB-CG-OD2	-7.42	111.62	118.30
1	A	252	ASP	CB-CG-OD2	-7.41	111.63	118.30
1	B	448	ARG	NE-CZ-NH2	-7.40	116.60	120.30
1	C	199	ASP	CB-CG-OD2	-7.40	111.64	118.30
1	A	199	ASP	CB-CG-OD2	-7.39	111.64	118.30
1	B	252	ASP	CB-CG-OD2	-7.39	111.65	118.30
1	D	211	ASP	CB-CG-OD2	-7.38	111.65	118.30
1	B	431[A]	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	B	431[B]	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	A	431[A]	ARG	NE-CZ-NH1	7.37	123.98	120.30
1	A	431[B]	ARG	NE-CZ-NH1	7.37	123.98	120.30
1	A	1004	SER	N-CA-CB	7.36	121.55	110.50
1	C	1004	SER	N-CA-CB	7.36	121.54	110.50
1	C	211	ASP	CB-CG-OD2	-7.36	111.68	118.30
1	D	1004	SER	N-CA-CB	7.36	121.53	110.50
1	B	211	ASP	CB-CG-OD2	-7.35	111.68	118.30
1	A	211	ASP	CB-CG-OD2	-7.34	111.69	118.30
1	D	199	ASP	CB-CG-OD2	-7.34	111.69	118.30
1	B	1004	SER	N-CA-CB	7.33	121.50	110.50
1	A	448	ARG	NE-CZ-NH2	-7.33	116.63	120.30
1	D	403	ASP	CB-CG-OD1	7.32	124.89	118.30
1	B	403	ASP	CB-CG-OD1	7.29	124.86	118.30
1	C	448	ARG	NE-CZ-NH2	-7.29	116.66	120.30
1	D	448	ARG	NE-CZ-NH2	-7.29	116.66	120.30
1	C	403	ASP	CB-CG-OD1	7.27	124.84	118.30
1	C	431[A]	ARG	NE-CZ-NH1	7.27	123.93	120.30
1	C	431[B]	ARG	NE-CZ-NH1	7.27	123.93	120.30
1	A	403	ASP	CB-CG-OD1	7.25	124.83	118.30
1	D	96	ASP	CB-CG-OD2	-7.22	111.80	118.30
1	B	648	ASP	CB-CG-OD1	7.20	124.78	118.30
1	C	96	ASP	CB-CG-OD2	-7.20	111.82	118.30
1	A	924	ASP	CB-CG-OD2	-7.20	111.82	118.30
1	B	924	ASP	CB-CG-OD2	-7.19	111.83	118.30
1	B	96	ASP	CB-CG-OD2	-7.19	111.83	118.30
1	A	96	ASP	CB-CG-OD2	-7.19	111.83	118.30
1	B	336	ARG	NE-CZ-NH1	7.19	123.89	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	924	ASP	CB-CG-OD1	7.18	124.77	118.30
1	D	924	ASP	CB-CG-OD1	7.18	124.77	118.30
1	B	126	THR	CA-CB-CG2	-7.17	102.36	112.40
1	C	924	ASP	CB-CG-OD2	-7.17	111.84	118.30
1	A	924	ASP	CB-CG-OD1	7.16	124.75	118.30
1	C	648	ASP	CB-CG-OD1	7.16	124.74	118.30
1	D	924	ASP	CB-CG-OD2	-7.16	111.86	118.30
1	A	126	THR	CA-CB-CG2	-7.15	102.39	112.40
1	C	126	THR	CA-CB-CG2	-7.15	102.39	112.40
1	D	126	THR	CA-CB-CG2	-7.14	102.40	112.40
1	B	924	ASP	CB-CG-OD1	7.14	124.73	118.30
1	A	648	ASP	CB-CG-OD1	7.14	124.72	118.30
1	C	336	ARG	NE-CZ-NH1	7.13	123.87	120.30
1	D	336	ARG	NE-CZ-NH1	7.13	123.86	120.30
1	A	336	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	D	648	ASP	CB-CG-OD1	7.11	124.70	118.30
1	A	553	TRP	CA-CB-CG	-7.08	100.25	113.70
1	B	553	TRP	CA-CB-CG	-7.08	100.25	113.70
1	C	553	TRP	CA-CB-CG	-7.08	100.25	113.70
1	C	252	ASP	CB-CG-OD1	7.08	124.67	118.30
1	B	746	ASP	CB-CG-OD2	-7.06	111.94	118.30
1	C	356	ARG	NE-CZ-NH2	-7.06	116.77	120.30
1	D	553	TRP	CA-CB-CG	-7.06	100.28	113.70
1	A	252	ASP	CB-CG-OD1	7.05	124.64	118.30
1	A	746	ASP	CB-CG-OD2	-7.05	111.96	118.30
1	C	746	ASP	CB-CG-OD2	-7.03	111.97	118.30
1	D	252	ASP	CB-CG-OD1	7.02	124.62	118.30
1	D	746	ASP	CB-CG-OD2	-7.02	111.98	118.30
1	D	400	THR	CA-CB-CG2	-7.01	102.59	112.40
1	B	252	ASP	CB-CG-OD1	7.00	124.60	118.30
1	B	859	ASP	CB-CG-OD1	6.99	124.59	118.30
1	A	400	THR	CA-CB-CG2	-6.97	102.64	112.40
1	C	400	THR	CA-CB-CG2	-6.97	102.64	112.40
1	D	356	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	B	356	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	D	859	ASP	CB-CG-OD1	6.96	124.56	118.30
1	A	233	ASP	CB-CG-OD2	-6.96	112.04	118.30
1	B	233	ASP	CB-CG-OD2	-6.96	112.04	118.30
1	B	287	ASP	CB-CG-OD1	6.95	124.55	118.30
1	C	591	ASP	CB-CG-OD1	6.95	124.55	118.30
1	A	859	ASP	CB-CG-OD1	6.94	124.55	118.30
1	B	400	THR	CA-CB-CG2	-6.94	102.68	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	233	ASP	CB-CG-OD2	-6.94	112.06	118.30
1	C	233	ASP	CB-CG-OD2	-6.93	112.06	118.30
1	A	287	ASP	CB-CG-OD1	6.93	124.53	118.30
1	A	591	ASP	CB-CG-OD1	6.92	124.53	118.30
1	B	429	ASP	CB-CG-OD2	-6.92	112.07	118.30
1	B	859	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	A	569	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	C	96	ASP	CB-CG-OD1	6.91	124.52	118.30
1	D	287	ASP	CB-CG-OD1	6.90	124.51	118.30
1	D	591	ASP	CB-CG-OD1	6.90	124.51	118.30
1	B	403	ASP	CB-CG-OD2	-6.89	112.10	118.30
1	C	859	ASP	CB-CG-OD1	6.89	124.50	118.30
1	D	859	ASP	CB-CG-OD2	-6.89	112.10	118.30
1	C	287	ASP	CB-CG-OD1	6.88	124.49	118.30
1	A	859	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	C	569	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	A	429	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	D	96	ASP	CB-CG-OD1	6.87	124.49	118.30
1	A	356	ARG	NE-CZ-NH2	-6.87	116.86	120.30
1	C	859	ASP	CB-CG-OD2	-6.87	112.12	118.30
1	D	569	ASP	CB-CG-OD2	-6.87	112.12	118.30
1	D	429	ASP	CB-CG-OD2	-6.86	112.12	118.30
1	B	591	ASP	CB-CG-OD1	6.86	124.47	118.30
1	A	96	ASP	CB-CG-OD1	6.86	124.47	118.30
1	C	429	ASP	CB-CG-OD2	-6.86	112.13	118.30
1	B	569	ASP	CB-CG-OD2	-6.84	112.15	118.30
1	D	403	ASP	CB-CG-OD2	-6.83	112.15	118.30
1	B	881	ARG	CD-NE-CZ	6.82	133.14	123.60
1	A	403	ASP	CB-CG-OD2	-6.82	112.17	118.30
1	C	881	ARG	CD-NE-CZ	6.81	133.13	123.60
1	D	881	ARG	CD-NE-CZ	6.81	133.13	123.60
1	A	881	ARG	CD-NE-CZ	6.80	133.12	123.60
1	B	96	ASP	CB-CG-OD1	6.79	124.42	118.30
1	C	403	ASP	CB-CG-OD2	-6.78	112.19	118.30
1	C	659	ASP	CB-CG-OD1	6.66	124.29	118.30
1	D	375	ASP	CB-CG-OD2	-6.65	112.31	118.30
1	A	659	ASP	CB-CG-OD1	6.65	124.28	118.30
1	C	571	VAL	CB-CA-C	-6.65	98.77	111.40
1	B	375	ASP	CB-CG-OD2	-6.65	112.32	118.30
1	C	375	ASP	CB-CG-OD2	-6.65	112.32	118.30
1	A	571	VAL	CB-CA-C	-6.63	98.80	111.40
1	D	571	VAL	CB-CA-C	-6.63	98.81	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	659	ASP	CB-CG-OD1	6.63	124.27	118.30
1	B	571	VAL	CB-CA-C	-6.62	98.83	111.40
1	A	375	ASP	CB-CG-OD2	-6.61	112.35	118.30
1	D	672	VAL	CB-CA-C	-6.60	98.86	111.40
1	C	672	VAL	CB-CA-C	-6.60	98.86	111.40
1	B	424	ASN	N-CA-CB	-6.59	98.74	110.60
1	D	659	ASP	CB-CG-OD1	6.59	124.23	118.30
1	D	424	ASN	N-CA-CB	-6.58	98.75	110.60
1	A	424	ASN	N-CA-CB	-6.58	98.75	110.60
1	A	672	VAL	CB-CA-C	-6.58	98.89	111.40
1	C	424	ASN	N-CA-CB	-6.57	98.77	110.60
1	B	672	VAL	CB-CA-C	-6.57	98.92	111.40
1	C	507	ASP	CB-CG-OD1	6.57	124.21	118.30
1	B	166	ARG	NE-CZ-NH1	6.55	123.57	120.30
1	A	507	ASP	CB-CG-OD1	6.53	124.18	118.30
1	D	507	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	166	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	B	507	ASP	CB-CG-OD1	6.49	124.14	118.30
1	D	166	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	D	919	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	B	15	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	A	15	ASP	CB-CG-OD2	-6.47	112.48	118.30
1	C	919	ASP	CB-CG-OD2	-6.46	112.49	118.30
1	D	15	ASP	CB-CG-OD1	6.45	124.11	118.30
1	D	15	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	A	919	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	C	15	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	C	166	ARG	NE-CZ-NH1	6.44	123.52	120.30
1	C	875	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	C	15	ASP	CB-CG-OD1	6.43	124.08	118.30
1	C	5	ASP	CB-CG-OD1	6.42	124.08	118.30
1	B	875	ASP	CB-CG-OD2	-6.42	112.53	118.30
1	A	15	ASP	CB-CG-OD1	6.41	124.07	118.30
1	A	875	ASP	CB-CG-OD2	-6.40	112.54	118.30
1	B	5	ASP	CB-CG-OD1	6.40	124.06	118.30
1	C	600	GLN	N-CA-CB	6.39	122.10	110.60
1	B	600	GLN	N-CA-CB	6.39	122.10	110.60
1	B	919	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	A	5	ASP	CB-CG-OD1	6.39	124.05	118.30
1	B	938	ARG	N-CA-CB	6.38	122.09	110.60
1	D	5	ASP	CB-CG-OD1	6.38	124.04	118.30
1	D	875	ASP	CB-CG-OD2	-6.38	112.56	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	938	ARG	N-CA-CB	6.38	122.08	110.60
1	B	15	ASP	CB-CG-OD1	6.38	124.04	118.30
1	A	600	GLN	N-CA-CB	6.37	122.07	110.60
1	D	938	ARG	N-CA-CB	6.37	122.07	110.60
1	D	750	GLU	N-CA-CB	6.37	122.06	110.60
1	C	938	ARG	N-CA-CB	6.37	122.06	110.60
1	C	750	GLU	N-CA-CB	6.36	122.05	110.60
1	B	750	GLU	N-CA-CB	6.35	122.03	110.60
1	D	319	ASP	CB-CG-OD2	-6.35	112.59	118.30
1	D	600	GLN	N-CA-CB	6.35	122.02	110.60
1	A	750	GLU	N-CA-CB	6.34	122.01	110.60
1	B	319	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	A	319	ASP	CB-CG-OD2	-6.32	112.61	118.30
1	B	782	ASP	CB-CG-OD1	6.31	123.98	118.30
1	A	782	ASP	CB-CG-OD1	6.31	123.98	118.30
1	D	782	ASP	CB-CG-OD1	6.30	123.97	118.30
1	C	319	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	C	782	ASP	CB-CG-OD1	6.27	123.94	118.30
1	C	908	ASP	CB-CG-OD1	6.27	123.94	118.30
1	B	439	ARG	NE-CZ-NH2	-6.27	117.17	120.30
1	A	439	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	651	LEU	CB-CA-C	-6.25	98.31	110.20
1	B	651	LEU	CB-CA-C	-6.25	98.32	110.20
1	D	651	LEU	CB-CA-C	-6.25	98.32	110.20
1	D	428	ASP	CB-CG-OD2	-6.24	112.69	118.30
1	D	439	ARG	NE-CZ-NH2	-6.24	117.18	120.30
1	C	651	LEU	CB-CA-C	-6.23	98.36	110.20
1	C	439	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	C	938	ARG	CG-CD-NE	-6.22	98.73	111.80
1	A	428	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	B	938	ARG	CG-CD-NE	-6.21	98.76	111.80
1	B	428	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	A	938	ARG	CG-CD-NE	-6.20	98.78	111.80
1	D	938	ARG	CG-CD-NE	-6.19	98.80	111.80
1	A	908	ASP	CB-CG-OD1	6.18	123.86	118.30
1	B	954	ASP	CB-CG-OD1	6.18	123.86	118.30
1	C	428	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	C	572	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	D	572	ASP	CB-CG-OD2	-6.16	112.76	118.30
1	B	908	ASP	CB-CG-OD1	6.16	123.84	118.30
1	B	172	ASP	CB-CG-OD2	-6.15	112.76	118.30
1	B	431[A]	ARG	NE-CZ-NH2	-6.14	117.23	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	431[B]	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	B	572	ASP	CB-CG-OD2	-6.13	112.78	118.30
1	D	954	ASP	CB-CG-OD1	6.13	123.82	118.30
1	A	572	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	954	ASP	CB-CG-OD1	6.12	123.81	118.30
1	B	772	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	D	908	ASP	CB-CG-OD1	6.12	123.81	118.30
1	A	172	ASP	CB-CG-OD2	-6.12	112.80	118.30
1	D	431[A]	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	D	431[B]	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	C	954	ASP	CB-CG-OD1	6.11	123.80	118.30
1	A	431[A]	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	A	431[B]	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	D	172	ASP	CB-CG-OD2	-6.10	112.81	118.30
1	C	172	ASP	CB-CG-OD2	-6.09	112.82	118.30
1	A	772	ASP	CB-CG-OD2	-6.08	112.83	118.30
1	D	772	ASP	CB-CG-OD2	-6.07	112.83	118.30
1	A	569	ASP	CB-CG-OD1	6.07	123.76	118.30
1	C	336	ARG	CB-CA-C	-6.07	98.27	110.40
1	C	772	ASP	CB-CG-OD2	-6.06	112.84	118.30
1	D	336	ARG	CB-CA-C	-6.05	98.30	110.40
1	A	336	ARG	CB-CA-C	-6.05	98.30	110.40
1	B	336	ARG	CB-CA-C	-6.05	98.31	110.40
1	C	431[A]	ARG	NE-CZ-NH2	-6.03	117.28	120.30
1	C	431[B]	ARG	NE-CZ-NH2	-6.03	117.28	120.30
1	C	679	LEU	CA-CB-CG	-6.03	101.44	115.30
1	A	679	LEU	CA-CB-CG	-6.01	101.48	115.30
1	D	679	LEU	CA-CB-CG	-6.00	101.50	115.30
1	B	679	LEU	CA-CB-CG	-6.00	101.51	115.30
1	A	136	GLU	CB-CA-C	-5.97	98.45	110.40
1	C	136	GLU	CB-CA-C	-5.97	98.45	110.40
1	C	569	ASP	CB-CG-OD1	5.97	123.68	118.30
1	B	136	GLU	CB-CA-C	-5.97	98.45	110.40
1	A	142	ILE	CB-CA-C	-5.97	99.66	111.60
1	B	142	ILE	CB-CA-C	-5.97	99.67	111.60
1	C	45	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	D	136	GLU	CB-CA-C	-5.97	98.47	110.40
1	C	142	ILE	CB-CA-C	-5.96	99.67	111.60
1	D	569	ASP	CB-CG-OD1	5.96	123.67	118.30
1	B	569	ASP	CB-CG-OD1	5.96	123.66	118.30
1	A	45	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	B	45	ASP	CB-CG-OD2	-5.95	112.94	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	5	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	D	45	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	D	142	ILE	CB-CA-C	-5.95	99.70	111.60
1	C	908	ASP	CB-CG-OD2	-5.95	112.95	118.30
1	D	5	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	D	908	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	A	908	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	B	5	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	C	199	ASP	CB-CG-OD1	5.91	123.62	118.30
1	B	1018	LEU	CB-CA-C	-5.89	99.01	110.20
1	A	1018	LEU	CB-CA-C	-5.88	99.02	110.20
1	B	43	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	B	199	ASP	CB-CG-OD1	5.88	123.59	118.30
1	A	769	TRP	CB-CA-C	-5.88	98.65	110.40
1	B	908	ASP	CB-CG-OD2	-5.87	113.01	118.30
1	D	769	TRP	CB-CA-C	-5.87	98.65	110.40
1	A	5	ASP	CB-CG-OD2	-5.87	113.02	118.30
1	C	769	TRP	CB-CA-C	-5.87	98.66	110.40
1	A	199	ASP	CB-CG-OD1	5.86	123.58	118.30
1	D	199	ASP	CB-CG-OD1	5.86	123.58	118.30
1	D	1018	LEU	CB-CA-C	-5.86	99.06	110.20
1	C	82	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	C	1018	LEU	CB-CA-C	-5.85	99.08	110.20
1	B	769	TRP	CB-CA-C	-5.85	98.70	110.40
1	D	77	ASP	CB-CG-OD2	-5.84	113.05	118.30
1	C	423	MET	C-N-CA	5.84	136.29	121.70
1	A	82	ASP	CB-CG-OD2	-5.83	113.05	118.30
1	C	77	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	A	77	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	A	423	MET	C-N-CA	5.82	136.24	121.70
1	D	82	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	D	77	ASP	CB-CG-OD1	5.82	123.53	118.30
1	A	77	ASP	CB-CG-OD1	5.81	123.53	118.30
1	B	144	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	B	423	MET	C-N-CA	5.80	136.21	121.70
1	D	423	MET	C-N-CA	5.80	136.21	121.70
1	B	954	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	B	610	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	D	130	ASP	CB-CG-OD1	5.80	123.52	118.30
1	D	368	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	B	77	ASP	CB-CG-OD1	5.79	123.51	118.30
1	C	130	ASP	CB-CG-OD1	5.79	123.51	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	82	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	D	610	ASP	CB-CG-OD2	-5.79	113.09	118.30
1	A	134	LEU	N-CA-CB	5.78	121.97	110.40
1	C	134	LEU	N-CA-CB	5.78	121.97	110.40
1	D	134	LEU	N-CA-CB	5.78	121.97	110.40
1	D	954	ASP	CB-CG-OD2	-5.78	113.09	118.30
1	A	144	ASP	CB-CG-OD2	-5.78	113.10	118.30
1	C	43	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	A	130	ASP	CB-CG-OD1	5.78	123.50	118.30
1	B	134	LEU	N-CA-CB	5.78	121.96	110.40
1	C	987	ASP	CB-CG-OD1	5.78	123.50	118.30
1	B	130	ASP	CB-CG-OD1	5.78	123.50	118.30
1	B	77	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	C	77	ASP	CB-CG-OD1	5.77	123.49	118.30
1	C	610	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	D	239	VAL	CA-CB-CG2	-5.77	102.25	110.90
1	C	239	VAL	CA-CB-CG2	-5.76	102.26	110.90
1	D	144	ASP	CB-CG-OD2	-5.75	113.12	118.30
1	B	792	ASP	CB-CG-OD1	5.75	123.48	118.30
1	A	610	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	A	43	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	A	954	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	C	954	ASP	CB-CG-OD2	-5.74	113.13	118.30
1	A	239	VAL	CA-CB-CG2	-5.74	102.29	110.90
1	C	144	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	368	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	987	ASP	CB-CG-OD1	5.72	123.45	118.30
1	C	368	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	B	368	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	D	43	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	D	792	ASP	CB-CG-OD1	5.72	123.45	118.30
1	C	292	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	C	792	ASP	CB-CG-OD1	5.72	123.44	118.30
1	A	469	ASP	CB-CG-OD1	5.71	123.44	118.30
1	B	239	VAL	CA-CB-CG2	-5.71	102.34	110.90
1	D	987	ASP	CB-CG-OD1	5.71	123.44	118.30
1	B	987	ASP	CB-CG-OD1	5.69	123.42	118.30
1	C	469	ASP	CB-CG-OD1	5.69	123.42	118.30
1	A	792	ASP	CB-CG-OD1	5.69	123.42	118.30
1	B	230	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	B	469	ASP	CB-CG-OD1	5.68	123.41	118.30
1	C	230	ARG	NE-CZ-NH1	5.68	123.14	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	144	ASP	CB-CG-OD1	5.67	123.41	118.30
1	A	164	ASP	CB-CG-OD2	-5.67	113.20	118.30
1	B	144	ASP	CB-CG-OD1	5.67	123.40	118.30
1	D	469	ASP	CB-CG-OD1	5.67	123.40	118.30
1	B	164	ASP	CB-CG-OD1	5.67	123.40	118.30
1	B	635	THR	CA-CB-CG2	-5.66	104.47	112.40
1	D	635	THR	CA-CB-CG2	-5.66	104.48	112.40
1	A	144	ASP	CB-CG-OD1	5.66	123.39	118.30
1	A	635	THR	CA-CB-CG2	-5.66	104.48	112.40
1	C	45	ASP	CB-CG-OD1	5.66	123.39	118.30
1	B	164	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	C	635	THR	CA-CB-CG2	-5.64	104.50	112.40
1	D	230	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	D	164	ASP	CB-CG-OD1	5.64	123.38	118.30
1	D	164	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	C	164	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	C	144	ASP	CB-CG-OD1	5.63	123.37	118.30
1	C	288	ARG	CD-NE-CZ	-5.63	115.72	123.60
1	A	164	ASP	CB-CG-OD1	5.63	123.36	118.30
1	A	288	ARG	CD-NE-CZ	-5.63	115.72	123.60
1	B	288	ARG	CD-NE-CZ	-5.62	115.72	123.60
1	D	45	ASP	CB-CG-OD1	5.62	123.36	118.30
1	B	772	ASP	CB-CG-OD1	5.62	123.36	118.30
1	B	45	ASP	CB-CG-OD1	5.62	123.36	118.30
1	D	594	ASP	CB-CG-OD2	-5.62	113.24	118.30
1	A	45	ASP	CB-CG-OD1	5.61	123.35	118.30
1	D	288	ARG	CD-NE-CZ	-5.61	115.74	123.60
1	B	210	ARG	N-CA-CB	5.61	120.69	110.60
1	A	210	ARG	N-CA-CB	5.61	120.69	110.60
1	D	210	ARG	N-CA-CB	5.60	120.68	110.60
1	A	594	ASP	CB-CG-OD2	-5.59	113.26	118.30
1	C	210	ARG	N-CA-CB	5.59	120.67	110.60
1	C	292	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	A	230	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	D	772	ASP	CB-CG-OD1	5.59	123.33	118.30
1	C	164	ASP	CB-CG-OD1	5.58	123.33	118.30
1	A	772	ASP	CB-CG-OD1	5.58	123.32	118.30
1	B	594	ASP	CB-CG-OD2	-5.58	113.28	118.30
1	D	916	ASP	CB-CG-OD1	5.57	123.31	118.30
1	C	594	ASP	CB-CG-OD2	-5.56	113.29	118.30
1	C	916	ASP	CB-CG-OD1	5.56	123.31	118.30
1	D	292	ARG	NE-CZ-NH2	-5.56	117.52	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	292	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	492	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	C	772	ASP	CB-CG-OD1	5.56	123.30	118.30
1	A	492	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	B	292	ARG	NE-CZ-NH1	5.55	123.07	120.30
1	A	292	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	828	ASP	CB-CG-OD1	5.53	123.28	118.30
1	B	916	ASP	CB-CG-OD1	5.53	123.27	118.30
1	C	492	ASP	CB-CG-OD2	-5.53	113.33	118.30
1	D	492	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	A	916	ASP	CB-CG-OD1	5.51	123.26	118.30
1	C	828	ASP	CB-CG-OD1	5.51	123.26	118.30
1	D	828	ASP	CB-CG-OD1	5.51	123.26	118.30
1	B	828	ASP	CB-CG-OD1	5.51	123.26	118.30
1	C	987	ASP	CB-CG-OD2	-5.50	113.34	118.30
1	B	292	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	D	292	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	B	561	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	D	561	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	D	987	ASP	CB-CG-OD2	-5.48	113.36	118.30
1	A	987	ASP	CB-CG-OD2	-5.48	113.37	118.30
1	B	987	ASP	CB-CG-OD2	-5.47	113.37	118.30
1	C	829	THR	CA-CB-CG2	-5.47	104.74	112.40
1	B	829	THR	CA-CB-CG2	-5.47	104.74	112.40
1	A	829	THR	CA-CB-CG2	-5.45	104.77	112.40
1	D	829	THR	CA-CB-CG2	-5.45	104.77	112.40
1	D	671	ASP	CB-CG-OD1	5.44	123.20	118.30
1	A	561	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	B	917	ARG	NE-CZ-NH2	-5.43	117.58	120.30
1	C	561	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	A	447	ASP	CB-CG-OD2	-5.43	113.42	118.30
1	C	447	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	B	863	GLN	CB-CA-C	-5.42	99.56	110.40
1	D	863	GLN	CB-CA-C	-5.42	99.56	110.40
1	A	863	GLN	CB-CA-C	-5.41	99.57	110.40
1	A	917	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	C	863	GLN	CB-CA-C	-5.41	99.58	110.40
1	D	447	ASP	CB-CG-OD2	-5.41	113.43	118.30
1	B	447	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	D	319	ASP	CB-CG-OD1	5.39	123.15	118.30
1	D	506	VAL	CA-CB-CG1	-5.38	102.82	110.90
1	A	671	ASP	CB-CG-OD1	5.38	123.14	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	219	THR	CA-CB-CG2	-5.38	104.88	112.40
1	A	219	THR	CA-CB-CG2	-5.37	104.88	112.40
1	A	506	VAL	CA-CB-CG1	-5.37	102.85	110.90
1	C	219	THR	CA-CB-CG2	-5.37	104.89	112.40
1	B	748	CYS	N-CA-CB	5.36	120.25	110.60
1	C	506	VAL	CA-CB-CG1	-5.36	102.86	110.90
1	C	671	ASP	CB-CG-OD1	5.36	123.12	118.30
1	B	506	VAL	CA-CB-CG1	-5.35	102.87	110.90
1	C	917	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	B	782	ASP	CB-CG-OD2	-5.35	113.49	118.30
1	A	319	ASP	CB-CG-OD1	5.34	123.11	118.30
1	B	219	THR	CA-CB-CG2	-5.34	104.92	112.40
1	D	748	CYS	N-CA-CB	5.34	120.20	110.60
1	A	748	CYS	N-CA-CB	5.33	120.20	110.60
1	B	671	ASP	CB-CG-OD1	5.33	123.10	118.30
1	C	748	CYS	N-CA-CB	5.33	120.19	110.60
1	B	319	ASP	CB-CG-OD1	5.32	123.09	118.30
1	C	579	ASP	CB-CG-OD1	5.32	123.09	118.30
1	C	319	ASP	CB-CG-OD1	5.32	123.09	118.30
1	B	980	GLU	N-CA-CB	5.31	120.16	110.60
1	D	579	ASP	CB-CG-OD1	5.30	123.07	118.30
1	D	917	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	782	ASP	CB-CG-OD2	-5.29	113.54	118.30
1	C	782	ASP	CB-CG-OD2	-5.29	113.54	118.30
1	C	980	GLU	N-CA-CB	5.29	120.12	110.60
1	A	980	GLU	N-CA-CB	5.29	120.12	110.60
1	D	261	TRP	CB-CA-C	-5.29	99.82	110.40
1	B	579	ASP	CB-CG-OD1	5.29	123.06	118.30
1	B	386	ALA	N-CA-CB	-5.29	102.70	110.10
1	D	980	GLU	N-CA-CB	5.28	120.11	110.60
1	D	782	ASP	CB-CG-OD2	-5.28	113.55	118.30
1	D	386	ALA	N-CA-CB	-5.28	102.71	110.10
1	B	261	TRP	CB-CA-C	-5.28	99.84	110.40
1	C	386	ALA	N-CA-CB	-5.28	102.71	110.10
1	A	261	TRP	CB-CA-C	-5.27	99.87	110.40
1	A	579	ASP	CB-CG-OD1	5.26	123.04	118.30
1	C	261	TRP	CB-CA-C	-5.26	99.87	110.40
1	A	386	ALA	N-CA-CB	-5.26	102.73	110.10
1	A	269	SER	N-CA-CB	5.24	118.36	110.50
1	C	916	ASP	CB-CG-OD2	-5.23	113.60	118.30
1	C	329	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	D	201	ASP	CB-CG-OD2	-5.22	113.61	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	D	572	ASP	CB-CG-OD1	5.21	122.99	118.30
1	B	269	SER	N-CA-CB	5.21	118.31	110.50
1	A	329	ASP	CB-CG-OD2	-5.21	113.62	118.30
1	C	599	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	D	916	ASP	CB-CG-OD2	-5.20	113.62	118.30
1	B	710	GLU	CB-CA-C	-5.20	100.00	110.40
1	D	269	SER	N-CA-CB	5.20	118.30	110.50
1	A	710	GLU	CB-CA-C	-5.19	100.01	110.40
1	D	710	GLU	CB-CA-C	-5.19	100.02	110.40
1	C	710	GLU	CB-CA-C	-5.19	100.03	110.40
1	B	104	THR	CA-CB-CG2	-5.18	105.14	112.40
1	C	269	SER	N-CA-CB	5.18	118.27	110.50
1	C	572	ASP	CB-CG-OD1	5.18	122.96	118.30
1	A	104	THR	CA-CB-CG2	-5.17	105.16	112.40
1	C	671	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	D	248	GLY	C-N-CA	-5.17	108.77	121.70
1	D	329	ASP	CB-CG-OD2	-5.17	113.64	118.30
1	A	201	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	D	46	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	A	518	TRP	CB-CA-C	-5.17	100.07	110.40
1	A	248	GLY	C-N-CA	-5.16	108.79	121.70
1	D	671	ASP	CB-CG-OD2	-5.16	113.65	118.30
1	C	46	ARG	C-N-CD	-5.16	109.25	120.60
1	C	201	ASP	CB-CG-OD2	-5.16	113.66	118.30
1	B	248	GLY	C-N-CA	-5.16	108.80	121.70
1	D	104	THR	CA-CB-CG2	-5.16	105.18	112.40
1	A	864	MET	N-CA-CB	5.16	119.88	110.60
1	A	599	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	B	916	ASP	CB-CG-OD2	-5.16	113.66	118.30
1	A	671	ASP	CB-CG-OD2	-5.15	113.66	118.30
1	C	518	TRP	CB-CA-C	-5.15	100.10	110.40
1	D	46	ARG	C-N-CD	-5.15	109.27	120.60
1	D	518	TRP	CB-CA-C	-5.15	100.09	110.40
1	C	248	GLY	C-N-CA	-5.15	108.82	121.70
1	C	864	MET	N-CA-CB	5.15	119.87	110.60
1	A	46	ARG	C-N-CD	-5.15	109.28	120.60
1	A	572	ASP	CB-CG-OD1	5.14	122.93	118.30
1	B	201	ASP	CB-CG-OD2	-5.14	113.67	118.30
1	D	599	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	B	572	ASP	CB-CG-OD1	5.14	122.92	118.30
1	D	610	ASP	CB-CG-OD1	5.14	122.93	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	864	MET	N-CA-CB	5.14	119.85	110.60
1	D	903[A]	GLN	N-CA-CB	5.14	119.85	110.60
1	D	903[B]	GLN	N-CA-CB	5.14	119.85	110.60
1	B	864	MET	N-CA-CB	5.14	119.85	110.60
1	C	104	THR	CA-CB-CG2	-5.14	105.21	112.40
1	B	193	ASP	CB-CG-OD2	-5.13	113.68	118.30
1	B	518	TRP	CB-CA-C	-5.13	100.13	110.40
1	B	903[A]	GLN	N-CA-CB	5.13	119.84	110.60
1	B	903[B]	GLN	N-CA-CB	5.13	119.84	110.60
1	A	903[A]	GLN	N-CA-CB	5.13	119.83	110.60
1	A	903[B]	GLN	N-CA-CB	5.13	119.83	110.60
1	C	903[A]	GLN	N-CA-CB	5.13	119.83	110.60
1	C	903[B]	GLN	N-CA-CB	5.13	119.83	110.60
1	D	651	LEU	CB-CG-CD2	-5.13	102.28	111.00
1	B	651	LEU	CB-CG-CD2	-5.12	102.29	111.00
1	B	46	ARG	C-N-CD	-5.12	109.34	120.60
1	B	671	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	A	916	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	D	237	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	C	193	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	A	651	LEU	CB-CG-CD2	-5.10	102.33	111.00
1	A	193	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	C	651	LEU	CB-CG-CD2	-5.09	102.34	111.00
1	B	599	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	A	610	ASP	CB-CG-OD1	5.08	122.88	118.30
1	D	310	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	610	ASP	CB-CG-OD1	5.07	122.86	118.30
1	C	610	ASP	CB-CG-OD1	5.07	122.86	118.30
1	B	46	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	D	193	ASP	CB-CG-OD2	-5.07	113.74	118.30
1	C	310	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	C	721	ARG	N-CA-CB	5.05	119.69	110.60
1	D	363	HIS	CA-CB-CG	-5.05	105.02	113.60
1	D	721	ARG	N-CA-CB	5.04	119.68	110.60
1	A	721	ARG	N-CA-CB	5.04	119.67	110.60
1	C	919	ASP	CB-CG-OD1	5.04	122.83	118.30
1	C	363	HIS	CA-CB-CG	-5.03	105.05	113.60
1	B	721	ARG	N-CA-CB	5.03	119.66	110.60
1	A	919	ASP	CB-CG-OD1	5.03	122.82	118.30
1	A	363	HIS	CA-CB-CG	-5.02	105.06	113.60
1	C	869	ASP	CB-CG-OD2	-5.02	113.78	118.30
1	B	869	ASP	CB-CG-OD2	-5.02	113.78	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	919	ASP	CB-CG-OD1	5.01	122.81	118.30
1	B	363	HIS	CA-CB-CG	-5.01	105.08	113.60
1	A	237	ARG	NE-CZ-NH2	-5.01	117.80	120.30
1	D	114	VAL	CA-CB-CG1	5.01	118.41	110.90
1	B	919	ASP	CB-CG-OD1	5.00	122.80	118.30
1	B	420	MET	CG-SD-CE	-5.00	92.19	100.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8238	0	7824	394	0
1	B	8238	0	7824	374	0
1	C	8238	0	7824	379	0
1	D	8238	0	7824	374	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	365	0	0	10	0
3	B	366	0	0	10	0
3	C	367	0	0	10	0
3	D	366	0	0	10	0
All	All	34424	0	31296	1496	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (1496) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:427:THR:HA	1:B:436:MET:HE1	1.21	1.11
1:B:746:ASP:HA	1:B:760:ARG:HG3	1.34	1.10

