



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2017 – 08:47 AM EDT

PDB ID : 5Y7O  
Title : Crystal structure of folding sensor region of UGGT from *Thermomyces dubon-  
tii*  
Authors : Satoh, T.; Song, C.; Zhu, T.; Toshimori, T.; Murata, K.; Hayashi, Y.;  
Kamikubo, H.; Uchihashi, T.; Kato, K.  
Deposited on : unknown  
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

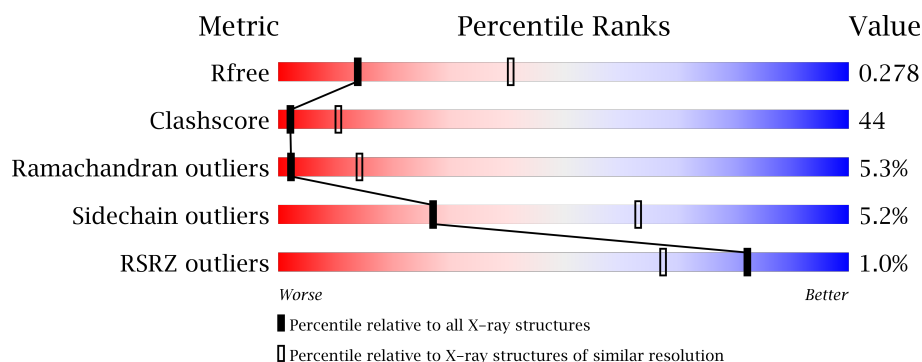
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1130	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; right: 0;">%</div> <div style="position: absolute; top: 10px; left: 0; right: 0;">29% 44% 6% • 19%</div> </div> </div>
1	B	1130	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; right: 0;">%</div> <div style="position: absolute; top: 10px; left: 0; right: 0;">29% 45% 6% • 19%</div> </div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14318 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

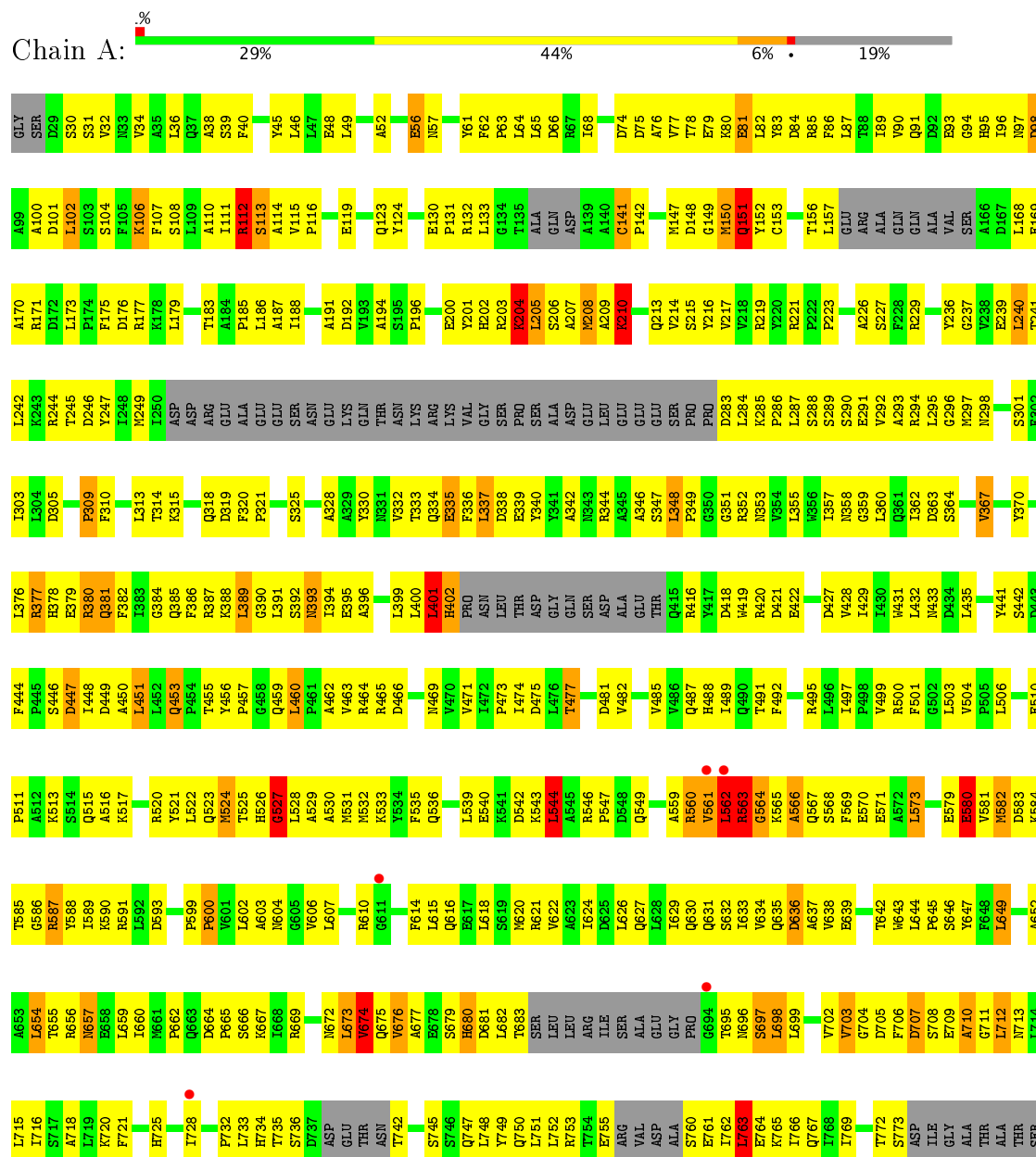
- Molecule 1 is a protein called UGGT.