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:746:ASP:HA	1:D:760:ARG:HG3	1.34	1.09
1:A:746:ASP:HA	1:A:760:ARG:HG3	1.34	1.09
1:C:427:THR:HA	1:C:436:MET:HE1	1.28	1.08
1:A:427:THR:HA	1:A:436:MET:HE1	1.32	1.07
1:C:746:ASP:HA	1:C:760:ARG:HG3	1.34	1.06
1:D:427:THR:HA	1:D:436:MET:HE1	1.35	1.05
1:B:693:GLN:HG2	1:B:721:ARG:HD3	1.39	1.05
1:D:693:GLN:HG2	1:D:721:ARG:HD3	1.39	1.04
1:A:693:GLN:HG2	1:A:721:ARG:HD3	1.39	1.03
1:C:693:GLN:HG2	1:C:721:ARG:HD3	1.39	1.01
1:B:434:PRO:HB3	1:C:434:PRO:HB3	1.44	0.99
1:C:597:ASN:HD22	1:C:599:ARG:H	1.11	0.98
1:D:597:ASN:HD22	1:D:599:ARG:H	1.11	0.98
1:C:597:ASN:ND2	1:C:599:ARG:H	1.65	0.95
1:B:38:ASN:ND2	1:B:41:GLU:H	1.66	0.94
1:A:38:ASN:ND2	1:A:41:GLU:H	1.66	0.94
1:A:597:ASN:ND2	1:A:599:ARG:H	1.65	0.94
1:D:597:ASN:ND2	1:D:599:ARG:H	1.65	0.94
1:B:427:THR:HA	1:B:436:MET:CE	1.99	0.93
1:A:255:ARG:HH11	1:A:255:ARG:HG2	1.34	0.93
1:B:255:ARG:HH11	1:B:255:ARG:HG2	1.34	0.93
1:C:38:ASN:ND2	1:C:41:GLU:H	1.66	0.93
1:B:597:ASN:ND2	1:B:599:ARG:H	1.65	0.92
1:C:255:ARG:HG2	1:C:255:ARG:HH11	1.34	0.92
1:D:38:ASN:ND2	1:D:41:GLU:H	1.66	0.92
1:C:427:THR:HA	1:C:436:MET:CE	1.99	0.92
1:A:427:THR:HA	1:A:436:MET:CE	1.99	0.92
1:B:597:ASN:HD22	1:B:599:ARG:H	1.11	0.92
1:D:427:THR:HA	1:D:436:MET:CE	1.99	0.91
1:A:597:ASN:HD22	1:A:599:ARG:H	1.11	0.91
1:D:255:ARG:HH11	1:D:255:ARG:HG2	1.34	0.89
1:C:673:ALA:HB1	1:C:674:PRO:HD2	1.58	0.86
1:C:734:SER:HB3	1:C:860:GLY:HA3	1.57	0.86
1:A:734:SER:HB3	1:A:860:GLY:HA3	1.57	0.86
1:A:673:ALA:HB1	1:A:674:PRO:HD2	1.58	0.85
1:D:673:ALA:HB1	1:D:674:PRO:HD2	1.58	0.85
1:B:673:ALA:HB1	1:B:674:PRO:HD2	1.58	0.85
1:D:734:SER:HB3	1:D:860:GLY:HA3	1.57	0.85
1:D:856:TYR:HB3	1:D:864:MET:CE	2.07	0.85
1:A:856:TYR:HB3	1:A:864:MET:CE	2.07	0.84
1:C:856:TYR:HB3	1:C:864:MET:CE	2.07	0.84
1:B:734:SER:HB3	1:B:860:GLY:HA3	1.57	0.84