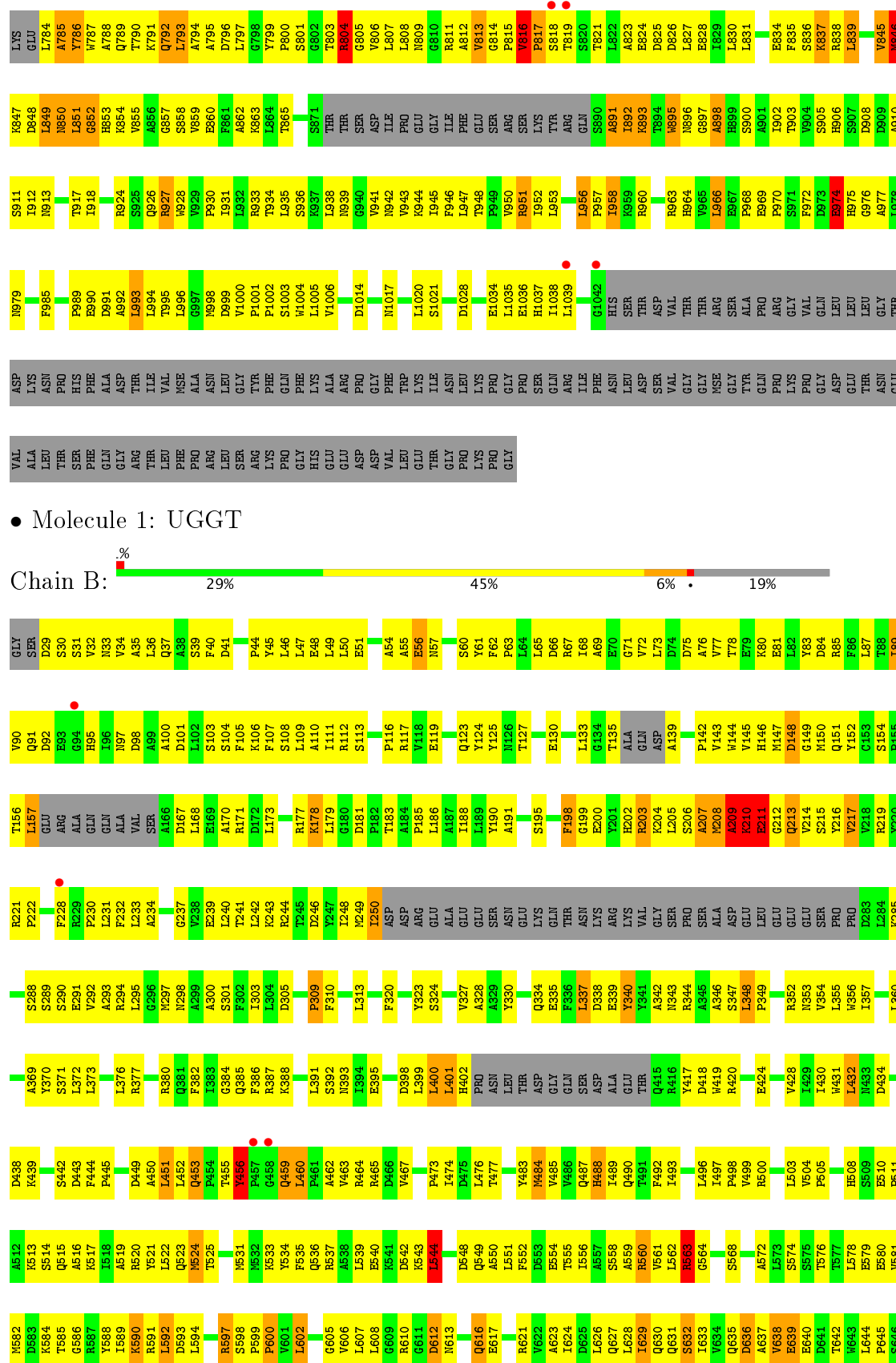
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	913	Total	C	N	O	S	Se	0	0	0
			7159	4556	1224	1362	2	15			
1	B	913	Total	C	N	O	S	Se	0	0	0
			7159	4556	1224	1362	2	15			

### 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 the various outlier classes 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: UGGT





LEU	ASP	SER	VAL	GLY	MSE	GLY	TYR	GLN	PRO	PRO	LYS	GLY	ASP	GLU	ASN	GLU	GLY	ASP	VAL	PRO	PRO	GLY																																							
SER	THR	ASP	VAL	THR	ARG	SER	ALA	ALA	PRO	ARG	GLY	VAL	GLN	ASP	LEU	LEU	LEU	THR	ASN	GLU	VAL	ALA																																							
H975	G976	A977	L978	N979	R980	S986	R987	L988	P989	E990	D991	A992	L993	L994	T995	L996	G997	M998	D999	V1000	P1001	P1002	L1003	W1004	L1005	V1006	S1007	P1008	K1009	E1010	L1015	R1019	L1020	S1021	S1022	L1023	R1024	E1025	G1026	S1027	D1028	V1029	D1030	A1031	I1032	Y1033	E1034	L1035	PRO	GLY	PRO	GLY	THR	GLY	PRO	LYS	PRO	PRO	GLY	HIS	
S905	H906	D909	A910	S911	I912	N913	D848	N850	L851	G852	H853	K854	S855	A856	G857	S858	F861	R827	W828	V929	P930	I931	L932	R933	T934	L938	N939	G940	V941	N942	V943	I945	F946	L947	T948	R951	I952	L953	L956	P957	I958	K959	R960	F961	Y962	L966	E969	P970	S971	F972	D973	E974									
L839	Y842	V845	M846	K847	D848	L849	N850	L851	G852	H853	K854	S855	A856	G857	S858	F861	R827	W828	V929	P930	I931	L932	R933	T934	L938	N939	G940	V941	N942	V943	I945	F946	L947	T948	R951	I952	L953	L956	P957	I958	K959	R960	F961	Y962	L966	E969	P970	S971	F972	D973	E974										
ILE	GLY	ALA	THR	ALA	THR	SER	LYS	GLU	L784	A785	Y786	A787	A788	Q789	K791	Q792	L793	A794	A795	D796	L797	G798	Y799	F800	S801	THR	ASN	R802	H743	T742	H743	G744	S745	W746	Q747	L748	Y749	Q750	ARG	R811	A812	W813	H753	T754	E755	ARG	P817	S818	T819	S820	T821	E824	D825	D826	I829	Y833	E834	F835	S836	K837	R838
Y647	F648	L649	S650	Q651	A652	T655	R656	N657	E658	L659	T660	H661	D664	P665	S666	G667	L668	N672	L673	V674	Q675	V676	A677	E678	S679	H680	T683	SER	LEU	LEU	ARG	ILE	SER	ALA	GLY	PRO	V694	T695	N696	S697	L698	W700	V703	E704	D705	F706	D707	S708	E709	A710	E711										
L712	N713	L714	L715	I716	S717	A718	L719	K720	F721	R722	L723	A724	H725	T728	E729	V730	L733	H734	T735	S736	D737	ASP	GLU	THR	ASN	H743	T742	H743	G744	S745	W746	Q747	L748	Y749	Q750	ARG	R811	A812	W813	H753	T754	E755	ARG	P817	S818	T819	S820	T821	E824	D825	D826	I829	Y833	E834	F835	S836	K837	R838			