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:856:TYR:HB3	1:B:864:MET:CE	2.07	0.83
1:D:734:SER:CB	1:D:860:GLY:HA3	2.08	0.83
1:D:654:TRP:NE1	1:D:666:GLY:HA3	1.94	0.83
1:B:734:SER:CB	1:B:860:GLY:HA3	2.08	0.82
1:A:734:SER:CB	1:A:860:GLY:HA3	2.09	0.82
1:C:654:TRP:NE1	1:C:666:GLY:HA3	1.94	0.82
1:C:949:HIS:CD2	1:C:1020:TRP:HE1	1.98	0.82
1:B:654:TRP:NE1	1:B:666:GLY:HA3	1.94	0.82
1:C:734:SER:CB	1:C:860:GLY:HA3	2.09	0.82
1:D:949:HIS:CD2	1:D:1020:TRP:HE1	1.98	0.82
1:A:654:TRP:NE1	1:A:666:GLY:HA3	1.94	0.81
1:B:830:LEU:CD2	1:B:835:LEU:HB2	2.11	0.81
1:A:830:LEU:CD2	1:A:835:LEU:HB2	2.11	0.81
1:C:830:LEU:CD2	1:C:835:LEU:HB2	2.11	0.81
1:B:949:HIS:CD2	1:B:1020:TRP:HE1	1.98	0.81
1:A:949:HIS:CD2	1:A:1020:TRP:HE1	1.98	0.80
1:D:830:LEU:CD2	1:D:835:LEU:HB2	2.11	0.80
1:C:134:LEU:N	1:C:134:LEU:HD12	1.97	0.80
1:A:360:HIS:ND1	1:A:361:PRO:HD2	1.97	0.80
1:C:360:HIS:ND1	1:C:361:PRO:HD2	1.97	0.80
1:A:134:LEU:HD12	1:A:134:LEU:N	1.97	0.79
1:D:360:HIS:ND1	1:D:361:PRO:HD2	1.97	0.79
1:B:77:ASP:O	1:B:78:LEU:HD23	1.83	0.79
1:D:436:MET:HE1	1:D:467:ASN:HD22	1.46	0.79
1:C:77:ASP:O	1:C:78:LEU:HD23	1.83	0.79
1:B:134:LEU:HD12	1:B:134:LEU:N	1.97	0.78
1:D:77:ASP:O	1:D:78:LEU:HD23	1.83	0.78
1:D:920:LEU:HB3	1:D:921:PRO:HD2	1.65	0.78
1:A:77:ASP:O	1:A:78:LEU:HD23	1.83	0.78
1:B:360:HIS:ND1	1:B:361:PRO:HD2	1.97	0.77
1:A:928:PRO:HB2	1:A:973:ARG:NH1	1.99	0.77
1:B:9:VAL:O	1:B:12:GLN:HB3	1.85	0.77
1:C:928:PRO:HB2	1:C:973:ARG:NH1	1.99	0.77
1:A:920:LEU:HB3	1:A:921:PRO:HD2	1.65	0.77
1:D:134:LEU:N	1:D:134:LEU:HD12	1.97	0.77
1:B:928:PRO:HB2	1:B:973:ARG:NH1	1.99	0.77
1:A:11:LEU:HD21	1:A:187:MET:CE	2.15	0.77
1:B:920:LEU:HB3	1:B:921:PRO:HD2	1.66	0.77
1:C:1004:SER:HB2	1:C:1006:GLU:OE2	1.85	0.77
1:D:928:PRO:HB2	1:D:973:ARG:NH1	1.99	0.77
1:A:1004:SER:HB2	1:A:1006:GLU:OE2	1.85	0.77
1:D:9:VAL:O	1:D:12:GLN:HB3	1.85	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:11:LEU:HD21	1:B:187:MET:CE	2.15	0.76
1:D:11:LEU:HD21	1:D:187:MET:CE	2.15	0.76
1:A:9:VAL:O	1:A:12:GLN:HB3	1.85	0.76
1:C:9:VAL:O	1:C:12:GLN:HB3	1.85	0.76
1:D:746:ASP:CA	1:D:760:ARG:HG3	2.14	0.76
1:A:746:ASP:CA	1:A:760:ARG:HG3	2.14	0.76
1:C:11:LEU:HD21	1:C:187:MET:CE	2.15	0.76
1:A:436:MET:HE1	1:A:467:ASN:HD22	1.49	0.76
1:C:920:LEU:HB3	1:C:921:PRO:HD2	1.65	0.76
1:B:685:LEU:HB3	1:B:686:PRO:HD2	1.68	0.76
1:D:1004:SER:HB2	1:D:1006:GLU:OE2	1.85	0.76
1:B:377:LEU:HD22	1:B:708:TRP:HA	1.69	0.75
1:D:377:LEU:HD22	1:D:708:TRP:HA	1.68	0.75
1:B:746:ASP:CA	1:B:760:ARG:HG3	2.14	0.75
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.68	0.75
1:A:949:HIS:HD2	1:A:1020:TRP:HE1	1.35	0.75
1:B:1004:SER:HB2	1:B:1006:GLU:OE2	1.85	0.75
1:D:685:LEU:HB3	1:D:686:PRO:HD2	1.68	0.75
1:A:685:LEU:HB3	1:A:686:PRO:HD2	1.68	0.74
1:C:38:ASN:HD22	1:C:41:GLU:H	1.35	0.74
1:A:38:ASN:HD22	1:A:41:GLU:H	1.35	0.74
1:C:377:LEU:HD22	1:C:708:TRP:HA	1.69	0.74
1:C:746:ASP:CA	1:C:760:ARG:HG3	2.14	0.74
1:C:685:LEU:HB3	1:C:686:PRO:HD2	1.68	0.74
1:D:655:MET:HG3	1:D:656:VAL:N	2.03	0.74
1:C:436:MET:HE1	1:C:467:ASN:HD22	1.53	0.73
1:D:579:ASP:OD1	1:D:583:ASN:HB2	1.89	0.73
1:D:778:THR:HG23	1:D:779:PRO:HD2	1.70	0.73
1:C:237:ARG:HH11	1:C:237:ARG:HB3	1.53	0.73
1:C:778:THR:HG23	1:C:779:PRO:HD2	1.70	0.73
1:B:237:ARG:HB3	1:B:237:ARG:HH11	1.54	0.73
1:B:579:ASP:OD1	1:B:583:ASN:HB2	1.89	0.73
1:C:579:ASP:OD1	1:C:583:ASN:HB2	1.89	0.73
1:C:559:TYR:HB2	1:C:562:LEU:HD12	1.71	0.73
1:C:237:ARG:HH11	1:C:237:ARG:CB	2.02	0.73
1:A:778:THR:HG23	1:A:779:PRO:HD2	1.70	0.72
1:A:579:ASP:OD1	1:A:583:ASN:HB2	1.89	0.72
1:A:237:ARG:HH11	1:A:237:ARG:HB3	1.54	0.72
1:D:237:ARG:HB3	1:D:237:ARG:HH11	1.54	0.72
1:B:778:THR:HG23	1:B:779:PRO:HD2	1.70	0.72
1:D:652:LEU:HD11	1:D:698:VAL:HB	1.71	0.72
1:C:949:HIS:HD2	1:C:1020:TRP:HE1	1.35	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:949:HIS:HD2	1:B:1020:TRP:HE1	1.35	0.72
1:D:559:TYR:HB2	1:D:562:LEU:HD12	1.71	0.72
1:B:652:LEU:HD11	1:B:698:VAL:HB	1.71	0.72
1:B:3:ILE:HG13	1:B:4:THR:N	2.04	0.72
1:D:380:LYS:HE2	3:D:4077:HOH:O	1.90	0.72
1:D:3:ILE:HG13	1:D:4:THR:N	2.04	0.72
1:A:559:TYR:HB2	1:A:562:LEU:HD12	1.71	0.72
1:D:436:MET:CE	1:D:467:ASN:HD22	2.03	0.72
1:D:928:PRO:HB2	1:D:973:ARG:HH11	1.55	0.72
1:A:652:LEU:HD11	1:A:698:VAL:HB	1.71	0.72
1:D:949:HIS:HD2	1:D:1020:TRP:HE1	1.35	0.72
1:B:237:ARG:CB	1:B:237:ARG:HH11	2.02	0.72
1:A:436:MET:CE	1:A:467:ASN:HD22	2.03	0.71
1:C:928:PRO:HB2	1:C:973:ARG:HH11	1.55	0.71
1:B:928:PRO:HB2	1:B:973:ARG:HH11	1.55	0.71
1:A:434:PRO:HB3	1:D:434:PRO:HB3	1.72	0.71
1:C:655:MET:HG3	1:C:656:VAL:N	2.03	0.71
1:B:38:ASN:HD22	1:B:41:GLU:H	1.35	0.71
1:A:3:ILE:HG13	1:A:4:THR:N	2.04	0.71
1:A:928:PRO:HB2	1:A:973:ARG:HH11	1.55	0.71
1:D:237:ARG:HH11	1:D:237:ARG:CB	2.02	0.71
1:A:237:ARG:HH11	1:A:237:ARG:CB	2.02	0.71
1:B:559:TYR:HB2	1:B:562:LEU:HD12	1.71	0.71
1:C:652:LEU:HD11	1:C:698:VAL:HB	1.71	0.71
1:C:436:MET:CE	1:C:467:ASN:HD22	2.03	0.71
1:C:3:ILE:HG13	1:C:4:THR:N	2.04	0.71
1:B:436:MET:CE	1:B:467:ASN:HD22	2.03	0.71
1:C:380:LYS:HE2	3:C:4174:HOH:O	1.90	0.71
1:B:380:LYS:HE2	3:B:4134:HOH:O	1.90	0.71
1:C:650:GLU:HB3	1:C:670:LEU:HD12	1.73	0.71
1:D:650:GLU:HB3	1:D:670:LEU:HD12	1.73	0.70
1:B:11:LEU:HD21	1:B:187:MET:HE3	1.72	0.70
1:D:38:ASN:HD22	1:D:41:GLU:H	1.35	0.69
1:C:836:ILE:N	1:C:836:ILE:HD13	2.07	0.69
1:A:655:MET:HG3	1:A:656:VAL:N	2.03	0.69
1:C:11:LEU:HD21	1:C:187:MET:HE3	1.74	0.69
1:A:836:ILE:N	1:A:836:ILE:HD13	2.07	0.69
1:A:380:LYS:HE2	3:A:4077:HOH:O	1.90	0.69
1:B:650:GLU:HB3	1:B:670:LEU:HD12	1.73	0.69
1:D:836:ILE:N	1:D:836:ILE:HD13	2.07	0.69
1:C:63:PHE:HB3	1:C:64:PRO:HD2	1.75	0.69
1:B:655:MET:HG3	1:B:656:VAL:N	2.03	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:836:ILE:HD13	1:B:836:ILE:N	2.07	0.69
1:A:650:GLU:HB3	1:A:670:LEU:HD12	1.73	0.68
1:B:63:PHE:HB3	1:B:64:PRO:HD2	1.75	0.68
1:C:255:ARG:HG2	1:C:255:ARG:NH1	2.07	0.68
1:A:1020:TRP:HD1	1:A:1021:CYS:N	1.92	0.68
1:A:11:LEU:HD21	1:A:187:MET:HE3	1.73	0.68
1:C:1020:TRP:HD1	1:C:1021:CYS:N	1.91	0.68
1:D:1020:TRP:HD1	1:D:1021:CYS:N	1.91	0.68
1:B:35:SER:OG	1:B:37:ARG:NH1	2.27	0.68
1:C:923:SER:HB3	3:C:4345:HOH:O	1.94	0.68
1:D:35:SER:OG	1:D:37:ARG:NH1	2.27	0.68
1:C:35:SER:OG	1:C:37:ARG:NH1	2.27	0.68
1:D:923:SER:HB3	3:D:4380:HOH:O	1.94	0.67
1:A:923:SER:HB3	3:A:4380:HOH:O	1.94	0.67
1:D:211:ASP:OD1	1:D:211:ASP:N	2.27	0.67
1:D:255:ARG:HG2	1:D:255:ARG:NH1	2.07	0.67
1:D:856:TYR:CD2	1:D:864:MET:HE1	2.29	0.67
1:D:965:GLN:O	1:D:969:GLU:HG3	1.94	0.67
1:B:30:HIS:HB2	1:B:31:PRO:HD2	1.76	0.67
1:C:59:ARG:NH2	1:C:81:ALA:O	2.28	0.67
1:B:965:GLN:O	1:B:969:GLU:HG3	1.94	0.67
1:B:1020:TRP:HD1	1:B:1021:CYS:N	1.91	0.67
1:C:965:GLN:O	1:C:969:GLU:HG3	1.94	0.67
1:A:30:HIS:HB2	1:A:31:PRO:HD2	1.77	0.67
1:A:211:ASP:N	1:A:211:ASP:OD1	2.27	0.67
1:D:63:PHE:HB3	1:D:64:PRO:HD2	1.75	0.67
1:A:35:SER:OG	1:A:37:ARG:NH1	2.27	0.67
1:B:255:ARG:NH1	1:B:255:ARG:HG2	2.07	0.66
1:C:65:ALA:HB1	1:C:66:PRO:HD2	1.77	0.66
1:C:375:ASP:O	1:C:379:MET:HG3	1.95	0.66
1:A:59:ARG:NH2	1:A:81:ALA:O	2.28	0.66
1:D:11:LEU:HD21	1:D:187:MET:HE3	1.76	0.66
1:D:30:HIS:HB2	1:D:31:PRO:HD2	1.77	0.66
1:A:965:GLN:O	1:A:969:GLU:HG3	1.94	0.66
1:A:7:LEU:N	1:A:71:GLU:OE2	2.28	0.66
1:A:63:PHE:HB3	1:A:64:PRO:HD2	1.75	0.66
1:B:923:SER:HB3	3:B:4305:HOH:O	1.94	0.66
1:B:824:GLN:HG3	1:B:825:CYS:N	2.11	0.66
1:C:856:TYR:HB3	1:C:864:MET:HE1	1.77	0.66
1:B:856:TYR:CD2	1:B:864:MET:HE1	2.31	0.66
1:D:824:GLN:HG3	1:D:825:CYS:N	2.11	0.66
1:A:856:TYR:HB3	1:A:864:MET:HE1	1.77	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:7:LEU:N	1:B:71:GLU:OE2	2.28	0.66
1:D:59:ARG:NH2	1:D:81:ALA:O	2.28	0.66
1:B:59:ARG:NH2	1:B:81:ALA:O	2.28	0.66
1:A:65:ALA:HB1	1:A:66:PRO:HD2	1.77	0.66
1:A:375:ASP:O	1:A:379:MET:HG3	1.95	0.66
1:C:30:HIS:HB2	1:C:31:PRO:HD2	1.77	0.65
1:B:211:ASP:OD1	1:B:211:ASP:N	2.27	0.65
1:C:824:GLN:HG3	1:C:825:CYS:N	2.11	0.65
1:D:856:TYR:HD2	1:D:864:MET:HE1	1.61	0.65
1:D:7:LEU:N	1:D:71:GLU:OE2	2.28	0.65
1:C:7:LEU:N	1:C:71:GLU:OE2	2.28	0.65
1:D:775:GLN:OE1	1:D:890:GLN:NE2	2.30	0.65
1:B:375:ASP:O	1:B:379:MET:HG3	1.95	0.65
1:B:856:TYR:HB3	1:B:864:MET:HE1	1.77	0.65
1:D:375:ASP:O	1:D:379:MET:HG3	1.95	0.65
1:C:210:ARG:HD3	3:C:4138:HOH:O	1.97	0.65
1:A:824:GLN:HG3	1:A:825:CYS:N	2.10	0.65
1:B:775:GLN:OE1	1:B:890:GLN:NE2	2.30	0.65
1:C:775:GLN:OE1	1:C:890:GLN:NE2	2.30	0.65
1:B:742:THR:HG22	1:B:743:SER:N	2.12	0.65
1:D:742:THR:HG22	1:D:743:SER:N	2.12	0.65
1:B:499:ILE:HB	1:B:533:LEU:HB2	1.80	0.64
1:A:742:THR:HG22	1:A:743:SER:N	2.12	0.64
1:B:65:ALA:HB1	1:B:66:PRO:HD2	1.77	0.64
1:C:742:THR:HG22	1:C:743:SER:N	2.12	0.64
1:A:499:ILE:HB	1:A:533:LEU:HB2	1.79	0.64
1:A:210:ARG:HD3	3:A:4036:HOH:O	1.97	0.64
1:B:436:MET:HE1	1:B:467:ASN:HD22	1.62	0.64
1:D:856:TYR:HB3	1:D:864:MET:HE1	1.78	0.64
1:A:775:GLN:OE1	1:A:890:GLN:NE2	2.30	0.64
1:A:287:ASP:OD2	1:D:425:ARG:NH2	2.31	0.64
1:D:499:ILE:HB	1:D:533:LEU:HB2	1.79	0.64
1:B:210:ARG:HD3	3:B:4098:HOH:O	1.97	0.64
1:D:65:ALA:HB1	1:D:66:PRO:HD2	1.77	0.64
1:B:797:GLU:O	1:B:801:ILE:HD12	1.98	0.64
1:D:210:ARG:HD3	3:D:4036:HOH:O	1.97	0.64
1:C:499:ILE:HB	1:C:533:LEU:HB2	1.79	0.64
1:A:287:ASP:CG	1:D:425:ARG:HH22	2.00	0.63
1:D:272:ALA:HB1	1:D:273:PRO:HD2	1.81	0.63
1:B:835:LEU:C	1:B:836:ILE:HD13	2.19	0.63
1:A:835:LEU:C	1:A:836:ILE:HD13	2.19	0.63
1:C:272:ALA:HB1	1:C:273:PRO:HD2	1.81	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:906:TYR:HB3	1:C:907:PRO:HD2	1.81	0.63
1:B:746:ASP:HA	1:B:760:ARG:CG	2.22	0.63
1:C:746:ASP:HA	1:C:760:ARG:CG	2.22	0.63
1:C:797:GLU:O	1:C:801:ILE:HD12	1.98	0.63
1:B:649:ASN:OD1	1:B:703:PRO:HD2	1.99	0.63
1:B:66:PRO:HD2	1:B:67:GLU:HG2	1.81	0.63
1:A:856:TYR:CD2	1:A:864:MET:HE1	2.34	0.63
1:A:66:PRO:HD2	1:A:67:GLU:HG2	1.81	0.63
1:C:211:ASP:N	1:C:211:ASP:OD1	2.27	0.63
1:D:649:ASN:OD1	1:D:703:PRO:HD2	1.99	0.63
1:B:272:ALA:HB1	1:B:273:PRO:HD2	1.81	0.63
1:B:166:ARG:HG3	1:B:392:TYR:HB2	1.81	0.62
1:D:100:TYR:HB2	1:D:203:TRP:CD2	2.34	0.62
1:D:746:ASP:HA	1:D:760:ARG:CG	2.22	0.62
1:A:797:GLU:O	1:A:801:ILE:HD12	1.98	0.62
1:A:255:ARG:HG2	1:A:255:ARG:NH1	2.07	0.62
1:A:649:ASN:OD1	1:A:703:PRO:HD2	1.99	0.62
1:C:100:TYR:HB2	1:C:203:TRP:CD2	2.34	0.62
1:A:100:TYR:HB2	1:A:203:TRP:CD2	2.34	0.62
1:B:906:TYR:HB3	1:B:907:PRO:HD2	1.81	0.62
1:C:649:ASN:OD1	1:C:703:PRO:HD2	1.99	0.62
1:B:100:TYR:HB2	1:B:203:TRP:CD2	2.34	0.62
1:C:835:LEU:C	1:C:836:ILE:HD13	2.19	0.62
1:A:272:ALA:HB1	1:A:273:PRO:HD2	1.81	0.62
1:C:767:GLN:HG3	1:C:768:MET:N	2.15	0.62
1:A:906:TYR:HB3	1:A:907:PRO:HD2	1.81	0.62
1:D:835:LEU:C	1:D:836:ILE:HD13	2.19	0.62
1:A:767:GLN:HG3	1:A:768:MET:N	2.15	0.62
1:C:778:THR:CG2	1:C:779:PRO:HD2	2.30	0.62
1:C:66:PRO:HD2	1:C:67:GLU:HG2	1.81	0.62
1:D:797:GLU:O	1:D:801:ILE:HD12	1.98	0.62
1:D:66:PRO:HD2	1:D:67:GLU:HG2	1.81	0.61
1:B:767:GLN:HG3	1:B:768:MET:N	2.15	0.61
1:A:778:THR:CG2	1:A:779:PRO:HD2	2.30	0.61
1:D:906:TYR:HB3	1:D:907:PRO:HD2	1.81	0.61
1:B:822:LEU:HD12	1:B:824:GLN:N	2.16	0.61
1:C:928:PRO:O	1:C:973:ARG:NH1	2.33	0.61
1:A:166:ARG:HG3	1:A:392:TYR:HB2	1.81	0.61
1:C:166:ARG:HG3	1:C:392:TYR:HB2	1.81	0.61
1:B:856:TYR:HD2	1:B:864:MET:HE1	1.63	0.61
1:A:651:LEU:HD12	1:A:669:PRO:HA	1.83	0.61
1:D:610:ASP:OD2	1:D:612:THR:HG23	2.01	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:928:PRO:O	1:A:973:ARG:NH1	2.34	0.61
1:C:227:VAL:HG13	1:C:240:LEU:HD11	1.83	0.61
1:B:778:THR:CG2	1:B:779:PRO:HD2	2.30	0.61
1:C:651:LEU:HD12	1:C:669:PRO:HA	1.83	0.61
1:D:166:ARG:HG3	1:D:392:TYR:HB2	1.81	0.61
1:B:928:PRO:O	1:B:973:ARG:NH1	2.34	0.61
1:D:928:PRO:O	1:D:973:ARG:NH1	2.34	0.61
1:D:778:THR:CG2	1:D:779:PRO:HD2	2.30	0.60
1:D:102:ASN:ND2	1:D:201:ASP:HB2	2.16	0.60
1:B:227:VAL:HG13	1:B:240:LEU:HD11	1.83	0.60
1:D:822:LEU:HD12	1:D:824:GLN:N	2.16	0.60
1:B:822:LEU:HD11	1:B:824:GLN:O	2.01	0.60
1:D:822:LEU:HD11	1:D:824:GLN:O	2.01	0.60
1:A:822:LEU:HD12	1:A:824:GLN:N	2.16	0.60
1:C:595:THR:HG23	1:C:596:PRO:HA	1.82	0.60
1:A:102:ASN:ND2	1:A:201:ASP:HB2	2.16	0.60
1:C:822:LEU:HD11	1:C:824:GLN:O	2.01	0.60
1:C:102:ASN:ND2	1:C:201:ASP:HB2	2.16	0.60
1:A:610:ASP:OD2	1:A:612:THR:HG23	2.01	0.60
1:C:870:VAL:HG12	1:C:871:GLU:N	2.16	0.60
1:D:595:THR:HG23	1:D:596:PRO:HA	1.82	0.60
1:B:830:LEU:HD21	1:B:835:LEU:HB2	1.84	0.60
1:B:102:ASN:ND2	1:B:201:ASP:HB2	2.16	0.60
1:A:595:THR:HG23	1:A:596:PRO:HA	1.82	0.60
1:C:856:TYR:CD2	1:C:864:MET:HE1	2.36	0.60
1:B:734:SER:HB3	1:B:860:GLY:CA	2.30	0.60
1:B:80:GLU:CD	1:B:80:GLU:H	2.01	0.60
1:C:822:LEU:HD12	1:C:824:GLN:N	2.16	0.60
1:B:595:THR:HG23	1:B:596:PRO:HA	1.82	0.60
1:B:140:ARG:NH1	1:B:170:GLU:OE1	2.31	0.60
1:C:734:SER:HB3	1:C:860:GLY:CA	2.30	0.60
1:C:511:PRO:HA	1:C:516:PRO:HB3	1.84	0.60
1:C:505:ARG:HG2	1:C:996:ASP:OD2	2.02	0.60
1:D:651:LEU:HD12	1:D:669:PRO:HA	1.83	0.60
1:A:282:ARG:HD3	1:D:418:HIS:O	2.01	0.60
1:B:651:LEU:HD12	1:B:669:PRO:HA	1.83	0.60
1:C:128:ASN:HA	1:C:180:GLY:O	2.02	0.60
1:B:610:ASP:OD2	1:B:612:THR:HG23	2.01	0.60
1:A:128:ASN:HA	1:A:180:GLY:O	2.02	0.60
1:A:734:SER:HB3	1:A:860:GLY:CA	2.30	0.59
1:A:830:LEU:HD21	1:A:835:LEU:HB2	1.84	0.59
1:D:830:LEU:HD21	1:D:835:LEU:HB2	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:870:VAL:HG12	1:B:871:GLU:N	2.16	0.59
1:D:227:VAL:HG13	1:D:240:LEU:HD11	1.83	0.59
1:D:734:SER:HB3	1:D:860:GLY:CA	2.30	0.59
1:C:759:ASN:OD1	1:C:761:GLN:N	2.35	0.59
1:B:505:ARG:HG2	1:B:996:ASP:OD2	2.02	0.59
1:D:701:VAL:HG12	1:D:702:GLN:N	2.17	0.59
1:A:822:LEU:HD11	1:A:824:GLN:O	2.01	0.59
1:A:227:VAL:HG13	1:A:240:LEU:HD11	1.83	0.59
1:D:767:GLN:HG3	1:D:768:MET:N	2.15	0.59
1:C:610:ASP:OD2	1:C:612:THR:HG23	2.01	0.59
1:A:759:ASN:OD1	1:A:761:GLN:N	2.35	0.59
1:A:696:LEU:HD12	1:A:697:THR:N	2.18	0.59
1:B:696:LEU:HD12	1:B:697:THR:N	2.18	0.59
1:A:870:VAL:HG12	1:A:871:GLU:N	2.16	0.59
1:D:128:ASN:HA	1:D:180:GLY:O	2.02	0.59
1:D:696:LEU:HD12	1:D:697:THR:N	2.18	0.59
1:A:505:ARG:HG2	1:A:996:ASP:OD2	2.02	0.59
1:A:282:ARG:HH12	1:D:419:GLY:C	2.06	0.59
1:D:870:VAL:HG12	1:D:871:GLU:N	2.16	0.59
1:D:505:ARG:HG2	1:D:996:ASP:OD2	2.02	0.59
1:B:128:ASN:HA	1:B:180:GLY:O	2.02	0.59
1:D:511:PRO:HA	1:D:516:PRO:HB3	1.84	0.59
1:A:701:VAL:HG12	1:A:702:GLN:N	2.17	0.58
1:B:336:ARG:NH2	1:B:338:GLU:OE1	2.36	0.58
1:C:696:LEU:HD12	1:C:697:THR:N	2.17	0.58
1:C:140:ARG:NH1	1:C:170:GLU:OE1	2.31	0.58
1:B:6:SER:HB2	1:B:71:GLU:OE2	2.04	0.58
1:A:511:PRO:HA	1:A:516:PRO:HB3	1.84	0.58
1:C:533:LEU:HD12	1:C:533:LEU:C	2.24	0.58
1:B:769:TRP:NE1	1:B:774:LYS:HG3	2.19	0.58
1:C:473:ARG:HD3	1:C:473:ARG:O	2.04	0.58
1:A:336:ARG:NH2	1:A:338:GLU:OE1	2.36	0.58
1:B:511:PRO:HA	1:B:516:PRO:HB3	1.84	0.58
1:D:62:TRP:CD1	1:D:95:TYR:HB3	2.39	0.58
1:C:336:ARG:NH2	1:C:338:GLU:OE1	2.36	0.58
1:B:473:ARG:HD3	1:B:473:ARG:O	2.04	0.58
1:B:701:VAL:HG12	1:B:702:GLN:N	2.17	0.58
1:A:62:TRP:CD1	1:A:95:TYR:HB3	2.39	0.58
1:B:737:ILE:HG13	1:B:738:PRO:N	2.17	0.58
1:A:473:ARG:O	1:A:473:ARG:HD3	2.04	0.58
1:A:856:TYR:HD2	1:A:864:MET:HE1	1.68	0.58
1:D:737:ILE:HG13	1:D:738:PRO:N	2.17	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:336:ARG:NH2	1:D:338:GLU:OE1	2.36	0.58
1:D:473:ARG:O	1:D:473:ARG:HD3	2.04	0.58
1:A:769:TRP:NE1	1:A:774:LYS:HG3	2.19	0.58
1:C:701:VAL:HG12	1:C:702:GLN:N	2.17	0.57
1:D:769:TRP:NE1	1:D:774:LYS:HG3	2.19	0.57
1:B:759:ASN:OD1	1:B:761:GLN:N	2.35	0.57
1:A:429:ASP:OD1	1:A:430:PRO:HD2	2.04	0.57
1:B:316:HIS:HD2	1:B:317:THR:O	1.87	0.57
1:D:6:SER:HB2	1:D:71:GLU:OE2	2.04	0.57
1:B:533:LEU:HD12	1:B:533:LEU:C	2.24	0.57
1:A:533:LEU:C	1:A:533:LEU:HD12	2.24	0.57
1:A:618:THR:HG22	1:A:912:ALA:HB1	1.86	0.57
1:C:618:THR:HG22	1:C:912:ALA:HB1	1.86	0.57
1:B:429:ASP:OD1	1:B:430:PRO:HD2	2.04	0.57
1:D:618:THR:HG22	1:D:912:ALA:HB1	1.86	0.57
1:D:80:GLU:H	1:D:80:GLU:CD	2.01	0.57
1:A:6:SER:HB2	1:A:71:GLU:OE2	2.03	0.57
1:C:737:ILE:HG13	1:C:738:PRO:N	2.17	0.57
1:C:769:TRP:NE1	1:C:774:LYS:HG3	2.19	0.57
1:B:62:TRP:CD1	1:B:95:TYR:HB3	2.39	0.57
1:C:830:LEU:HD21	1:C:835:LEU:HB2	1.84	0.57
1:C:134:LEU:H	1:C:134:LEU:HD12	1.69	0.57
1:D:533:LEU:HD12	1:D:533:LEU:C	2.24	0.57
1:C:62:TRP:CD1	1:C:95:TYR:HB3	2.39	0.57
1:B:460:ASN:ND2	1:B:461:GLU:HG2	2.20	0.57
1:B:618:THR:HG22	1:B:912:ALA:HB1	1.86	0.57
1:A:737:ILE:HG13	1:A:738:PRO:N	2.17	0.57
1:D:140:ARG:NH1	1:D:170:GLU:OE1	2.31	0.57
1:C:429:ASP:OD1	1:C:430:PRO:HD2	2.04	0.57
1:C:26:ARG:HD2	1:C:169:SER:HA	1.87	0.57
1:D:316:HIS:HD2	1:D:317:THR:O	1.87	0.57
1:A:597:ASN:HD22	1:A:599:ARG:N	1.94	0.57
1:D:360:HIS:CE1	1:D:362:LEU:HB2	2.40	0.57
1:C:166:ARG:HD3	3:C:4137:HOH:O	2.05	0.57
1:A:360:HIS:CE1	1:A:362:LEU:HB2	2.40	0.57
1:B:360:HIS:CE1	1:B:362:LEU:HB2	2.40	0.57
1:C:6:SER:HB2	1:C:71:GLU:OE2	2.03	0.57
1:B:763:GLY:HA3	1:B:822:LEU:HD21	1.87	0.57
1:A:763:GLY:HA3	1:A:822:LEU:HD21	1.87	0.57
1:C:460:ASN:ND2	1:C:461:GLU:HG2	2.20	0.57
1:A:419:GLY:C	1:D:282:ARG:HH12	2.08	0.57
1:A:316:HIS:HD2	1:A:317:THR:O	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:26:ARG:HD2	1:B:169:SER:HA	1.87	0.57
1:A:460:ASN:ND2	1:A:461:GLU:HG2	2.20	0.57
1:B:360:HIS:CE1	1:B:361:PRO:HD2	2.40	0.56
1:B:834:VAL:HG12	1:B:835:LEU:N	2.19	0.56
1:B:166:ARG:HD3	3:B:4097:HOH:O	2.05	0.56
1:A:166:ARG:HD3	3:A:4035:HOH:O	2.05	0.56
1:D:460:ASN:ND2	1:D:461:GLU:HG2	2.20	0.56
1:A:457:SER:HA	1:A:485:GLN:O	2.06	0.56
1:A:360:HIS:CE1	1:A:361:PRO:HD2	2.41	0.56
1:D:763:GLY:HA3	1:D:822:LEU:HD21	1.87	0.56
1:C:763:GLY:HA3	1:C:822:LEU:HD21	1.87	0.56
1:C:429:ASP:OD1	1:C:431[B]:ARG:HG3	2.05	0.56
1:B:18:ASN:OD1	1:B:19:PRO:HD2	2.06	0.56
1:D:18:ASN:OD1	1:D:19:PRO:HD2	2.06	0.56
1:D:38:ASN:HD21	1:D:41:GLU:H	1.53	0.56
1:C:834:VAL:HG12	1:C:835:LEU:N	2.19	0.56
1:D:166:ARG:HD3	3:D:4035:HOH:O	2.05	0.56
1:D:457:SER:HA	1:D:485:GLN:O	2.06	0.56
1:A:26:ARG:HD2	1:A:169:SER:HA	1.87	0.56
1:A:834:VAL:HG12	1:A:835:LEU:N	2.19	0.56
1:D:834:VAL:HG12	1:D:835:LEU:N	2.19	0.56
1:A:304:GLU:C	1:A:305:ILE:HG13	2.26	0.56
1:A:531:ARG:O	1:A:561:ARG:NH1	2.39	0.56
1:C:457:SER:HA	1:C:485:GLN:O	2.06	0.56
1:B:531:ARG:O	1:B:561:ARG:NH1	2.39	0.56
1:C:360:HIS:CE1	1:C:362:LEU:HB2	2.40	0.56
1:D:134:LEU:H	1:D:134:LEU:HD12	1.69	0.56
1:B:763:GLY:HA3	1:B:822:LEU:CD2	2.36	0.56
1:B:429:ASP:OD1	1:B:431[B]:ARG:HG3	2.05	0.56
1:D:429:ASP:OD1	1:D:431[B]:ARG:HG3	2.05	0.56
1:A:577:LYS:O	1:A:584:PRO:HA	2.06	0.56
1:A:80:GLU:CD	1:A:80:GLU:H	2.01	0.56
1:A:18:ASN:OD1	1:A:19:PRO:HD2	2.06	0.56
1:C:316:HIS:HD2	1:C:317:THR:O	1.88	0.56
1:B:457:SER:HA	1:B:485:GLN:O	2.05	0.56
1:C:833:ALA:HB1	1:C:858:ILE:O	2.06	0.56
1:C:856:TYR:HD2	1:C:864:MET:HE1	1.71	0.56
1:A:763:GLY:HA3	1:A:822:LEU:CD2	2.36	0.56
1:A:429:ASP:OD1	1:A:431[B]:ARG:HG3	2.05	0.56
1:D:429:ASP:OD1	1:D:430:PRO:HD2	2.04	0.55
1:A:1020:TRP:CD1	1:A:1021:CYS:N	2.74	0.55
1:C:360:HIS:CE1	1:C:361:PRO:HD2	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:425:ARG:NH2	1:C:287:ASP:OD2	2.39	0.55
1:D:395:HIS:ND1	1:D:396:PRO:HD2	2.22	0.55
1:A:100:TYR:HB2	1:A:203:TRP:CE3	2.42	0.55
1:A:833:ALA:HB1	1:A:858:ILE:O	2.06	0.55
1:D:763:GLY:HA3	1:D:822:LEU:CD2	2.36	0.55
1:C:100:TYR:HB2	1:C:203:TRP:CE3	2.42	0.55
1:B:38:ASN:HD21	1:B:41:GLU:H	1.53	0.55
1:B:833:ALA:HB1	1:B:858:ILE:O	2.06	0.55
1:B:134:LEU:H	1:B:134:LEU:HD12	1.69	0.55
1:C:304:GLU:C	1:C:305:ILE:HG13	2.26	0.55
1:C:395:HIS:ND1	1:C:396:PRO:HD2	2.22	0.55
1:C:531:ARG:O	1:C:561:ARG:NH1	2.39	0.55
1:B:395:HIS:ND1	1:B:396:PRO:HD2	2.22	0.55
1:D:304:GLU:C	1:D:305:ILE:HG13	2.26	0.55
1:B:100:TYR:HB2	1:B:203:TRP:CE3	2.42	0.55
1:A:140:ARG:NH1	1:A:170:GLU:OE1	2.31	0.55
1:C:18:ASN:OD1	1:C:19:PRO:HD2	2.06	0.55
1:D:360:HIS:CE1	1:D:361:PRO:HD2	2.41	0.55
1:B:304:GLU:C	1:B:305:ILE:HG13	2.26	0.55
1:B:577:LYS:O	1:B:584:PRO:HA	2.06	0.55
1:C:942:ARG:HA	1:C:953:GLY:O	2.07	0.55
1:A:942:ARG:HA	1:A:953:GLY:O	2.07	0.55
1:D:833:ALA:HB1	1:D:858:ILE:O	2.06	0.55
1:D:668:VAL:HG13	1:D:669:PRO:HD2	1.89	0.55
1:C:763:GLY:HA3	1:C:822:LEU:CD2	2.36	0.55
1:D:577:LYS:O	1:D:584:PRO:HA	2.06	0.55
1:C:786:ARG:HA	1:C:964:GLN:OE1	2.07	0.55
1:C:577:LYS:O	1:C:584:PRO:HA	2.06	0.54
1:D:531:ARG:O	1:D:561:ARG:NH1	2.39	0.54
1:B:668:VAL:HG13	1:B:669:PRO:HD2	1.89	0.54
1:C:749:ILE:O	1:C:755:ARG:HG3	2.07	0.54
1:A:425:ARG:HH22	1:D:287:ASP:CG	2.11	0.54
1:A:786:ARG:HA	1:A:964:GLN:OE1	2.07	0.54
1:D:100:TYR:HB2	1:D:203:TRP:CE3	2.42	0.54
1:B:942:ARG:HA	1:B:953:GLY:O	2.07	0.54
1:A:749:ILE:O	1:A:755:ARG:HG3	2.08	0.54
1:B:894:ARG:NH1	1:B:919:ASP:OD1	2.34	0.54
1:D:26:ARG:HD2	1:D:169:SER:HA	1.87	0.54
1:B:786:ARG:HA	1:B:964:GLN:OE1	2.07	0.54
1:A:746:ASP:HA	1:A:760:ARG:CG	2.22	0.54
1:D:1020:TRP:CD1	1:D:1021:CYS:N	2.74	0.54
1:B:79:PRO:N	1:B:80:GLU:OE2	2.41	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:79:PRO:N	1:D:80:GLU:OE2	2.41	0.54
1:D:942:ARG:HA	1:D:953:GLY:O	2.07	0.54
1:A:134:LEU:HD12	1:A:134:LEU:H	1.69	0.54
1:C:79:PRO:N	1:C:80:GLU:OE2	2.41	0.54
1:C:645:ARG:HH22	1:C:650:GLU:CD	2.11	0.54
1:D:759:ASN:OD1	1:D:761:GLN:N	2.35	0.54
1:D:38:ASN:ND2	1:D:41:GLU:N	2.48	0.54
1:A:79:PRO:N	1:A:80:GLU:OE2	2.41	0.54
1:C:668:VAL:HG13	1:C:669:PRO:HD2	1.89	0.54
1:B:166:ARG:HG3	1:B:392:TYR:CB	2.38	0.54
1:A:418:HIS:O	1:D:282:ARG:HD3	2.08	0.54
1:D:749:ILE:O	1:D:755:ARG:HG3	2.08	0.54
1:B:29:ALA:HA	3:B:4295:HOH:O	2.07	0.54
1:A:395:HIS:ND1	1:A:396:PRO:HD2	2.22	0.54
1:C:38:ASN:HD21	1:C:41:GLU:H	1.53	0.54
1:C:80:GLU:H	1:C:80:GLU:CD	2.01	0.54
1:B:645:ARG:HH22	1:B:650:GLU:CD	2.11	0.54
1:A:166:ARG:HG3	1:A:392:TYR:CB	2.38	0.54
1:D:29:ALA:HA	3:D:4347:HOH:O	2.07	0.54
1:C:1020:TRP:CD1	1:C:1021:CYS:N	2.74	0.54
1:C:30:HIS:HB2	1:C:31:PRO:CD	2.38	0.54
1:C:357:HIS:HD2	1:C:392:TYR:OH	1.91	0.54
1:D:786:ARG:HA	1:D:964:GLN:OE1	2.07	0.54
1:C:903[A]:GLN:HB2	3:C:4239:HOH:O	2.08	0.54
1:A:668:VAL:HG13	1:A:669:PRO:HD2	1.89	0.53
1:B:30:HIS:HB2	1:B:31:PRO:CD	2.38	0.53
1:A:645:ARG:HH22	1:A:650:GLU:CD	2.11	0.53
1:B:749:ILE:O	1:B:755:ARG:HG3	2.07	0.53
1:A:357:HIS:HD2	1:A:392:TYR:OH	1.91	0.53
1:A:29:ALA:HA	3:A:4347:HOH:O	2.07	0.53
1:A:903[A]:GLN:HB2	3:A:4157:HOH:O	2.09	0.53
1:D:166:ARG:HG3	1:D:392:TYR:CB	2.38	0.53
1:A:1017:GLN:O	1:A:1018:LEU:HD23	2.09	0.53
1:B:1017:GLN:O	1:B:1018:LEU:HD23	2.09	0.53
1:C:6:SER:OG	1:C:9:VAL:HB	2.09	0.53
1:D:30:HIS:HB2	1:D:31:PRO:CD	2.38	0.53
1:B:742:THR:HG22	1:B:743:SER:H	1.74	0.53
1:C:110:ASN:O	1:C:113:PHE:N	2.39	0.53
1:D:597:ASN:HD22	1:D:599:ARG:N	1.94	0.53
1:C:894:ARG:NH1	1:C:919:ASP:OD1	2.34	0.53
1:D:696:LEU:HD12	1:D:697:THR:H	1.74	0.53
1:D:645:ARG:HH22	1:D:650:GLU:CD	2.11	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:357:HIS:HD2	1:D:392:TYR:OH	1.92	0.53
1:B:597:ASN:HD22	1:B:599:ARG:N	1.94	0.53
1:D:654:TRP:CE2	1:D:666:GLY:HA3	2.44	0.53
1:A:959:ILE:O	1:A:959:ILE:HG23	2.09	0.53
1:C:166:ARG:HG3	1:C:392:TYR:CB	2.38	0.53
1:A:6:SER:OG	1:A:9:VAL:HB	2.09	0.52
1:C:416:GLU:OE1	1:C:461:GLU:HG3	2.09	0.52
1:D:416:GLU:OE1	1:D:461:GLU:HG3	2.09	0.52
1:A:355:ASN:OD1	1:A:388:ARG:HD3	2.09	0.52
1:C:29:ALA:HA	3:C:4335:HOH:O	2.07	0.52
1:D:742:THR:HG22	1:D:743:SER:H	1.74	0.52
1:C:696:LEU:HD12	1:C:697:THR:H	1.74	0.52
1:C:1017:GLN:O	1:C:1018:LEU:HD23	2.09	0.52
1:C:959:ILE:HG23	1:C:959:ILE:O	2.09	0.52
1:A:920:LEU:HB3	1:A:921:PRO:CD	2.39	0.52
1:A:416:GLU:OE1	1:A:461:GLU:HG3	2.09	0.52
1:B:355:ASN:OD1	1:B:388:ARG:HD3	2.09	0.52
1:D:251:ARG:NH1	1:D:251:ARG:HG2	2.25	0.52
1:A:696:LEU:HD12	1:A:697:THR:H	1.74	0.52
1:C:355:ASN:OD1	1:C:388:ARG:HD3	2.09	0.52
1:B:959:ILE:HG23	1:B:959:ILE:O	2.09	0.52
1:D:808:GLU:HA	1:D:808:GLU:OE1	2.10	0.52
1:D:355:ASN:OD1	1:D:388:ARG:HD3	2.09	0.52
1:C:654:TRP:CE2	1:C:666:GLY:HA3	2.44	0.52
1:B:1020:TRP:CD1	1:B:1021:CYS:N	2.74	0.52
1:B:696:LEU:HD12	1:B:697:THR:H	1.74	0.52
1:C:749:ILE:N	1:C:749:ILE:HD12	2.25	0.52
1:A:749:ILE:N	1:A:749:ILE:HD12	2.25	0.52
1:B:251:ARG:HG2	1:B:251:ARG:NH1	2.25	0.52
1:B:436:MET:HE3	1:B:467:ASN:HD22	1.72	0.52
1:B:357:HIS:HD2	1:B:392:TYR:OH	1.91	0.52
1:A:878:HIS:HB3	1:A:1009:LEU:O	2.10	0.52
1:A:742:THR:HG22	1:A:743:SER:H	1.74	0.52
1:D:749:ILE:N	1:D:749:ILE:HD12	2.25	0.52
1:D:1017:GLN:O	1:D:1018:LEU:HD23	2.09	0.52
1:C:808:GLU:OE1	1:C:808:GLU:HA	2.10	0.52
1:A:30:HIS:HB2	1:A:31:PRO:CD	2.38	0.52
1:D:110:ASN:O	1:D:113:PHE:N	2.39	0.52
1:B:903[A]:GLN:HB2	3:B:4199:HOH:O	2.08	0.52
1:D:6:SER:OG	1:D:9:VAL:HB	2.09	0.52
1:A:425:ARG:NH2	1:D:287:ASP:OD2	2.43	0.52
1:B:130:ASP:OD2	1:B:132:SER:OG	2.28	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:130:ASP:OD2	1:D:132:SER:OG	2.28	0.52
1:D:148:SER:HB3	1:D:190:ARG:O	2.10	0.52
1:B:770:ILE:HG22	1:B:770:ILE:O	2.10	0.52
1:A:654:TRP:CE2	1:A:666:GLY:HA3	2.44	0.51
1:B:6:SER:OG	1:B:9:VAL:HB	2.09	0.51
1:C:742:THR:HG22	1:C:743:SER:H	1.74	0.51
1:D:542:MET:HA	1:D:604:ASN:HA	1.92	0.51
1:B:531:ARG:HB3	1:B:532:PRO:HD2	1.92	0.51
1:B:749:ILE:HD12	1:B:749:ILE:N	2.25	0.51
1:B:148:SER:HB3	1:B:190:ARG:O	2.10	0.51
1:C:878:HIS:HB3	1:C:1009:LEU:O	2.10	0.51
1:B:654:TRP:CE2	1:B:666:GLY:HA3	2.44	0.51
1:C:894:ARG:HD3	1:C:919:ASP:OD1	2.11	0.51
1:C:542:MET:HA	1:C:604:ASN:HA	1.92	0.51
1:B:808:GLU:HA	1:B:808:GLU:OE1	2.10	0.51
1:B:416:GLU:OE1	1:B:461:GLU:HG3	2.09	0.51
1:D:878:HIS:HB3	1:D:1009:LEU:O	2.10	0.51
1:D:959:ILE:HG23	1:D:959:ILE:O	2.09	0.51
1:C:65:ALA:HB1	1:C:66:PRO:CD	2.41	0.51
1:C:531:ARG:HB3	1:C:532:PRO:HD2	1.92	0.51
1:B:878:HIS:HB3	1:B:1009:LEU:O	2.10	0.51
1:A:251:ARG:NH1	1:A:251:ARG:HG2	2.25	0.51
1:C:38:ASN:ND2	1:C:41:GLU:N	2.48	0.51
1:A:531:ARG:HB3	1:A:532:PRO:HD2	1.92	0.51
1:D:903[A]:GLN:HB2	3:D:4157:HOH:O	2.08	0.51
1:A:808:GLU:HA	1:A:808:GLU:OE1	2.10	0.51
1:D:230:ARG:CG	1:D:230:ARG:HH11	2.24	0.51
1:A:130:ASP:OD2	1:A:132:SER:OG	2.28	0.51
1:B:822:LEU:HD12	1:B:824:GLN:H	1.76	0.51