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	195.09Å 195.09Å 142.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.97 – 3.10 19.97 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.97-3.10) 98.0 (19.97-3.10)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.37 (at 3.09Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.232 , 0.278 0.232 , 0.278	Depositor DCC
$R_{free}$ test set	2730 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	110.4	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 108.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.55$ , $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	0.478 for -h,-k,l	Xtriage
Reported twinning fraction	0.500 for -h,-k,l	Depositor
Outliers	0 of 54601 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	14318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.66	3/7286 (0.0%)	1.09	30/9871 (0.3%)
1	B	0.62	3/7286 (0.0%)	1.02	29/9871 (0.3%)
All	All	0.64	6/14572 (0.0%)	1.05	59/19742 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	14
1	B	0	9
All	All	0	23

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	211	GLU	CB-CG	-8.01	1.36	1.52
1	B	209	ALA	CA-CB	-7.33	1.37	1.52
1	A	895	TRP	CB-CG	-7.16	1.37	1.50
1	B	211	GLU	CG-CD	-6.12	1.42	1.51
1	A	563	ARG	CG-CD	-5.51	1.38	1.51
1	A	141	CYS	CB-SG	-5.06	1.73	1.81

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	LEU	CB-CG-CD2	-18.33	79.83	111.00
1	A	763	LEU	CB-CG-CD1	-13.06	88.80	111.00
1	A	205	LEU	CA-CB-CG	-8.87	94.90	115.30
1	A	573	LEU	CB-CG-CD2	-8.71	96.20	111.00
1	A	564	GLY	N-CA-C	8.65	134.73	113.10
1	A	401	LEU	CB-CG-CD1	8.59	125.61	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	664	ASP	C-N-CD	8.12	145.46	128.40
1	A	102	LEU	CB-CG-CD1	-8.12	97.19	111.00
1	B	211	GLU	CA-CB-CG	-7.64	96.59	113.40
1	B	401	LEU	CA-CB-CG	7.44	132.41	115.30
1	B	210	LYS	CD-CE-NZ	-7.35	94.80	111.70
1	B	674	VAL	N-CA-C	-7.29	91.33	111.00
1	A	573	LEU	CA-CB-CG	7.13	131.70	115.30
1	A	451	LEU	CA-CB-CG	7.06	131.53	115.30
1	A	401	LEU	CA-CB-CG	6.95	131.29	115.30
1	B	544	LEU	CA-CB-CG	6.86	131.08	115.30
1	A	664	ASP	C-N-CD	6.79	142.65	128.40
1	B	337	LEU	CA-CB-CG	6.71	130.73	115.30
1	A	698	LEU	CA-CB-CG	6.68	130.66	115.30
1	A	804	ARG	N-CA-C	6.59	128.78	111.00
1	A	562	LEU	CB-CG-CD1	-6.37	100.17	111.00
1	A	377	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	B	751	LEU	CB-CG-CD1	6.31	121.73	111.00