1:A:26:ARG:CD	1:A:169:SER:HB3	2.41	0.51
1:B:425:ARG:HH22	1:C:287:ASP:CG	2.14	0.51
1:C:148:SER:HB3	1:C:190:ARG:O	2.10	0.51
1:C:597:ASN:HD22	1:C:599:ARG:N	1.94	0.51
1:A:254:LEU:O	1:A:255:ARG:NH1	2.44	0.51
1:A:894:ARG:HD3	1:A:919:ASP:OD1	2.11	0.51
1:A:906:TYR:HB3	1:A:907:PRO:CD	2.41	0.51
1:B:254:LEU:O	1:B:255:ARG:NH1	2.44	0.51
1:B:26:ARG:CD	1:B:169:SER:HB3	2.41	0.51
1:A:38:ASN:ND2	1:A:41:GLU:N	2.48	0.51
1:D:254:LEU:O	1:D:255:ARG:NH1	2.44	0.50
1:D:894:ARG:NH1	1:D:919:ASP:OD1	2.34	0.50
1:B:906:TYR:HB3	1:B:907:PRO:CD	2.41	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:95:TYR:N	1:C:95:TYR:CD1	2.79	0.50
1:C:26:ARG:CD	1:C:169:SER:HB3	2.41	0.50
1:A:770:ILE:HG22	1:A:770:ILE:O	2.10	0.50
1:A:134:LEU:N	1:A:134:LEU:CD1	2.73	0.50
1:D:65:ALA:HB1	1:D:66:PRO:CD	2.41	0.50
1:A:282:ARG:CG	1:D:423:MET:HB2	2.42	0.50
1:D:531:ARG:HB3	1:D:532:PRO:HD2	1.92	0.50
1:B:542:MET:HA	1:B:604:ASN:HA	1.92	0.50
1:D:73:TRP:CZ2	1:D:122:CYS:HB3	2.47	0.50
1:A:836:ILE:HG22	1:A:837:THR:N	2.26	0.50
1:D:822:LEU:HD12	1:D:824:GLN:H	1.76	0.50
1:D:906:TYR:HB3	1:D:907:PRO:CD	2.41	0.50
1:A:73:TRP:CZ2	1:A:122:CYS:HB3	2.47	0.50
1:A:38:ASN:HD21	1:A:41:GLU:H	1.53	0.50
1:B:134:LEU:CD1	1:B:134:LEU:N	2.73	0.50
1:A:767:GLN:CG	1:A:768:MET:N	2.75	0.50
1:D:770:ILE:O	1:D:770:ILE:HG22	2.10	0.50
1:C:230:ARG:CG	1:C:230:ARG:HH11	2.24	0.50
1:B:100:TYR:CZ	1:B:602:CYS:HB3	2.47	0.50
1:D:26:ARG:CD	1:D:169:SER:HB3	2.41	0.50
1:C:100:TYR:CZ	1:C:602:CYS:HB3	2.47	0.50
1:A:542:MET:HA	1:A:604:ASN:HA	1.92	0.50
1:B:662:PRO:C	1:B:663:LEU:HD23	2.32	0.50
1:A:662:PRO:C	1:A:663:LEU:HD23	2.32	0.50
1:A:230:ARG:CG	1:A:230:ARG:HH11	2.24	0.50
1:A:100:TYR:CZ	1:A:602:CYS:HB3	2.47	0.50
1:A:360:HIS:CG	1:A:361:PRO:HD2	2.47	0.50
1:B:65:ALA:HB1	1:B:66:PRO:CD	2.41	0.50
1:B:882:ILE:O	1:B:882:ILE:HG22	2.12	0.50
1:B:433:LEU:O	1:B:437:SER:HB3	2.12	0.50
1:B:836:ILE:HG22	1:B:837:THR:N	2.26	0.50
1:C:360:HIS:CG	1:C:361:PRO:HD2	2.47	0.50
1:B:360:HIS:CG	1:B:361:PRO:HD2	2.47	0.50
1:A:652:LEU:HD12	1:A:699:ARG:O	2.12	0.50
1:C:767:GLN:CG	1:C:768:MET:N	2.75	0.50
1:B:73:TRP:CZ2	1:B:122:CYS:HB3	2.47	0.50
1:B:90:TRP:HE1	1:B:96:ASP:CG	2.16	0.50
1:C:73:TRP:CZ2	1:C:122:CYS:HB3	2.47	0.50
1:B:230:ARG:HH11	1:B:230:ARG:CG	2.24	0.50
1:D:894:ARG:HD3	1:D:919:ASP:OD1	2.11	0.50
1:B:894:ARG:HD3	1:B:919:ASP:OD1	2.11	0.50
1:D:100:TYR:CZ	1:D:602:CYS:HB3	2.47	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:95:TYR:N	1:D:95:TYR:CD1	2.79	0.50
1:C:662:PRO:C	1:C:663:LEU:HD23	2.32	0.50
1:C:433:LEU:O	1:C:437:SER:HB3	2.12	0.49
1:C:254:LEU:O	1:C:255:ARG:NH1	2.44	0.49
1:C:30:HIS:ND1	1:C:31:PRO:O	2.40	0.49
1:C:822:LEU:HD12	1:C:824:GLN:H	1.76	0.49
1:A:148:SER:HB3	1:A:190:ARG:O	2.10	0.49
1:A:12:GLN:HG3	1:A:13:ARG:N	2.27	0.49
1:A:822:LEU:HD12	1:A:824:GLN:H	1.76	0.49
1:B:767:GLN:CG	1:B:768:MET:N	2.75	0.49
1:C:90:TRP:HE1	1:C:96:ASP:CG	2.16	0.49
1:A:638:VAL:O	1:A:677:LYS:HA	2.12	0.49
1:C:251:ARG:NH1	1:C:251:ARG:HG2	2.25	0.49
1:D:708:TRP:CE3	1:D:709:SER:HB3	2.47	0.49
1:A:708:TRP:CE3	1:A:709:SER:HB3	2.48	0.49
1:A:763:GLY:CA	1:A:822:LEU:HD21	2.42	0.49
1:D:638:VAL:O	1:D:677:LYS:HA	2.12	0.49
1:D:882:ILE:O	1:D:882:ILE:HG22	2.12	0.49
1:D:12:GLN:HG3	1:D:13:ARG:N	2.27	0.49
1:B:763:GLY:CA	1:B:822:LEU:HD21	2.42	0.49
1:A:65:ALA:HB1	1:A:66:PRO:CD	2.41	0.49
1:C:272:ALA:HB1	1:C:273:PRO:CD	2.43	0.49
1:A:272:ALA:HB1	1:A:273:PRO:CD	2.43	0.49
1:C:595:THR:HG23	1:C:596:PRO:CA	2.43	0.49
1:D:595:THR:HG23	1:D:596:PRO:CA	2.43	0.49
1:C:638:VAL:O	1:C:677:LYS:HA	2.12	0.49
1:C:153:TRP:HA	1:C:157:ARG:O	2.13	0.49
1:C:770:ILE:HG22	1:C:770:ILE:O	2.10	0.49
1:B:638:VAL:O	1:B:677:LYS:HA	2.12	0.49
1:B:652:LEU:HD12	1:B:699:ARG:O	2.12	0.49
1:A:95:TYR:N	1:A:95:TYR:CD1	2.79	0.49
1:A:90:TRP:HE1	1:A:96:ASP:CG	2.16	0.49
1:B:105:TYR:CE2	1:B:199:ASP:HB2	2.48	0.49
1:A:153:TRP:HA	1:A:157:ARG:O	2.13	0.49
1:B:153:TRP:HA	1:B:157:ARG:O	2.13	0.49
1:A:105:TYR:CE2	1:A:199:ASP:HB2	2.48	0.49
1:C:763:GLY:CA	1:C:822:LEU:HD21	2.42	0.49
1:C:660:GLY:O	1:C:662:PRO:HD3	2.13	0.49
1:D:660:GLY:O	1:D:662:PRO:HD3	2.13	0.49
1:A:110:ASN:O	1:A:113:PHE:N	2.39	0.49
1:A:200:GLN:N	1:A:200:GLN:OE1	2.44	0.49
1:D:360:HIS:CG	1:D:361:PRO:HD2	2.47	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:12:GLN:HG3	1:B:13:ARG:N	2.27	0.49
1:D:767:GLN:CG	1:D:768:MET:N	2.75	0.49
1:A:660:GLY:O	1:A:662:PRO:HD3	2.13	0.49
1:C:143:PHE:N	1:C:143:PHE:CD1	2.81	0.49
1:C:830:LEU:HD22	1:C:835:LEU:HB2	1.95	0.49
1:D:920:LEU:HB3	1:D:921:PRO:CD	2.39	0.49
1:C:708:TRP:CE3	1:C:709:SER:HB3	2.48	0.49
1:D:652:LEU:HD12	1:D:699:ARG:O	2.12	0.49
1:C:906:TYR:HB3	1:C:907:PRO:CD	2.41	0.49
1:C:938:ARG:NH2	3:C:4307:HOH:O	2.45	0.49
1:C:130:ASP:OD2	1:C:132:SER:OG	2.28	0.49
1:D:836:ILE:HG22	1:D:837:THR:N	2.26	0.49
1:C:134:LEU:N	1:C:134:LEU:CD1	2.73	0.49
1:D:763:GLY:CA	1:D:822:LEU:HD21	2.42	0.49
1:B:595:THR:HG23	1:B:596:PRO:CA	2.43	0.49
1:D:662:PRO:C	1:D:663:LEU:HD23	2.32	0.49
1:B:938:ARG:NH2	3:B:4267:HOH:O	2.45	0.49
1:C:835:LEU:CD1	1:C:857:ARG:HB2	2.43	0.48
1:C:836:ILE:HG22	1:C:837:THR:N	2.26	0.48
1:B:708:TRP:CE3	1:B:709:SER:HB3	2.48	0.48
1:A:651:LEU:HA	1:A:651:LEU:HD12	1.46	0.48
1:A:433:LEU:O	1:A:437:SER:HB3	2.12	0.48
1:D:105:TYR:CE2	1:D:199:ASP:HB2	2.48	0.48
1:A:143:PHE:N	1:A:143:PHE:CD1	2.81	0.48
1:D:90:TRP:HE1	1:D:96:ASP:CG	2.16	0.48
1:B:646:HIS:O	1:B:648:ASP:N	2.47	0.48
1:C:882:ILE:HG22	1:C:882:ILE:O	2.12	0.48
1:C:12:GLN:HG3	1:C:13:ARG:N	2.27	0.48
1:C:652:LEU:HD12	1:C:699:ARG:O	2.12	0.48
1:A:787:ALA:HA	1:A:788:PRO:HD3	1.66	0.48
1:D:153:TRP:HA	1:D:157:ARG:O	2.13	0.48
1:D:143:PHE:CD1	1:D:143:PHE:N	2.81	0.48
1:B:597:ASN:ND2	1:B:599:ARG:N	2.48	0.48
1:B:835:LEU:CD1	1:B:857:ARG:HB2	2.43	0.48
1:A:835:LEU:CD1	1:A:857:ARG:HB2	2.43	0.48
1:B:651:LEU:HD12	1:B:651:LEU:HA	1.46	0.48
1:B:668:VAL:CG1	1:B:669:PRO:HD2	2.44	0.48
1:D:433:LEU:O	1:D:437:SER:HB3	2.12	0.48
1:B:660:GLY:O	1:B:662:PRO:HD3	2.13	0.48
1:D:646:HIS:O	1:D:648:ASP:N	2.47	0.48
1:D:651:LEU:HD12	1:D:651:LEU:HA	1.46	0.48
1:C:26:ARG:HD3	1:C:169:SER:HB3	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:257:THR:OG1	1:C:316:HIS:HE1	1.97	0.48
1:C:147:ASN:HA	1:C:148:SER:HA	1.65	0.48
1:A:651:LEU:HD23	1:A:653[A]:HIS:HE1	1.79	0.48
1:C:651:LEU:HD23	1:C:653[A]:HIS:HE1	1.79	0.48
1:D:30:HIS:ND1	1:D:31:PRO:O	2.40	0.48
1:A:595:THR:HG23	1:A:596:PRO:CA	2.43	0.48
1:B:257:THR:OG1	1:B:316:HIS:HE1	1.97	0.48
1:D:26:ARG:HD3	1:D:169:SER:HB3	1.96	0.48
1:D:251:ARG:HH11	1:D:251:ARG:HG2	1.79	0.48
1:C:646:HIS:O	1:C:648:ASP:N	2.46	0.48
1:C:599:ARG:HD2	1:C:600:GLN:OE1	2.14	0.48
1:A:597:ASN:ND2	1:A:599:ARG:N	2.48	0.48
1:A:599:ARG:HD2	1:A:600:GLN:OE1	2.14	0.48
1:A:100:TYR:CE1	1:A:602:CYS:HB3	2.49	0.48
1:C:856:TYR:HD2	1:C:864:MET:CE	2.27	0.48
1:A:894:ARG:NH1	1:A:919:ASP:OD1	2.34	0.48
1:C:568:TRP:HE1	1:C:604:ASN:HD22	1.62	0.48
1:A:513:PRO:O	1:A:514:ALA:HB3	2.14	0.48
1:A:646:HIS:O	1:A:648:ASP:N	2.46	0.48
1:A:668:VAL:CG1	1:A:669:PRO:HD2	2.43	0.48
1:C:668:VAL:CG1	1:C:669:PRO:HD2	2.44	0.48
1:A:257:THR:OG1	1:A:316:HIS:HE1	1.97	0.48
1:B:26:ARG:HD3	1:B:169:SER:HB3	1.96	0.48
1:B:147:ASN:HA	1:B:148:SER:HA	1.65	0.48
1:B:143:PHE:CD1	1:B:143:PHE:N	2.81	0.48
1:D:513:PRO:O	1:D:514:ALA:HB3	2.14	0.48
1:A:30:HIS:ND1	1:A:31:PRO:O	2.40	0.47
1:B:67:GLU:H	1:B:67:GLU:HG2	1.15	0.47
1:D:100:TYR:CE1	1:D:602:CYS:HB3	2.49	0.47
1:C:573:GLN:HB2	1:C:602:CYS:O	2.14	0.47
1:B:100:TYR:CE1	1:B:602:CYS:HB3	2.49	0.47
1:B:970:THR:CG2	1:B:975:LEU:HB2	2.44	0.47
1:D:835:LEU:CD1	1:D:857:ARG:HB2	2.43	0.47
1:A:668:VAL:HA	1:A:669:PRO:HD3	1.66	0.47
1:A:701:VAL:CG1	1:A:702:GLN:N	2.77	0.47
1:C:742:THR:CG2	1:C:743:SER:N	2.77	0.47
1:A:210:ARG:NH1	1:A:358:GLU:OE1	2.47	0.47
1:D:734:SER:HB2	1:D:860:GLY:HA3	1.95	0.47
1:D:668:VAL:CG1	1:D:669:PRO:HD2	2.44	0.47
1:A:305:ILE:HD11	1:A:645:ARG:HB3	1.96	0.47
1:C:210:ARG:NH1	1:C:358:GLU:OE1	2.47	0.47
1:C:100:TYR:CE1	1:C:602:CYS:HB3	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:568:TRP:HE1	1:D:604:ASN:HD22	1.62	0.47
1:D:599:ARG:HD2	1:D:600:GLN:OE1	2.14	0.47
1:A:830:LEU:HD22	1:A:835:LEU:HB2	1.95	0.47
1:D:210:ARG:NH1	1:D:358:GLU:OE1	2.47	0.47
1:A:568:TRP:HE1	1:A:604:ASN:HD22	1.62	0.47
1:C:105:TYR:CE2	1:C:199:ASP:HB2	2.48	0.47
1:C:780:LEU:HA	1:C:886:CYS:HB3	1.97	0.47
1:A:635:THR:OG1	1:A:681:GLU:HG3	2.15	0.47
1:A:292:ARG:C	1:A:293:LEU:HD23	2.35	0.47
1:A:882:ILE:O	1:A:882:ILE:HG22	2.12	0.47
1:A:856:TYR:HD2	1:A:864:MET:CE	2.27	0.47
1:D:651:LEU:HD23	1:D:653[A]:HIS:HE1	1.79	0.47
1:C:701:VAL:CG1	1:C:702:GLN:N	2.77	0.47
1:A:423:MET:HB2	1:D:282:ARG:CG	2.43	0.47
1:A:18:ASN:HA	1:A:19:PRO:HD3	1.56	0.47
1:B:251:ARG:HH11	1:B:251:ARG:HG2	1.79	0.47
1:A:970:THR:CG2	1:A:975:LEU:HB2	2.44	0.47
1:D:635:THR:OG1	1:D:681:GLU:HG3	2.15	0.47
1:B:651:LEU:HD23	1:B:653[A]:HIS:HE1	1.79	0.47
1:D:305:ILE:HD11	1:D:645:ARG:HB3	1.96	0.47
1:A:26:ARG:HD3	1:A:169:SER:HB3	1.96	0.47
1:A:780:LEU:HA	1:A:886:CYS:HB3	1.97	0.47
1:B:780:LEU:HA	1:B:886:CYS:HB3	1.97	0.47
1:D:780:LEU:HA	1:D:886:CYS:HB3	1.97	0.47
1:B:110:ASN:O	1:B:113:PHE:N	2.39	0.47
1:A:573:GLN:HB2	1:A:602:CYS:O	2.14	0.47
1:B:599:ARG:HD2	1:B:600:GLN:OE1	2.14	0.47
1:D:830:LEU:HD22	1:D:835:LEU:HB2	1.95	0.47
1:B:701:VAL:CG1	1:B:702:GLN:N	2.78	0.47
1:D:272:ALA:HB1	1:D:273:PRO:CD	2.43	0.47
1:D:257:THR:OG1	1:D:316:HIS:HE1	1.97	0.47
1:C:661:LYS:HA	1:C:662:PRO:HD2	1.71	0.47
1:D:938:ARG:NH2	3:D:4279:HOH:O	2.45	0.47
1:C:970:THR:CG2	1:C:975:LEU:HB2	2.44	0.47
1:C:214:LEU:HA	1:C:214:LEU:HD23	1.61	0.47
1:C:513:PRO:O	1:C:514:ALA:HB3	2.14	0.47
1:D:970:THR:CG2	1:D:975:LEU:HB2	2.44	0.47
1:A:80:GLU:OE2	1:A:80:GLU:N	2.29	0.47
1:D:742:THR:CG2	1:D:743:SER:N	2.77	0.47
1:B:568:TRP:HE1	1:B:604:ASN:HD22	1.62	0.47
1:A:261:TRP:N	1:A:261:TRP:CD1	2.83	0.47
1:B:210:ARG:NH1	1:B:358:GLU:OE1	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:127:PHE:HE2	1:B:184:LEU:HG	1.80	0.47
1:C:292:ARG:C	1:C:293:LEU:HD23	2.35	0.47
1:B:830:LEU:HD22	1:B:835:LEU:HB2	1.95	0.47
1:B:305:ILE:HD11	1:B:645:ARG:HB3	1.96	0.47
1:A:251:ARG:HG2	1:A:251:ARG:HH11	1.79	0.47
1:D:73:TRP:CE2	1:D:122:CYS:HB3	2.50	0.47
1:A:849:LEU:HD23	1:A:849:LEU:N	2.30	0.47
1:D:701:VAL:CG1	1:D:702:GLN:N	2.77	0.46
1:B:272:ALA:HB1	1:B:273:PRO:CD	2.43	0.46
1:D:573:GLN:HB2	1:D:602:CYS:O	2.14	0.46
1:A:282:ARG:NH1	1:D:419:GLY:C	2.68	0.46
1:A:419:GLY:C	1:D:282:ARG:NH1	2.68	0.46
1:B:73:TRP:CE2	1:B:122:CYS:HB3	2.50	0.46
1:D:441:THR:HG22	1:D:474:TRP:CH2	2.50	0.46
1:B:200:GLN:OE1	1:B:200:GLN:N	2.44	0.46
1:B:573:GLN:HB2	1:B:602:CYS:O	2.14	0.46
1:B:95:TYR:CD1	1:B:95:TYR:N	2.79	0.46
1:D:230:ARG:HG2	1:D:230:ARG:HH11	1.81	0.46
1:D:292:ARG:C	1:D:293:LEU:HD23	2.35	0.46
1:B:513:PRO:O	1:B:514:ALA:HB3	2.14	0.46
1:C:234:ASP:O	1:C:235:PHE:HB2	2.15	0.46
1:D:234:ASP:O	1:D:235:PHE:HB2	2.15	0.46
1:C:635:THR:OG1	1:C:681:GLU:HG3	2.15	0.46
1:B:292:ARG:C	1:B:293:LEU:HD23	2.35	0.46
1:D:834:VAL:CG1	1:D:835:LEU:N	2.79	0.46
1:B:202:MET:HE3	1:B:357:HIS:CD2	2.50	0.46
1:A:282:ARG:HG2	1:D:423:MET:HB2	1.97	0.46
1:A:429:ASP:OD1	1:A:431[A]:ARG:HG3	2.16	0.46
1:C:429:ASP:OD1	1:C:431[A]:ARG:HG3	2.16	0.46
1:A:230:ARG:HH11	1:A:230:ARG:HG2	1.81	0.46
1:A:13:ARG:NH1	1:D:13:ARG:NH1	2.63	0.46
1:C:227:VAL:HG12	1:C:228:ALA:N	2.31	0.46
1:B:429:ASP:HA	1:B:430:PRO:HD3	1.82	0.46
1:B:429:ASP:OD1	1:B:431[A]:ARG:HG3	2.16	0.46
1:C:1018:LEU:HD23	1:C:1018:LEU:HA	1.53	0.46
1:D:261:TRP:N	1:D:261:TRP:CD1	2.83	0.46
1:B:873:ALA:O	1:B:876:THR:HG22	2.16	0.46
1:B:226:HIS:CD2	1:B:226:HIS:N	2.83	0.46
1:C:226:HIS:CD2	1:C:226:HIS:N	2.83	0.46
1:C:11:LEU:CD2	1:C:187:MET:HE3	2.45	0.46
1:A:166:ARG:HG3	1:A:392:TYR:CG	2.51	0.46
1:D:878:HIS:HA	1:D:879:PRO:HD3	1.69	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:127:PHE:HE2	1:C:184:LEU:HG	1.80	0.46
1:B:234:ASP:O	1:B:235:PHE:HB2	2.15	0.46
1:C:84:VAL:HG13	1:C:85:VAL:N	2.31	0.46
1:B:441:THR:HG22	1:B:474:TRP:CH2	2.50	0.46
1:D:200:GLN:N	1:D:200:GLN:OE1	2.44	0.46
1:A:403:ASP:CG	1:A:451:PRO:HD2	2.36	0.46
1:D:597:ASN:ND2	1:D:599:ARG:N	2.48	0.46
1:B:254:LEU:C	1:B:255:ARG:HG2	2.36	0.46
1:C:305:ILE:HD11	1:C:645:ARG:HB3	1.96	0.46
1:A:742:THR:CG2	1:A:743:SER:N	2.77	0.46
1:B:166:ARG:HG3	1:B:392:TYR:CG	2.51	0.46
1:A:423:MET:HB2	1:D:282:ARG:HG2	1.97	0.46
1:B:261:TRP:N	1:B:261:TRP:CD1	2.83	0.46
1:C:620:ALA:O	1:C:624:GLN:HG3	2.16	0.46
1:C:261:TRP:CD1	1:C:261:TRP:N	2.83	0.46
1:D:630:ARG:HB3	1:D:630:ARG:HE	1.31	0.46
1:D:227:VAL:HG12	1:D:228:ALA:N	2.31	0.46
1:A:737:ILE:HA	1:A:738:PRO:HD3	1.78	0.46
1:C:73:TRP:CE2	1:C:122:CYS:HB3	2.51	0.46
1:D:873:ALA:O	1:D:876:THR:HG22	2.16	0.46
1:B:620:ALA:O	1:B:624:GLN:HG3	2.16	0.46
1:B:635:THR:OG1	1:B:681:GLU:HG3	2.15	0.46
1:B:849:LEU:N	1:B:849:LEU:HD23	2.30	0.46
1:B:945:ASN:OD1	1:B:950:GLN:HB2	2.16	0.46
1:B:856:TYR:HD2	1:B:864:MET:CE	2.27	0.46
1:B:834:VAL:CG1	1:B:835:LEU:N	2.79	0.46
1:D:894:ARG:NH2	1:D:921:PRO:HD3	2.31	0.46
1:D:701:VAL:O	1:D:703:PRO:HD3	2.16	0.46
1:B:742:THR:CG2	1:B:743:SER:N	2.77	0.46
1:D:316:HIS:HB2	1:D:321:THR:O	2.16	0.46
1:D:127:PHE:HE2	1:D:184:LEU:HG	1.80	0.46
1:C:141:ILE:CG1	1:C:142:ILE:N	2.79	0.46
1:C:881:ARG:HD3	1:C:987:ASP:CG	2.36	0.46
1:B:369:GLU:O	1:B:373:VAL:HG23	2.16	0.46
1:A:679:LEU:HD23	1:A:679:LEU:HA	1.13	0.46
1:B:111:PRO:HA	1:B:112:PRO:HA	1.57	0.46
1:D:254:LEU:C	1:D:255:ARG:HG2	2.36	0.46
1:B:701:VAL:O	1:B:703:PRO:HD3	2.16	0.46
1:D:870:VAL:CG1	1:D:871:GLU:N	2.79	0.46
1:A:881:ARG:HD3	1:A:987:ASP:CG	2.36	0.46
1:D:658:LEU:O	1:D:659:ASP:C	2.54	0.46
1:C:441:THR:HG22	1:C:474:TRP:CH2	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:894:ARG:NH2	1:A:921:PRO:HD3	2.31	0.46
1:B:870:VAL:CG1	1:B:871:GLU:N	2.79	0.46
1:B:168:PRO:O	1:B:442:ARG:NH2	2.48	0.46
1:A:141:ILE:CG1	1:A:142:ILE:N	2.79	0.46
1:B:881:ARG:HD3	1:B:987:ASP:CG	2.36	0.46
1:D:84:VAL:HG13	1:D:85:VAL:N	2.31	0.46
1:A:369:GLU:O	1:A:373:VAL:HG23	2.16	0.46
1:B:908:ASP:HB3	1:B:1007:PHE:CD1	2.51	0.46
1:A:254:LEU:C	1:A:255:ARG:HG2	2.36	0.45
1:D:856:TYR:HD2	1:D:864:MET:CE	2.27	0.45
1:C:834:VAL:CG1	1:C:835:LEU:N	2.79	0.45
1:B:3:ILE:HD12	1:B:3:ILE:O	2.16	0.45
1:B:316:HIS:HB2	1:B:321:THR:O	2.16	0.45
1:C:230:ARG:HG2	1:C:230:ARG:HH11	1.81	0.45
1:A:234:ASP:O	1:A:235:PHE:HB2	2.15	0.45
1:C:403:ASP:CG	1:C:451:PRO:HD2	2.36	0.45
1:C:908:ASP:HB3	1:C:1007:PHE:CD1	2.52	0.45
1:B:38:ASN:ND2	1:B:41:GLU:HG3	2.31	0.45
1:A:38:ASN:ND2	1:A:41:GLU:HG3	2.32	0.45
1:B:80:GLU:N	1:B:80:GLU:OE2	2.29	0.45
1:A:3:ILE:HD12	1:A:3:ILE:O	2.16	0.45
1:C:701:VAL:O	1:C:703:PRO:HD3	2.16	0.45
1:B:1018:LEU:HD23	1:B:1018:LEU:HA	1.53	0.45
1:D:945:ASN:OD1	1:D:950:GLN:HB2	2.16	0.45
1:A:441:THR:HG22	1:A:474:TRP:CH2	2.50	0.45
1:C:242:ALA:O	1:C:290:THR:HA	2.16	0.45
1:D:881:ARG:HD3	1:D:987:ASP:CG	2.36	0.45
1:B:403:ASP:CG	1:B:451:PRO:HD2	2.36	0.45
1:A:658:LEU:O	1:A:659:ASP:C	2.54	0.45
1:A:938:ARG:NH2	3:A:4279:HOH:O	2.45	0.45
1:D:908:ASP:HB3	1:D:1007:PHE:CD1	2.52	0.45
1:A:226:HIS:N	1:A:226:HIS:CD2	2.83	0.45
1:D:226:HIS:N	1:D:226:HIS:CD2	2.83	0.45
1:D:369:GLU:O	1:D:373:VAL:HG23	2.16	0.45
1:A:834:VAL:CG1	1:A:835:LEU:N	2.79	0.45
1:A:701:VAL:O	1:A:703:PRO:HD3	2.16	0.45
1:A:227:VAL:HG12	1:A:228:ALA:N	2.31	0.45
1:D:531:ARG:CB	1:D:532:PRO:HD2	2.46	0.45
1:A:1018:LEU:HD23	1:A:1018:LEU:HA	1.53	0.45
1:C:230:ARG:CG	1:C:230:ARG:NH1	2.79	0.45
1:B:230:ARG:CG	1:B:230:ARG:NH1	2.79	0.45
1:C:369:GLU:O	1:C:373:VAL:HG23	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:757:GLN:HG2	1:B:758:PHE:N	2.31	0.45
1:B:832:ASP:N	1:B:832:ASP:OD1	2.50	0.45
1:C:80:GLU:OE2	1:C:80:GLU:N	2.29	0.45
1:B:920:LEU:HB3	1:B:921:PRO:CD	2.39	0.45
1:D:3:ILE:O	1:D:3:ILE:HD12	2.16	0.45
1:D:63:PHE:HB3	1:D:64:PRO:CD	2.45	0.45
1:C:67:GLU:HG2	1:C:67:GLU:H	1.15	0.45
1:A:202:MET:HE3	1:A:357:HIS:CD2	2.52	0.45
1:A:524:LEU:HB2	3:A:4198:HOH:O	2.16	0.45
1:B:531:ARG:CB	1:B:532:PRO:HD2	2.46	0.45
1:C:251:ARG:HG2	1:C:251:ARG:HH11	1.79	0.45
1:B:141:ILE:CG1	1:B:142:ILE:N	2.79	0.45
1:C:873:ALA:O	1:C:876:THR:HG22	2.16	0.45
1:A:620:ALA:O	1:A:624:GLN:HG3	2.16	0.45
1:B:352:ARG:O	1:B:385:ASN:HB2	2.17	0.45
1:A:242:ALA:O	1:A:290:THR:HA	2.16	0.45
1:B:242:ALA:O	1:B:290:THR:HA	2.16	0.45
1:D:620:ALA:O	1:D:624:GLN:HG3	2.16	0.45
1:A:214:LEU:HD23	1:A:214:LEU:HA	1.61	0.45
1:A:84:VAL:HG13	1:A:85:VAL:N	2.31	0.45
1:C:38:ASN:ND2	1:C:41:GLU:HG3	2.32	0.45
1:A:559:TYR:HA	1:A:560:PRO:HD2	1.85	0.45
1:C:63:PHE:HB3	1:C:64:PRO:CD	2.45	0.45
1:C:531:ARG:CB	1:C:532:PRO:HD2	2.46	0.45
1:D:403:ASP:CG	1:D:451:PRO:HD2	2.36	0.45
1:A:915:PHE:O	1:A:916:ASP:HB2	2.17	0.45
1:A:352:ARG:O	1:A:385:ASN:HB2	2.17	0.45
1:B:658:LEU:O	1:B:659:ASP:C	2.54	0.45
1:B:679:LEU:HD23	1:B:679:LEU:HA	1.13	0.45
1:B:650:GLU:HA	1:B:701:VAL:O	2.17	0.45
1:D:166:ARG:HG3	1:D:392:TYR:CG	2.51	0.45
1:B:227:VAL:HG12	1:B:228:ALA:N	2.31	0.45
1:D:111:PRO:HA	1:D:112:PRO:HA	1.56	0.45
1:B:287:ASP:OD2	1:C:425:ARG:NH2	2.50	0.45
1:D:38:ASN:ND2	1:D:41:GLU:HG3	2.32	0.45
1:B:734:SER:HB2	1:B:860:GLY:HA3	1.95	0.45
1:C:650:GLU:HA	1:C:701:VAL:O	2.17	0.45
1:C:524:LEU:HB2	3:C:4262:HOH:O	2.16	0.45
1:B:878:HIS:HA	1:B:879:PRO:HD3	1.69	0.45
1:A:73:TRP:CE2	1:A:122:CYS:HB3	2.50	0.45
1:D:757:GLN:HG2	1:D:758:PHE:N	2.31	0.45
1:A:945:ASN:OD1	1:A:950:GLN:HB2	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:308:LEU:HA	1:D:308:LEU:HD23	1.80	0.45
1:C:658:LEU:O	1:C:659:ASP:C	2.54	0.45
1:B:894:ARG:NH2	1:B:921:PRO:HD3	2.31	0.45
1:C:3:ILE:HD12	1:C:3:ILE:O	2.16	0.45
1:D:143:PHE:O	1:D:168:PRO:HA	2.17	0.45
1:A:873:ALA:O	1:A:876:THR:HG22	2.16	0.45
1:B:84:VAL:HG13	1:B:85:VAL:N	2.31	0.45
1:B:86:VAL:HG13	1:B:87:PRO:HA	1.99	0.45
1:C:730:LEU:HG	1:C:730:LEU:H	1.41	0.45
1:C:832:ASP:OD1	1:C:832:ASP:N	2.49	0.45
1:B:255:ARG:NH1	1:B:255:ARG:CG	2.79	0.45
1:D:429:ASP:OD1	1:D:431[A]:ARG:HG3	2.16	0.45
1:D:524:LEU:HB2	3:D:4198:HOH:O	2.16	0.45
1:A:878:HIS:HA	1:A:879:PRO:HD3	1.69	0.45
1:A:127:PHE:HE2	1:A:184:LEU:HG	1.80	0.45
1:B:915:PHE:O	1:B:916:ASP:HB2	2.17	0.45
1:C:849:LEU:N	1:C:849:LEU:HD23	2.30	0.45
1:B:599:ARG:HB2	1:B:600:GLN:H	1.54	0.45
1:C:77:ASP:C	1:C:78:LEU:HD23	2.37	0.45
1:A:77:ASP:C	1:A:78:LEU:HD23	2.37	0.45
1:B:230:ARG:HG2	1:B:230:ARG:HH11	1.81	0.45
1:D:441:THR:HG22	1:D:474:TRP:CZ3	2.52	0.45
1:C:945:ASN:OD1	1:C:950:GLN:HB2	2.16	0.45
1:D:832:ASP:N	1:D:832:ASP:OD1	2.50	0.45
1:A:399:TYR:CD1	1:A:399:TYR:N	2.85	0.45
1:B:38:ASN:ND2	1:B:41:GLU:N	2.48	0.44
1:C:254:LEU:C	1:C:255:ARG:HG2	2.36	0.44
1:D:1018:LEU:HA	1:D:1018:LEU:HD23	1.53	0.44
1:D:230:ARG:NH1	1:D:230:ARG:CG	2.79	0.44
1:C:143:PHE:O	1:C:168:PRO:HA	2.17	0.44
1:D:43:ARG:HD2	1:D:261:TRP:CD2	2.52	0.44
1:C:118:ASN:HA	1:C:119:PRO:HD2	1.61	0.44
1:C:86:VAL:HG13	1:C:87:PRO:HA	1.99	0.44
1:C:352:ARG:O	1:C:385:ASN:HB2	2.17	0.44
1:C:399:TYR:N	1:C:399:TYR:CD1	2.85	0.44
1:A:86:VAL:HG13	1:A:87:PRO:HA	1.99	0.44
1:D:352:ARG:O	1:D:385:ASN:HB2	2.17	0.44
1:C:433:LEU:HB3	1:C:434:PRO:HD3	2.00	0.44
1:A:78:LEU:HB3	1:A:80:GLU:OE2	2.18	0.44
1:C:894:ARG:NH2	1:C:921:PRO:HD3	2.31	0.44
1:C:668:VAL:HA	1:C:669:PRO:HD3	1.66	0.44
1:D:650:GLU:HA	1:D:701:VAL:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:166:ARG:HG3	1:C:392:TYR:CG	2.51	0.44
1:A:531:ARG:CB	1:A:532:PRO:HD2	2.46	0.44
1:C:18:ASN:HA	1:C:19:PRO:HD3	1.56	0.44
1:B:136:GLU:O	1:B:216:HIS:HE1	2.01	0.44
1:D:141:ILE:CG1	1:D:142:ILE:N	2.79	0.44
1:A:908:ASP:HB3	1:A:1007:PHE:CD1	2.52	0.44
1:A:708:TRP:N	1:A:708:TRP:CD1	2.85	0.44
1:C:870:VAL:CG1	1:C:871:GLU:N	2.79	0.44
1:A:870:VAL:CG1	1:A:871:GLU:N	2.79	0.44
1:C:316:HIS:HB2	1:C:321:THR:O	2.16	0.44
1:B:786:ARG:HH11	1:B:990:HIS:CE1	2.36	0.44
1:A:230:ARG:NH1	1:A:230:ARG:CG	2.79	0.44
1:B:43:ARG:HD2	1:B:261:TRP:CD2	2.52	0.44
1:C:43:ARG:HD2	1:C:261:TRP:CD2	2.52	0.44
1:C:881:ARG:HD3	1:C:987:ASP:OD2	2.17	0.44
1:A:989:PHE:CD1	1:A:989:PHE:N	2.86	0.44
1:D:849:LEU:HD23	1:D:849:LEU:N	2.30	0.44
1:B:77:ASP:C	1:B:78:LEU:HD23	2.37	0.44
1:D:708:TRP:CD1	1:D:708:TRP:N	2.85	0.44
1:C:708:TRP:N	1:C:708:TRP:CD1	2.85	0.44
1:C:395:HIS:CG	1:C:396:PRO:HD2	2.53	0.44
1:A:786:ARG:HH11	1:A:990:HIS:CE1	2.36	0.44
1:B:143:PHE:O	1:B:168:PRO:HA	2.17	0.44
1:D:86:VAL:HG13	1:D:87:PRO:HA	1.99	0.44
1:A:136:GLU:O	1:A:216:HIS:HE1	2.01	0.44
1:D:78:LEU:HB3	1:D:80:GLU:OE2	2.18	0.44
1:D:77:ASP:C	1:D:78:LEU:HD23	2.38	0.44
1:D:433:LEU:HB3	1:D:434:PRO:HD3	2.00	0.44
1:C:645:ARG:NH2	1:C:650:GLU:OE1	2.51	0.44
1:A:650:GLU:HA	1:A:701:VAL:O	2.17	0.44
1:A:63:PHE:N	1:A:63:PHE:CD1	2.86	0.44
1:C:737:ILE:HA	1:C:738:PRO:HD3	1.78	0.44
1:B:441:THR:HG22	1:B:474:TRP:CZ3	2.52	0.44
1:C:989:PHE:CD1	1:C:989:PHE:N	2.86	0.44
1:B:947:GLY:HA3	1:B:948:PRO:HD2	1.89	0.44
1:C:78:LEU:HB3	1:C:80:GLU:OE2	2.18	0.44
1:C:79:PRO:HB2	1:C:80:GLU:HG3	2.00	0.44
1:D:18:ASN:HA	1:D:19:PRO:HD3	1.56	0.44
1:A:395:HIS:HA	1:A:396:PRO:HD3	1.83	0.44
1:A:168:PRO:O	1:A:442:ARG:NH2	2.48	0.44
1:D:242:ALA:O	1:D:290:THR:HA	2.16	0.44
1:A:118:ASN:HA	1:A:119:PRO:HD2	1.61	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:63:PHE:N	1:C:63:PHE:CD1	2.86	0.44
1:A:645:ARG:NH2	1:A:650:GLU:OE1	2.51	0.44
1:C:202:MET:HE3	1:C:357:HIS:CD2	2.53	0.44
1:D:136:GLU:O	1:D:216:HIS:HE1	2.01	0.44
1:B:524:LEU:HB2	3:B:4222:HOH:O	2.16	0.44
1:B:399:TYR:N	1:B:399:TYR:CD1	2.85	0.44
1:B:78:LEU:HB3	1:B:80:GLU:OE2	2.18	0.44
1:B:30:HIS:CE1	1:B:33:PHE:CD1	3.06	0.44
1:C:441:THR:HG22	1:C:474:TRP:CZ3	2.52	0.44
1:D:694:LEU:HD12	1:D:694:LEU:HA	1.82	0.44
1:D:134:LEU:N	1:D:134:LEU:CD1	2.73	0.44
1:B:11:LEU:CD2	1:B:187:MET:HE3	2.44	0.44
1:A:441:THR:HG22	1:A:474:TRP:CZ3	2.52	0.44
1:C:136:GLU:O	1:C:216:HIS:HE1	2.01	0.44
1:D:989:PHE:CD1	1:D:989:PHE:N	2.86	0.44
1:A:433:LEU:HB3	1:A:434:PRO:HD3	2.00	0.43
1:C:145:GLY:HA3	1:C:210:ARG:HG3	2.00	0.43
1:A:316:HIS:HB2	1:A:321:THR:O	2.16	0.43
1:C:786:ARG:HH11	1:C:990:HIS:CE1	2.36	0.43
1:B:881:ARG:HD3	1:B:987:ASP:OD2	2.18	0.43
1:C:915:PHE:O	1:C:916:ASP:HB2	2.17	0.43
1:A:832:ASP:OD1	1:A:832:ASP:N	2.50	0.43
1:C:597:ASN:ND2	1:C:599:ARG:N	2.48	0.43
1:C:255:ARG:NH1	1:C:255:ARG:CG	2.79	0.43
1:D:79:PRO:HB2	1:D:80:GLU:HG3	2.00	0.43
1:A:3:ILE:C	1:A:5:ASP:H	2.22	0.43
1:B:645:ARG:NH2	1:B:650:GLU:OE1	2.51	0.43
1:A:30:HIS:CE1	1:A:33:PHE:CD1	3.06	0.43
1:D:30:HIS:CE1	1:D:33:PHE:CD1	3.06	0.43
1:A:227:VAL:CG1	1:A:240:LEU:HD11	2.48	0.43
1:B:748:CYS:C	1:B:749:ILE:HD12	2.39	0.43
1:D:915:PHE:O	1:D:916:ASP:HB2	2.17	0.43
1:B:989:PHE:CD1	1:B:989:PHE:N	2.86	0.43
1:B:630:ARG:HB3	1:B:630:ARG:HE	1.31	0.43
1:A:78:LEU:HA	1:A:79:PRO:HD2	1.59	0.43
1:C:3:ILE:C	1:C:5:ASP:H	2.22	0.43
1:D:63:PHE:N	1:D:63:PHE:CD1	2.86	0.43
1:A:742:THR:CG2	1:A:743:SER:H	2.31	0.43
1:D:145:GLY:HA3	1:D:210:ARG:HG3	2.00	0.43
1:B:395:HIS:CG	1:B:396:PRO:HD2	2.53	0.43
1:D:786:ARG:HH11	1:D:990:HIS:CE1	2.36	0.43
1:A:43:ARG:HD2	1:A:261:TRP:CD2	2.52	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:634:GLN:NE2	1:C:682:LEU:O	2.51	0.43
1:B:433:LEU:HB3	1:B:434:PRO:HD3	2.00	0.43
1:C:168:PRO:O	1:C:442:ARG:NH2	2.48	0.43
1:A:881:ARG:HD3	1:A:987:ASP:OD2	2.17	0.43
1:D:881:ARG:HD3	1:D:987:ASP:OD2	2.18	0.43
1:B:682:LEU:HA	1:B:683:PRO:HD3	1.91	0.43
1:B:225:PHE:HA	1:B:243:GLU:O	2.19	0.43
1:C:225:PHE:HA	1:C:243:GLU:O	2.19	0.43
1:C:657:ALA:O	1:C:694:LEU:HD12	2.18	0.43
1:A:285:TYR:OH	1:D:424:ASN:HB3	2.19	0.43
1:D:399:TYR:N	1:D:399:TYR:CD1	2.85	0.43
1:B:79:PRO:HB2	1:B:80:GLU:HG3	2.00	0.43
1:A:79:PRO:HB2	1:A:80:GLU:HG3	2.00	0.43
1:D:11:LEU:CD2	1:D:187:MET:HE3	2.48	0.43
1:D:645:ARG:NH2	1:D:650:GLU:OE1	2.51	0.43
1:A:67:GLU:H	1:A:67:GLU:HG2	1.15	0.43
1:B:742:THR:CG2	1:B:743:SER:H	2.31	0.43
1:B:145:GLY:HA3	1:B:210:ARG:HG3	2.00	0.43
1:D:429:ASP:HA	1:D:430:PRO:HD3	1.82	0.43
1:A:143:PHE:O	1:A:168:PRO:HA	2.17	0.43
1:C:920:LEU:HB3	1:C:921:PRO:CD	2.39	0.43
1:A:685:LEU:HA	1:A:686:PRO:HD3	1.84	0.43
1:D:748:CYS:C	1:D:749:ILE:HD12	2.39	0.43
1:C:878:HIS:HA	1:C:879:PRO:HD3	1.69	0.43
1:D:657:ALA:O	1:D:694:LEU:HD12	2.18	0.43
1:B:657:ALA:O	1:B:694:LEU:HD12	2.18	0.43
1:C:217:LYS:HB3	1:C:218:PRO:HD2	2.00	0.43
1:C:482:ARG:HH11	1:C:482:ARG:HD2	1.57	0.43
1:C:176:PHE:CD1	1:C:176:PHE:N	2.87	0.43
1:B:118:ASN:HA	1:B:119:PRO:HD2	1.61	0.43
1:A:734:SER:HB2	1:A:860:GLY:HA3	1.95	0.43
1:A:77:ASP:HA	3:A:4132:HOH:O	2.19	0.43
1:C:645:ARG:NH2	1:C:650:GLU:OE2	2.45	0.43
1:C:30:HIS:CE1	1:C:33:PHE:CD1	3.06	0.43
1:A:822:LEU:HD12	1:A:823:LEU:N	2.34	0.43
1:C:429:ASP:HA	1:C:430:PRO:HD3	1.82	0.43
1:D:395:HIS:CG	1:D:396:PRO:HD2	2.53	0.43
1:C:114:VAL:HA	1:C:115:PRO:HD3	1.77	0.43
1:D:787:ALA:HA	1:D:788:PRO:HD3	1.66	0.43
1:C:200:GLN:OE1	1:C:200:GLN:N	2.44	0.43
1:C:679:LEU:HD23	1:C:679:LEU:HA	1.13	0.43
1:C:630:ARG:HE	1:C:630:ARG:HB3	1.31	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:708:TRP:CD1	1:B:708:TRP:N	2.85	0.43
1:A:748:CYS:C	1:A:749:ILE:HD12	2.39	0.43
1:D:354:VAL:HG22	1:D:355:ASN:N	2.34	0.43
1:A:634:GLN:NE2	1:A:682:LEU:O	2.51	0.43
1:A:217:LYS:HB3	1:A:218:PRO:HD2	2.00	0.43
1:D:910:LEU:HD12	1:D:910:LEU:C	2.39	0.43
1:A:630:ARG:HE	1:A:630:ARG:HB3	1.31	0.43
1:A:730:LEU:H	1:A:730:LEU:HG	1.41	0.43
1:C:173:LEU:HA	1:C:173:LEU:HD23	1.80	0.43
1:C:734:SER:HB2	1:C:860:GLY:HA3	1.95	0.43
1:D:685:LEU:CB	1:D:686:PRO:HD2	2.38	0.43
1:B:227:VAL:CG1	1:B:240:LEU:HD11	2.48	0.43
1:A:257:THR:HA	1:A:270:GLY:O	2.19	0.43
1:C:748:CYS:C	1:C:749:ILE:HD12	2.39	0.43
1:B:251:ARG:HH11	1:B:251:ARG:CG	2.32	0.43
1:D:147:ASN:HA	1:D:148:SER:HA	1.65	0.43
1:A:251:ARG:CG	1:A:251:ARG:HH11	2.32	0.43
1:A:105:TYR:HB3	1:A:106:PRO:HD2	2.01	0.43
1:B:634:GLN:NE2	1:B:682:LEU:O	2.51	0.43
1:A:687:GLN:HA	1:A:688:PRO:HD3	1.82	0.43
1:C:436:MET:HE3	1:C:467:ASN:HD22	1.81	0.43
1:A:360:HIS:HA	1:A:361:PRO:HD3	1.89	0.43
1:B:187:MET:O	1:B:187:MET:HG3	2.19	0.43