1	A	895	TRP	N-CA-C	6.25	127.89	111.00
1	B	743	HIS	N-CA-C	6.24	127.86	111.00
1	B	456	TYR	C-N-CD	6.23	141.48	128.40
1	B	563	ARG	CG-CD-NE	6.14	124.69	111.80
1	A	527	GLY	N-CA-C	6.03	128.18	113.10
1	A	846	MSE	CA-CB-CG	5.97	123.45	113.30
1	B	751	LEU	CA-CB-CG	5.96	129.02	115.30
1	A	956	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	893	LYS	CD-CE-NZ	-5.70	98.59	111.70
1	B	157	LEU	CA-CB-CG	5.67	128.33	115.30
1	A	337	LEU	N-CA-C	5.64	126.23	111.00
1	B	592	LEU	CB-CG-CD2	-5.59	101.49	111.00
1	B	602	LEU	CA-CB-CG	-5.59	102.44	115.30
1	A	895	TRP	CB-CA-C	-5.57	99.26	110.40
1	B	974	GLU	N-CA-C	-5.55	96.02	111.00
1	B	400	LEU	CA-CB-CG	-5.47	102.73	115.30
1	A	204	LYS	CA-CB-CG	5.40	125.28	113.40
1	A	113	SER	N-CA-C	5.38	125.52	111.00
1	B	978	LEU	CA-CB-CG	5.31	127.52	115.30
1	A	102	LEU	CA-CB-CG	5.31	127.50	115.30
1	A	563	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	B	563	ARG	CB-CG-CD	5.29	125.36	111.60
1	B	560	ARG	CB-CG-CD	5.26	125.27	111.60
1	B	451	LEU	N-CA-C	-5.25	96.84	111.00
1	B	798	GLY	N-CA-C	-5.24	100.00	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	664	ASP	C-N-CA	-5.22	100.06	122.00
1	A	649	LEU	CB-CG-CD2	-5.17	102.20	111.00
1	A	956	LEU	CB-CG-CD2	-5.16	102.22	111.00
1	A	682	LEU	CA-CB-CG	5.15	127.14	115.30
1	B	719	LEU	CA-CB-CG	-5.13	103.49	115.30
1	B	839	LEU	CA-CB-CG	5.13	127.09	115.30
1	B	810	GLY	N-CA-C	-5.12	100.29	113.10
1	B	340	TYR	CA-CB-CG	-5.09	103.72	113.40
1	B	456	TYR	CB-CA-C	-5.05	100.30	110.40
1	B	976	GLY	N-CA-C	5.05	125.73	113.10
1	A	240	LEU	CA-CB-CG	-5.03	103.74	115.30

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	MSE	Peptide
1	A	151	GLN	Peptide
1	A	204	LYS	Peptide
1	A	391	LEU	Peptide
1	A	456	TYR	Peptide
1	A	562	LEU	Peptide
1	A	580	GLU	Peptide
1	A	816	VAL	Peptide
1	A	845	VAL	Peptide
1	A	846	MSE	Peptide
1	A	849	LEU	Peptide
1	A	852	GLY	Peptide
1	A	891	ALA	Peptide
1	A	974	GLU	Peptide
1	B	198	PHE	Peptide
1	B	207	ALA	Peptide
1	B	208	MSE	Peptide
1	B	209	ALA	Peptide
1	B	210	LYS	Peptide
1	B	211	GLU	Peptide
1	B	638	VAL	Peptide
1	B	743	HIS	Peptide
1	B	820	SER	Peptide

## 5.2 Too-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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7159	0	7156	685	0
1	B	7159	0	7156	576	1
All	All	14318	0	14312	1254	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 44.