1:B:63:PHE:CD1	1:B:63:PHE:N	2.86	0.43
1:B:30:HIS:ND1	1:B:31:PRO:O	2.40	0.43
1:D:257:THR:HA	1:D:270:GLY:O	2.19	0.43
1:D:105:TYR:HB3	1:D:106:PRO:HD2	2.01	0.43
1:C:234:ASP:OD1	1:C:236:SER:OG	2.31	0.43
1:B:622:HIS:HD2	1:B:625:GLN:OE1	2.02	0.43
1:A:570:TRP:CD1	1:A:571:VAL:HG22	2.54	0.43
1:D:622:HIS:HD2	1:D:625:GLN:OE1	2.02	0.43
1:C:840:HIS:ND1	1:C:840:HIS:N	2.67	0.43
1:B:77:ASP:HA	3:B:4178:HOH:O	2.19	0.42
1:A:11:LEU:CD2	1:A:187:MET:HE3	2.45	0.42
1:C:187:MET:O	1:C:187:MET:HG3	2.19	0.42
1:A:822:LEU:HD13	1:A:822:LEU:HA	1.79	0.42
1:A:145:GLY:HA3	1:A:210:ARG:HG3	2.01	0.42
1:B:257:THR:HA	1:B:270:GLY:O	2.19	0.42
1:A:395:HIS:CG	1:A:396:PRO:HD2	2.53	0.42
1:A:354:VAL:HG22	1:A:355:ASN:N	2.34	0.42
1:A:635:THR:HA	1:A:680:ILE:O	2.19	0.42
1:D:634:GLN:NE2	1:D:682:LEU:O	2.51	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:910:LEU:C	1:B:910:LEU:HD12	2.39	0.42
1:B:114:VAL:HA	1:B:115:PRO:HD3	1.77	0.42
1:A:429:ASP:HA	1:A:430:PRO:HD3	1.82	0.42
1:B:787:ALA:HA	1:B:788:PRO:HD3	1.66	0.42
1:D:217:LYS:HB3	1:D:218:PRO:HD2	2.00	0.42
1:B:570:TRP:CD1	1:B:571:VAL:HG22	2.54	0.42
1:D:225:PHE:HA	1:D:243:GLU:O	2.19	0.42
1:D:187:MET:HG3	1:D:187:MET:O	2.19	0.42
1:C:257:THR:HA	1:C:270:GLY:O	2.19	0.42
1:B:635:THR:HA	1:B:680:ILE:O	2.19	0.42
1:A:225:PHE:HA	1:A:243:GLU:O	2.19	0.42
1:A:657:ALA:O	1:A:694:LEU:HD12	2.18	0.42
1:C:367:MET:HB3	1:C:372:MET:CE	2.50	0.42
1:C:183:ARG:HD3	1:C:183:ARG:HH11	1.55	0.42
1:C:822:LEU:HD12	1:C:823:LEU:N	2.34	0.42
1:C:227:VAL:CG1	1:C:240:LEU:HD11	2.48	0.42
1:C:576:ILE:HD13	1:C:584:PRO:HB2	2.02	0.42
1:C:124:SER:HA	1:C:184:LEU:O	2.20	0.42
1:D:479:ASP:HA	1:D:480:PRO:HD2	1.73	0.42
1:A:622:HIS:HD2	1:A:625:GLN:OE1	2.02	0.42
1:D:782:ASP:OD1	1:D:854:LYS:NZ	2.52	0.42
1:B:278:ILE:HD12	1:B:278:ILE:HA	1.88	0.42
1:B:227:VAL:CG1	1:B:228:ALA:N	2.83	0.42
1:A:282:ARG:NH1	1:D:418:HIS:O	2.52	0.42
1:B:737:ILE:HA	1:B:738:PRO:HD3	1.78	0.42
1:D:576:ILE:HD13	1:D:584:PRO:HB2	2.02	0.42
1:C:635:THR:HA	1:C:680:ILE:O	2.19	0.42
1:A:124:SER:HA	1:A:184:LEU:O	2.20	0.42
1:B:52[A]:ARG:HH11	1:B:52[A]:ARG:HD3	1.65	0.42
1:A:255:ARG:CG	1:A:255:ARG:NH1	2.79	0.42
1:A:858:ILE:HG12	1:A:864:MET:HB3	2.02	0.42
1:A:187:MET:HG3	1:A:187:MET:O	2.19	0.42
1:C:742:THR:CG2	1:C:743:SER:H	2.31	0.42
1:D:367:MET:HB3	1:D:372:MET:CE	2.50	0.42
1:C:570:TRP:CD1	1:C:571:VAL:HG22	2.54	0.42
1:D:472:TYR:O	1:D:476:LYS:HG2	2.20	0.42
1:C:274:PHE:HB3	1:C:286:ALA:O	2.20	0.42
1:A:367:MET:HB3	1:A:372:MET:CE	2.50	0.42
1:B:472:TYR:O	1:B:476:LYS:HG2	2.20	0.42
1:C:77:ASP:HA	3:C:4218:HOH:O	2.19	0.42
1:B:360:HIS:HE1	1:B:362:LEU:HB2	1.84	0.42
1:B:105:TYR:HB3	1:B:106:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:105:TYR:HA	1:A:106:PRO:HD3	1.91	0.42
1:C:479:ASP:HA	1:C:480:PRO:HD2	1.73	0.42
1:D:570:TRP:CD1	1:D:571:VAL:HG22	2.54	0.42
1:A:274:PHE:HB3	1:A:286:ALA:O	2.20	0.42
1:D:214:LEU:HD23	1:D:214:LEU:HA	1.61	0.42
1:D:835:LEU:HA	1:D:835:LEU:HD12	1.90	0.42
1:B:685:LEU:CB	1:B:686:PRO:HD2	2.38	0.42
1:C:237:ARG:CB	1:C:237:ARG:NH1	2.78	0.42
1:B:822:LEU:HD12	1:B:823:LEU:N	2.34	0.42
1:D:822:LEU:HD12	1:D:823:LEU:N	2.34	0.42
1:D:251:ARG:CG	1:D:251:ARG:HH11	2.32	0.42
1:C:354:VAL:HG22	1:C:355:ASN:N	2.34	0.42
1:C:757:GLN:HG2	1:C:758:PHE:N	2.31	0.42
1:C:787:ALA:HA	1:C:788:PRO:HD3	1.66	0.42
1:C:622:HIS:HD2	1:C:625:GLN:OE1	2.02	0.42
1:A:910:LEU:HD12	1:A:910:LEU:C	2.39	0.42
1:D:274:PHE:HB3	1:D:286:ALA:O	2.20	0.42
1:D:858:ILE:HG12	1:D:864:MET:HB3	2.02	0.42
1:B:11:LEU:N	1:B:11:LEU:HD23	2.35	0.42
1:C:63:PHE:CB	1:C:64:PRO:CD	2.98	0.42
1:D:202:MET:HE3	1:D:357:HIS:CD2	2.54	0.42
1:C:251:ARG:CG	1:C:251:ARG:HH11	2.32	0.42
1:D:635:THR:HA	1:D:680:ILE:O	2.19	0.42
1:B:217:LYS:HB3	1:B:218:PRO:HD2	2.01	0.42
1:B:274:PHE:HB3	1:B:286:ALA:O	2.20	0.42
1:B:308:LEU:HD23	1:B:308:LEU:HA	1.80	0.42
1:A:424:ASN:HD22	1:A:424:ASN:HA	1.40	0.42
1:D:840:HIS:ND1	1:D:840:HIS:N	2.67	0.42
1:D:856:TYR:CD1	1:D:856:TYR:N	2.88	0.42
1:C:856:TYR:CD1	1:C:856:TYR:N	2.88	0.42
1:D:360:HIS:HE1	1:D:362:LEU:HB2	1.84	0.42
1:A:11:LEU:HD23	1:A:11:LEU:N	2.35	0.42
1:B:3:ILE:C	1:B:5:ASP:H	2.22	0.42
1:C:651:LEU:HD12	1:C:651:LEU:HA	1.46	0.42
1:B:124:SER:HA	1:B:184:LEU:O	2.20	0.42
1:B:441:THR:O	1:B:445:GLN:HG3	2.20	0.42
1:C:474:TRP:CZ2	1:C:478:VAL:HG21	2.55	0.42
1:A:441:THR:O	1:A:445:GLN:HG3	2.20	0.42
1:A:474:TRP:CZ2	1:A:478:VAL:HG21	2.55	0.42
1:D:378:LEU:HD23	1:D:378:LEU:HA	1.75	0.42
1:C:910:LEU:HD12	1:C:910:LEU:C	2.39	0.42
1:C:472:TYR:O	1:C:476:LYS:HG2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:856:TYR:N	1:A:856:TYR:CD1	2.88	0.41
1:A:645:ARG:NH2	1:A:650:GLU:OE2	2.46	0.41
1:B:576:ILE:HD13	1:B:584:PRO:HB2	2.02	0.41
1:D:441:THR:O	1:D:445:GLN:HG3	2.20	0.41
1:A:111:PRO:HA	1:A:112:PRO:HA	1.56	0.41
1:B:262:GLN:HG2	1:B:262:GLN:O	2.19	0.41
1:A:721:ARG:HE	1:B:874:SER:CB	2.32	0.41
1:C:599:ARG:HB2	1:C:600:GLN:H	1.54	0.41
1:A:7:LEU:HA	1:A:7:LEU:HD23	1.85	0.41
1:D:559:TYR:HB2	1:D:562:LEU:CD1	2.47	0.41
1:C:227:VAL:CG1	1:C:228:ALA:N	2.83	0.41
1:C:395:HIS:HA	1:C:396:PRO:HD3	1.83	0.41
1:C:105:TYR:HB3	1:C:106:PRO:HD2	2.01	0.41
1:D:474:TRP:CZ2	1:D:478:VAL:HG21	2.55	0.41
1:D:141:ILE:HG12	1:D:142:ILE:N	2.35	0.41
1:A:757:GLN:HG2	1:A:758:PHE:N	2.31	0.41
1:D:262:GLN:O	1:D:262:GLN:HG2	2.19	0.41
1:A:176:PHE:CD1	1:A:176:PHE:N	2.87	0.41
1:B:176:PHE:N	1:B:176:PHE:CD1	2.87	0.41
1:B:288:ARG:HD3	1:B:288:ARG:HH11	1.48	0.41
1:C:858:ILE:HG12	1:C:864:MET:HB3	2.02	0.41
1:D:835:LEU:HD12	1:D:857:ARG:HB2	2.03	0.41
1:C:578:TYR:HA	1:C:583:ASN:O	2.20	0.41
1:A:524:LEU:O	1:A:561:ARG:NH2	2.50	0.41
1:C:141:ILE:HG12	1:C:142:ILE:N	2.35	0.41
1:A:141:ILE:HG12	1:A:142:ILE:N	2.35	0.41
1:B:23:GLN:HG2	3:B:4413:HOH:O	2.20	0.41
1:D:407:LEU:HD23	1:D:407:LEU:HA	1.86	0.41
1:C:262:GLN:O	1:C:262:GLN:HG2	2.19	0.41
1:B:41:GLU:HG2	1:B:46:ARG:NH1	2.35	0.41
1:D:41:GLU:HG2	1:D:46:ARG:NH1	2.35	0.41
1:A:835:LEU:HD12	1:A:857:ARG:HB2	2.03	0.41
1:B:78:LEU:HA	1:B:79:PRO:HD2	1.58	0.41
1:B:559:TYR:HA	1:B:560:PRO:HD2	1.85	0.41
1:A:63:PHE:CB	1:A:64:PRO:CD	2.98	0.41
1:D:742:THR:CG2	1:D:743:SER:H	2.32	0.41
1:D:524:LEU:O	1:D:561:ARG:NH2	2.50	0.41
1:A:682:LEU:HA	1:A:683:PRO:HD3	1.91	0.41
1:A:892:ALA:HB3	1:A:946:TYR:CE1	2.56	0.41
1:D:892:ALA:HB3	1:D:946:TYR:CE1	2.55	0.41
1:A:23:GLN:HG2	3:A:7533:HOH:O	2.20	0.41
1:B:407:LEU:HD23	1:B:407:LEU:HA	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:250:LEU:HD23	1:B:250:LEU:HA	1.90	0.41
1:A:599:ARG:HB2	1:A:600:GLN:H	1.54	0.41
1:D:77:ASP:HA	3:D:4132:HOH:O	2.19	0.41
1:D:559:TYR:HA	1:D:560:PRO:HD2	1.86	0.41
1:B:63:PHE:CB	1:B:64:PRO:CD	2.98	0.41
1:B:822:LEU:HA	1:B:822:LEU:HD13	1.79	0.41
1:D:124:SER:HA	1:D:184:LEU:O	2.20	0.41
1:D:352:ARG:NH2	1:D:641:GLU:OE1	2.54	0.41
1:B:856:TYR:CD1	1:B:856:TYR:N	2.88	0.41
1:C:11:LEU:N	1:C:11:LEU:HD23	2.35	0.41
1:A:652:LEU:O	1:A:667:GLU:HA	2.20	0.41
1:B:649:ASN:O	1:B:702:GLN:HG3	2.21	0.41
1:B:272:ALA:HA	1:B:273:PRO:HD3	1.88	0.41
1:B:354:VAL:HG22	1:B:355:ASN:N	2.34	0.41
1:C:892:ALA:HB3	1:C:946:TYR:CE1	2.56	0.41
1:B:367:MET:HB3	1:B:372:MET:CE	2.50	0.41
1:C:41:GLU:HG2	1:C:46:ARG:NH1	2.35	0.41
1:C:559:TYR:HB2	1:C:562:LEU:CD1	2.47	0.41
1:A:578:TYR:HA	1:A:583:ASN:O	2.20	0.41
1:B:652:LEU:O	1:B:667:GLU:HA	2.21	0.41
1:C:649:ASN:O	1:C:702:GLN:HG3	2.21	0.41
1:A:380:LYS:HE3	1:A:406:GLY:O	2.21	0.41
1:B:655:MET:O	1:B:696:LEU:HD12	2.21	0.41
1:B:63:PHE:HB3	1:B:64:PRO:CD	2.45	0.41
1:D:63:PHE:CB	1:D:64:PRO:CD	2.98	0.41
1:B:619:GLU:HA	1:B:912:ALA:HB2	2.03	0.41
1:C:26:ARG:HD2	1:C:169:SER:HB3	2.02	0.41
1:C:970:THR:HG22	1:C:972:HIS:O	2.21	0.41
1:B:352:ARG:NH2	1:B:641:GLU:OE1	2.54	0.41
1:C:682:LEU:HA	1:C:683:PRO:HD3	1.91	0.41
1:B:69:VAL:HG13	1:B:70:PRO:HD2	2.03	0.41
1:A:278:ILE:HA	1:A:278:ILE:HD12	1.88	0.41
1:B:892:ALA:HB3	1:B:946:TYR:CE1	2.56	0.41
1:A:949:HIS:CD2	1:A:1020:TRP:NE1	2.79	0.41
1:A:685:LEU:CB	1:A:686:PRO:HD2	2.38	0.41
1:C:511:PRO:HA	1:C:516:PRO:CB	2.51	0.41
1:A:282:ARG:HG3	1:D:423:MET:HB2	2.03	0.41
1:A:227:VAL:CG1	1:A:228:ALA:N	2.83	0.41
1:D:26:ARG:HD2	1:D:169:SER:HB3	2.02	0.41
1:D:127:PHE:CE2	1:D:184:LEU:HG	2.56	0.41
1:C:441:THR:O	1:C:445:GLN:HG3	2.20	0.41
1:D:844:HIS:ND1	1:D:845:GLN:HG2	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:844:HIS:ND1	1:A:845:GLN:HG2	2.36	0.41
1:A:840:HIS:N	1:A:840:HIS:ND1	2.67	0.41
1:A:41:GLU:HG2	1:A:46:ARG:NH1	2.35	0.41
1:B:858:ILE:HG12	1:B:864:MET:HB3	2.02	0.41
1:C:835:LEU:HD12	1:C:857:ARG:HB2	2.03	0.41
1:D:11:LEU:N	1:D:11:LEU:HD23	2.35	0.41
1:D:655:MET:O	1:D:696:LEU:HD12	2.21	0.41
1:D:778:THR:CG2	1:D:779:PRO:CD	2.99	0.41
1:D:778:THR:HG22	1:D:779:PRO:N	2.35	0.41
1:A:778:THR:HG22	1:A:779:PRO:N	2.35	0.41
1:B:778:THR:HG22	1:B:779:PRO:N	2.35	0.41
1:C:652:LEU:O	1:C:667:GLU:HA	2.20	0.41
1:C:380:LYS:HE3	1:C:406:GLY:O	2.21	0.41
1:C:305:ILE:HA	1:C:306:PRO:HD2	1.88	0.41
1:D:649:ASN:O	1:D:702:GLN:HG3	2.21	0.41
1:A:655:MET:O	1:A:696:LEU:HD12	2.21	0.41
1:A:649:ASN:O	1:A:702:GLN:HG3	2.21	0.41
1:A:63:PHE:HB3	1:A:64:PRO:CD	2.45	0.41
1:C:619:GLU:HA	1:C:912:ALA:HB2	2.03	0.41
1:C:524:LEU:O	1:C:561:ARG:NH2	2.50	0.41
1:B:105:TYR:HA	1:B:106:PRO:HD3	1.91	0.41
1:D:168:PRO:O	1:D:442:ARG:NH2	2.48	0.41
1:A:970:THR:HG22	1:A:972:HIS:O	2.21	0.41
1:B:474:TRP:CZ2	1:B:478:VAL:HG21	2.55	0.41
1:A:127:PHE:CE2	1:A:184:LEU:HG	2.56	0.41
1:A:262:GLN:HG2	1:A:262:GLN:O	2.19	0.41
1:D:917:ARG:NH2	1:D:943:GLU:OE1	2.54	0.41
1:B:687:GLN:HA	1:B:688:PRO:HD3	1.81	0.41
1:D:114:VAL:HA	1:D:115:PRO:HD3	1.77	0.41
1:A:472:TYR:O	1:A:476:LYS:HG2	2.20	0.41
1:C:360:HIS:HE1	1:C:362:LEU:HB2	1.84	0.41
1:D:578:TYR:HA	1:D:583:ASN:O	2.21	0.41
1:C:778:THR:HG22	1:C:779:PRO:N	2.35	0.41
1:B:581:ASN:HD22	1:B:583:ASN:ND2	2.19	0.41
1:A:26:ARG:HD2	1:A:169:SER:HB3	2.02	0.41
1:D:970:THR:HG22	1:D:972:HIS:O	2.21	0.41
1:B:287:ASP:CG	1:C:425:ARG:HH22	2.23	0.41
1:B:588:TYR:O	1:B:589:GLY:C	2.59	0.41
1:B:868:VAL:HG12	1:B:869:ASP:N	2.36	0.41
1:A:161:TYR:OH	1:A:163:GLN:NE2	2.50	0.41
1:A:868:VAL:HG12	1:A:869:ASP:N	2.36	0.41
1:D:176:PHE:N	1:D:176:PHE:CD1	2.87	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:378:LEU:HD23	1:A:378:LEU:HA	1.75	0.41
1:B:26:ARG:HD2	1:B:169:SER:HB3	2.02	0.40
1:B:18:ASN:HA	1:B:19:PRO:HD3	1.56	0.40
1:A:576:ILE:HD13	1:A:584:PRO:HB2	2.02	0.40
1:B:141:ILE:HG12	1:B:142:ILE:N	2.35	0.40
1:C:352:ARG:NH2	1:C:641:GLU:OE1	2.54	0.40
1:A:149:ALA:O	1:A:150:PHE:HB3	2.21	0.40
1:D:69:VAL:HG13	1:D:70:PRO:HD2	2.03	0.40
1:B:840:HIS:ND1	1:B:840:HIS:N	2.67	0.40
1:B:579:ASP:CG	1:B:583:ASN:HB2	2.42	0.40
1:B:380:LYS:HE3	1:B:406:GLY:O	2.21	0.40
1:C:762:SER:C	1:C:822:LEU:HD23	2.42	0.40
1:A:272:ALA:CB	1:A:273:PRO:CD	2.99	0.40
1:B:658:LEU:HG	1:B:661:LYS:HZ2	1.86	0.40
1:A:278:ILE:HD13	1:A:278:ILE:N	2.37	0.40
1:D:23:GLN:HG2	3:D:7533:HOH:O	2.20	0.40
1:C:149:ALA:O	1:C:150:PHE:HB3	2.21	0.40
1:A:917:ARG:NH2	1:A:943:GLU:OE1	2.54	0.40
1:C:23:GLN:HG2	3:C:4454:HOH:O	2.20	0.40
1:B:214:LEU:HD23	1:B:214:LEU:HA	1.61	0.40
1:D:3:ILE:C	1:D:5:ASP:H	2.22	0.40
1:B:272:ALA:CB	1:B:273:PRO:CD	2.99	0.40
1:B:780:LEU:HD12	1:B:780:LEU:HA	1.89	0.40
1:C:89:ASN:O	1:C:92:MET:HB2	2.21	0.40
1:A:502:MET:HA	1:A:537:GLU:O	2.22	0.40
1:D:149:ALA:O	1:D:150:PHE:HB3	2.21	0.40
1:C:502:MET:HA	1:C:537:GLU:O	2.22	0.40
1:A:588:TYR:O	1:A:589:GLY:C	2.59	0.40
1:C:407:LEU:HD23	1:C:407:LEU:HA	1.86	0.40
1:C:38:ASN:HD21	1:C:41:GLU:N	2.17	0.40
1:B:578:TYR:HA	1:B:583:ASN:O	2.21	0.40
1:D:702:GLN:O	1:D:712:GLY:N	2.50	0.40
1:C:65:ALA:CB	1:C:66:PRO:CD	3.00	0.40
1:A:762:SER:C	1:A:822:LEU:HD23	2.42	0.40
1:C:128:ASN:HD22	1:C:180:GLY:C	2.25	0.40
1:D:227:VAL:CG1	1:D:240:LEU:HD11	2.48	0.40
1:A:147:ASN:HA	1:A:148:SER:HA	1.65	0.40
1:A:90:TRP:NE1	1:A:96:ASP:OD1	2.55	0.40
1:B:970:THR:HG22	1:B:972:HIS:O	2.21	0.40
1:D:868:VAL:HG12	1:D:869:ASP:N	2.36	0.40
1:D:89:ASN:O	1:D:92:MET:HB2	2.22	0.40
1:A:244:VAL:O	1:A:288:ARG:HA	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:100:TYR:O	1:A:597:ASN:HB2	2.22	0.40
1:C:579:ASP:CG	1:C:583:ASN:HB2	2.42	0.40
1:C:559:TYR:HA	1:C:560:PRO:HD2	1.86	0.40
1:D:237:ARG:NH1	1:D:237:ARG:CB	2.79	0.40
1:C:702:GLN:O	1:C:712:GLY:N	2.50	0.40
1:A:128:ASN:HD22	1:A:180:GLY:C	2.25	0.40
1:D:619:GLU:HA	1:D:912:ALA:HB2	2.03	0.40
1:B:90:TRP:CD1	1:B:90:TRP:C	2.95	0.40
1:C:486:TYR:CE2	1:C:488:GLY:HA3	2.56	0.40
1:B:844:HIS:ND1	1:B:845:GLN:HG2	2.36	0.40
1:C:868:VAL:HG12	1:C:869:ASP:N	2.36	0.40
1:C:244:VAL:O	1:C:288:ARG:HA	2.22	0.40
1:C:917:ARG:NH2	1:C:943:GLU:OE1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1026/1021 (100%)	953 (93%)	67 (6%)	6 (1%)	33	72
1	B	1026/1021 (100%)	953 (93%)	67 (6%)	6 (1%)	33	72
1	C	1026/1021 (100%)	953 (93%)	67 (6%)	6 (1%)	33	72
1	D	1026/1021 (100%)	953 (93%)	67 (6%)	6 (1%)	33	72
All	All	4104/4084 (100%)	3812 (93%)	268 (6%)	24 (1%)	33	72

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	647	SER
1	B	647	SER
1	C	647	SER
1	D	647	SER
1	A	77	ASP

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Mol	Chain	Res	Type
1	A	601	PHE
1	B	77	ASP
1	B	601	PHE
1	C	77	ASP
1	C	601	PHE
1	D	77	ASP
1	D	601	PHE
1	A	164	ASP
1	B	164	ASP
1	C	164	ASP
1	D	164	ASP
1	A	690	SER
1	B	690	SER
1	C	690	SER
1	D	690	SER
1	A	10	VAL
1	B	10	VAL
1	C	10	VAL
1	D	10	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	880/873 (101%)	755 (86%)	125 (14%)	5	14
1	B	880/873 (101%)	755 (86%)	125 (14%)	5	14
1	C	880/873 (101%)	755 (86%)	125 (14%)	5	14
1	D	880/873 (101%)	755 (86%)	125 (14%)	5	14
All	All	3520/3492 (101%)	3020 (86%)	500 (14%)	5	14

All (500) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	12	GLN
1	A	24	LEU

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Mol	Chain	Res	Type
1	A	37	ARG
1	A	38	ASN
1	A	39	SER
1	A	49	GLN
1	A	67	GLU
1	A	71	GLU
1	A	72	SER
1	A	80	GLU
1	A	85	VAL
1	A	90	TRP
1	A	102	ASN
1	A	114	VAL
1	A	116	THR
1	A	134	LEU
1	A	135	GLN
1	A	136	GLU
1	A	138	GLN
1	A	148	SER
1	A	169	SER
1	A	187	MET
1	A	190	ARG
1	A	202	MET
1	A	210	ARG
1	A	211	ASP
1	A	214	LEU
1	A	219	THR
1	A	223	SER
1	A	230	ARG
1	A	237	ARG
1	A	246	MET
1	A	249	GLU
1	A	251	ARG
1	A	255	ARG
1	A	259	SER
1	A	269	SER
1	A	277	GLU
1	A	278	ILE
1	A	279	ILE
1	A	282	ARG
1	A	288	ARG
1	A	310	ARG
1	A	322	LEU

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Mol	Chain	Res	Type
1	A	333	ARG
1	A	347	LYS
1	A	385	ASN
1	A	394	ASN
1	A	424	ASN
1	A	425	ARG
1	A	437	SER
1	A	448	ARG
1	A	473	ARG
1	A	481	SER
1	A	519	SER
1	A	521	LYS
1	A	525	SER
1	A	526	LEU
1	A	529	GLU
1	A	533	LEU
1	A	545	SER
1	A	546	LEU
1	A	554	GLN
1	A	571	VAL
1	A	576	ILE
1	A	580	GLU
1	A	581	ASN
1	A	600	GLN
1	A	645	ARG
1	A	647	SER
1	A	655	MET
1	A	661	LYS
1	A	665	SER
1	A	672	VAL
1	A	675	GLN
1	A	687	GLN
1	A	690	SER
1	A	719	GLN
1	A	721	ARG
1	A	728	VAL
1	A	730	LEU
1	A	734	SER
1	A	737	ILE
1	A	743	SER
1	A	746	ASP
1	A	750	GLU

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Mol	Chain	Res	Type
1	A	755	ARG
1	A	761	GLN
1	A	765	LEU
1	A	766	SER
1	A	768	MET
1	A	770	ILE
1	A	772	ASP
1	A	773	LYS
1	A	774	LYS
1	A	797	GLU
1	A	800	ARG
1	A	801	ILE
1	A	811	LYS
1	A	817	GLN
1	A	822	LEU
1	A	824	GLN
1	A	830	LEU
1	A	843	GLN
1	A	845	GLN
1	A	856	TYR
1	A	857	ARG
1	A	867	THR
1	A	874	SER
1	A	881	ARG
1	A	894	ARG
1	A	917	ARG
1	A	923	SER
1	A	931	PHE
1	A	938	ARG
1	A	950	GLN
1	A	958	ASN
1	A	969	GLU
1	A	986	ILE
1	A	991	MET
1	A	1004	SER
1	A	1006	GLU
1	A	1017	GLN
1	A	1023	LYS
1	B	3	ILE
1	B	12	GLN
1	B	24	LEU
1	B	37	ARG

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Mol	Chain	Res	Type
1	B	38	ASN
1	B	39	SER
1	B	49	GLN
1	B	67	GLU
1	B	71	GLU
1	B	72	SER
1	B	80	GLU
1	B	85	VAL
1	B	90	TRP
1	B	102	ASN
1	B	114	VAL
1	B	116	THR
1	B	134	LEU
1	B	135	GLN
1	B	136	GLU
1	B	138	GLN
1	B	148	SER
1	B	169	SER
1	B	187	MET
1	B	190	ARG
1	B	202	MET
1	B	210	ARG
1	B	211	ASP
1	B	214	LEU
1	B	219	THR
1	B	223	SER
1	B	230	ARG
1	B	237	ARG
1	B	246	MET
1	B	249	GLU
1	B	251	ARG
1	B	255	ARG
1	B	259	SER
1	B	269	SER
1	B	277	GLU
1	B	278	ILE
1	B	279	ILE
1	B	282	ARG
1	B	288	ARG
1	B	310	ARG
1	B	322	LEU
1	B	333	ARG

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Mol	Chain	Res	Type
1	B	347	LYS
1	B	385	ASN
1	B	394	ASN
1	B	424	ASN
1	B	425	ARG
1	B	437	SER
1	B	448	ARG
1	B	473	ARG
1	B	481	SER
1	B	519	SER
1	B	521	LYS
1	B	525	SER
1	B	526	LEU
1	B	529	GLU
1	B	533	LEU
1	B	545	SER
1	B	546	LEU
1	B	554	GLN
1	B	571	VAL
1	B	576	ILE
1	B	580	GLU
1	B	581	ASN
1	B	600	GLN
1	B	645	ARG
1	B	647	SER
1	B	655	MET
1	B	661	LYS
1	B	665	SER
1	B	672	VAL
1	B	675	GLN
1	B	687	GLN
1	B	690	SER
1	B	719	GLN
1	B	721	ARG
1	B	728	VAL
1	B	730	LEU
1	B	734	SER
1	B	737	ILE
1	B	743	SER
1	B	746	ASP
1	B	750	GLU
1	B	755	ARG

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Mol	Chain	Res	Type
1	B	761	GLN
1	B	765	LEU
1	B	766	SER
1	B	768	MET
1	B	770	ILE
1	B	772	ASP
1	B	773	LYS
1	B	774	LYS
1	B	797	GLU
1	B	800	ARG
1	B	801	ILE
1	B	811	LYS
1	B	817	GLN
1	B	822	LEU
1	B	824	GLN
1	B	830	LEU
1	B	843	GLN
1	B	845	GLN
1	B	856	TYR
1	B	857	ARG
1	B	867	THR
1	B	874	SER
1	B	881	ARG
1	B	894	ARG
1	B	917	ARG
1	B	923	SER
1	B	931	PHE
1	B	938	ARG
1	B	950	GLN
1	B	958	ASN
1	B	969	GLU
1	B	986	ILE
1	B	991	MET
1	B	1004	SER
1	B	1006	GLU
1	B	1017	GLN
1	B	1023	LYS
1	C	3	ILE
1	C	12	GLN
1	C	24	LEU
1	C	37	ARG
1	C	38	ASN

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Mol	Chain	Res	Type
1	C	39	SER
1	C	49	GLN
1	C	67	GLU
1	C	71	GLU
1	C	72	SER
1	C	80	GLU
1	C	85	VAL
1	C	90	TRP
1	C	102	ASN
1	C	114	VAL
1	C	116	THR
1	C	134	LEU
1	C	135	GLN
1	C	136	GLU
1	C	138	GLN
1	C	148	SER
1	C	169	SER
1	C	187	MET
1	C	190	ARG
1	C	202	MET
1	C	210	ARG
1	C	211	ASP
1	C	214	LEU
1	C	219	THR
1	C	223	SER
1	C	230	ARG
1	C	237	ARG
1	C	246	MET
1	C	249	GLU
1	C	251	ARG
1	C	255	ARG
1	C	259	SER
1	C	269	SER
1	C	277	GLU
1	C	278	ILE
1	C	279	ILE
1	C	282	ARG
1	C	288	ARG
1	C	310	ARG
1	C	322	LEU
1	C	333	ARG
1	C	347	LYS

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Mol	Chain	Res	Type
1	C	385	ASN
1	C	394	ASN
1	C	424	ASN
1	C	425	ARG
1	C	437	SER
1	C	448	ARG
1	C	473	ARG
1	C	481	SER
1	C	519	SER
1	C	521	LYS
1	C	525	SER
1	C	526	LEU
1	C	529	GLU
1	C	533	LEU
1	C	545	SER
1	C	546	LEU
1	C	554	GLN
1	C	571	VAL
1	C	576	ILE
1	C	580	GLU
1	C	581	ASN
1	C	600	GLN
1	C	645	ARG
1	C	647	SER
1	C	655	MET
1	C	661	LYS
1	C	665	SER
1	C	672	VAL
1	C	675	GLN
1	C	687	GLN
1	C	690	SER
1	C	719	GLN
1	C	721	ARG
1	C	728	VAL
1	C	730	LEU
1	C	734	SER
1	C	737	ILE
1	C	743	SER
1	C	746	ASP
1	C	750	GLU
1	C	755	ARG
1	C	761	GLN

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Mol	Chain	Res	Type
1	C	765	LEU
1	C	766	SER
1	C	768	MET
1	C	770	ILE
1	C	772	ASP
1	C	773	LYS
1	C	774	LYS
1	C	797	GLU
1	C	800	ARG
1	C	801	ILE
1	C	811	LYS
1	C	817	GLN
1	C	822	LEU
1	C	824	GLN
1	C	830	LEU
1	C	843	GLN
1	C	845	GLN
1	C	856	TYR
1	C	857	ARG
1	C	867	THR
1	C	874	SER
1	C	881	ARG
1	C	894	ARG
1	C	917	ARG
1	C	923	SER
1	C	931	PHE
1	C	938	ARG
1	C	950	GLN
1	C	958	ASN
1	C	969	GLU
1	C	986	ILE
1	C	991	MET
1	C	1004	SER
1	C	1006	GLU
1	C	1017	GLN
1	C	1023	LYS
1	D	3	ILE
1	D	12	GLN
1	D	24	LEU
1	D	37	ARG
1	D	38	ASN
1	D	39	SER

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Mol	Chain	Res	Type
1	D	49	GLN
1	D	67	GLU
1	D	71	GLU
1	D	72	SER
1	D	80	GLU
1	D	85	VAL
1	D	90	TRP
1	D	102	ASN
1	D	114	VAL
1	D	116	THR
1	D	134	LEU
1	D	135	GLN
1	D	136	GLU
1	D	138	GLN
1	D	148	SER
1	D	169	SER
1	D	187	MET
1	D	190	ARG
1	D	202	MET
1	D	210	ARG
1	D	211	ASP
1	D	214	LEU
1	D	219	THR
1	D	223	SER
1	D	230	ARG
1	D	237	ARG
1	D	246	MET
1	D	249	GLU
1	D	251	ARG
1	D	255	ARG
1	D	259	SER
1	D	269	SER
1	D	277	GLU
1	D	278	ILE
1	D	279	ILE
1	D	282	ARG
1	D	288	ARG
1	D	310	ARG
1	D	322	LEU
1	D	333	ARG
1	D	347	LYS
1	D	385	ASN

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Mol	Chain	Res	Type
1	D	394	ASN
1	D	424	ASN
1	D	425	ARG
1	D	437	SER
1	D	448	ARG
1	D	473	ARG
1	D	481	SER
1	D	519	SER
1	D	521	LYS
1	D	525	SER
1	D	526	LEU
1	D	529	GLU
1	D	533	LEU
1	D	545	SER
1	D	546	LEU
1	D	554	GLN
1	D	571	VAL
1	D	576	ILE
1	D	580	GLU
1	D	581	ASN
1	D	600	GLN
1	D	645	ARG
1	D	647	SER
1	D	655	MET
1	D	661	LYS
1	D	665	SER
1	D	672	VAL
1	D	675	GLN
1	D	687	GLN
1	D	690	SER
1	D	719	GLN
1	D	721	ARG
1	D	728	VAL
1	D	730	LEU
1	D	734	SER
1	D	737	ILE
1	D	743	SER
1	D	746	ASP
1	D	750	GLU
1	D	755	ARG
1	D	761	GLN
1	D	765	LEU

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Mol	Chain	Res	Type
1	D	766	SER
1	D	768	MET
1	D	770	ILE
1	D	772	ASP
1	D	773	LYS
1	D	774	LYS
1	D	797	GLU
1	D	800	ARG
1	D	801	ILE
1	D	811	LYS
1	D	817	GLN
1	D	822	LEU
1	D	824	GLN
1	D	830	LEU
1	D	843	GLN
1	D	845	GLN
1	D	856	TYR
1	D	857	ARG
1	D	867	THR
1	D	874	SER
1	D	881	ARG
1	D	894	ARG
1	D	917	ARG
1	D	923	SER
1	D	931	PHE
1	D	938	ARG
1	D	950	GLN
1	D	958	ASN
1	D	969	GLU
1	D	986	ILE
1	D	991	MET
1	D	1004	SER
1	D	1006	GLU
1	D	1017	GLN
1	D	1023	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	50	GLN
1	A	102	ASN

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Mol	Chain	Res	Type
1	A	128	ASN
1	A	163	GLN
1	A	216	HIS
1	A	226	HIS
1	A	316	HIS
1	A	357	HIS
1	A	385	ASN
1	A	424	ASN
1	A	467	ASN
1	A	554	GLN
1	A	581	ASN
1	A	597	ASN
1	A	604	ASN
1	A	622	HIS
1	A	624	GLN
1	A	634	GLN
1	A	817	GLN
1	A	890	GLN
1	A	949	HIS
1	A	990	HIS
1	A	1017	GLN
1	B	38	ASN
1	B	50	GLN
1	B	102	ASN
1	B	128	ASN
1	B	163	GLN
1	B	216	HIS
1	B	226	HIS
1	B	316	HIS
1	B	357	HIS
1	B	385	ASN
1	B	424	ASN
1	B	467	ASN
1	B	554	GLN
1	B	581	ASN
1	B	597	ASN
1	B	604	ASN
1	B	622	HIS
1	B	624	GLN
1	B	634	GLN
1	B	817	GLN
1	B	890	GLN

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Mol	Chain	Res	Type
1	B	949	HIS
1	B	990	HIS
1	B	1017	GLN
1	C	38	ASN
1	C	50	GLN
1	C	102	ASN
1	C	128	ASN
1	C	216	HIS
1	C	226	HIS
1	C	316	HIS
1	C	357	HIS
1	C	385	ASN
1	C	424	ASN
1	C	467	ASN
1	C	554	GLN
1	C	581	ASN
1	C	597	ASN
1	C	604	ASN
1	C	622	HIS
1	C	624	GLN
1	C	634	GLN
1	C	817	GLN
1	C	890	GLN
1	C	949	HIS
1	C	990	HIS
1	C	1017	GLN
1	D	38	ASN
1	D	50	GLN
1	D	102	ASN
1	D	128	ASN
1	D	216	HIS
1	D	226	HIS
1	D	316	HIS
1	D	357	HIS
1	D	385	ASN
1	D	424	ASN
1	D	467	ASN
1	D	554	GLN
1	D	581	ASN
1	D	597	ASN
1	D	604	ASN
1	D	622	HIS

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Mol	Chain	Res	Type
1	D	624	GLN
1	D	634	GLN
1	D	817	GLN
1	D	890	GLN
1	D	949	HIS
1	D	990	HIS
1	D	1017	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1021/1021 (100%)	-0.93	6 (0%) 86 88	8, 29, 70, 100	19 (1%)
1	B	1021/1021 (100%)	-0.91	4 (0%) 90 91	8, 29, 70, 100	19 (1%)
1	C	1021/1021 (100%)	-0.96	3 (0%) 91 93	8, 29, 70, 100	19 (1%)
1	D	1021/1021 (100%)	-0.94	4 (0%) 90 91	8, 29, 70, 100	19 (1%)
All	All	4084/4084 (100%)	-0.93	17 (0%) 90 91	8, 29, 71, 100	76 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	732	ALA	4.1
1	D	732	ALA	4.0
1	C	732	ALA	3.5
1	B	732	ALA	3.5
1	C	581	ASN	3.3
1	A	581	ASN	3.1
1	A	801	ILE	3.1
1	B	583	ASN	2.7
1	A	733	ALA	2.7
1	D	733	ALA	2.6
1	A	734	SER	2.5
1	A	730	LEU	2.4
1	D	582	GLY	2.2
1	D	734	SER	2.1
1	B	745	MET	2.1
1	B	731	PRO	2.1
1	C	731	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MG	D	3002	1/1	0.10	1.45	31,31,31,31	0
2	MG	A	3002	1/1	0.10	1.43	31,31,31,31	0
2	MG	C	3002	1/1	0.09	-0.23	31,31,31,31	0
2	MG	B	3002	1/1	0.08	-0.84	31,31,31,31	0
2	MG	B	3001	1/1	0.07	-1.29	28,28,28,28	0
2	MG	D	3001	1/1	0.07	-1.90	28,28,28,28	0
2	MG	A	3001	1/1	0.06	-2.22	28,28,28,28	0
2	MG	C	3001	1/1	0.04	-2.31	28,28,28,28	0

6.5 Other polymers

There are no such residues in this entry.