All (1254) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:VAL:HG22	1:A:804:ARG:HH11	1.15	1.10
1:A:380:ARG:HH11	1:A:912:ILE:HD12	1.02	1.07
1:B:210:LYS:HB2	1:B:211:GLU:HG2	1.11	1.06
1:A:433:ASN:HD22	1:A:500:ARG:HA	1.21	1.04
1:B:420:ARG:HE	1:B:649:LEU:HD21	1.22	1.00
1:A:380:ARG:NH1	1:A:912:ILE:HD12	1.78	0.97
1:A:703:VAL:HG13	1:A:804:ARG:HE	1.27	0.95
1:B:453:GLN:HA	1:B:453:GLN:HE21	1.31	0.94
1:B:613:ASN:OD1	1:B:616:GLN:NE2	2.01	0.94
1:A:386:PHE:HA	1:A:388:LYS:HE2	1.50	0.94
1:B:385:GLN:HA	1:B:388:LYS:HD2	1.48	0.94
1:A:913:ASN:HA	1:A:942:ASN:OD1	1.68	0.94
1:B:845:VAL:HA	1:B:848:ASP:HB2	1.46	0.94
1:A:748:LEU:HD12	1:A:751:LEU:HD21	1.52	0.92
1:B:202:HIS:O	1:B:206:SER:N	2.03	0.92
1:A:378:HIS:HA	1:A:381:GLN:HE22	1.34	0.91
1:A:809:ASN:HB3	1:A:839:LEU:HD11	1.52	0.91
1:B:170:ALA:HB1	1:B:186:LEU:HD23	1.50	0.91
1:A:200:GLU:OE1	1:A:203:ARG:NH1	2.02	0.91
1:A:813:VAL:HG23	1:A:814:GLY:H	1.35	0.90
1:B:918:ILE:HD13	1:B:945:ILE:HG23	1.54	0.90
1:B:452:LEU:O	1:B:453:GLN:NE2	2.02	0.90
1:A:151:GLN:HG2	1:A:152:TYR:H	1.36	0.89
1:B:211:GLU:HG3	1:B:212:GLY:N	1.86	0.89
1:A:559:ALA:HB1	1:A:563:ARG:HA	1.52	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:522:LEU:HD23	1:B:531:MSE:HA	1.54	0.88
1:B:249:MSE:SE	1:B:292:VAL:HG21	2.24	0.88
1:B:519:ALA:HB1	1:B:531:MSE:HE3	1.56	0.88
1:A:339:GLU:HA	1:A:342:ALA:HB3	1.54	0.87
1:A:716:ILE:HG22	1:A:767:GLN:HE21	1.39	0.87
1:B:108:SER:HA	1:B:373:LEU:HD21	1.56	0.87
1:A:388:LYS:HD2	1:A:389:LEU:HD13	1.57	0.86
1:A:710:ALA:HA	1:A:713:ASN:HB2	1.58	0.86
1:A:111:ILE:O	1:A:113:SER:N	2.08	0.86
1:A:956:LEU:HD12	1:A:957:PRO:HD2	1.57	0.85
1:A:847:LYS:NZ	1:A:854:LYS:H	1.73	0.85
1:B:335:GLU:HA	1:B:338:ASP:HB3	1.58	0.85
1:A:100:ALA:HB1	1:A:380:ARG:HH21	1.38	0.84
1:B:451:LEU:HG	1:B:460:LEU:HD13	1.58	0.84
1:A:131:PRO:O	1:B:508:HIS:NE2	2.10	0.84
1:A:580:GLU:OE1	1:A:580:GLU:HA	1.76	0.84
1:B:297:MSE:HE2	1:B:951:ARG:HA	1.61	0.82
1:A:202:HIS:O	1:A:206:SER:N	2.13	0.82
1:A:246:ASP:H	1:A:285:LYS:HD2	1.44	0.82
1:A:847:LYS:HB3	1:A:850:ASN:O	1.78	0.82
1:B:98:ASP:HB2	1:B:101:ASP:HB2	1.62	0.82
1:B:444:PHE:O	1:B:464:ARG:NE	2.13	0.82
1:A:151:GLN:HG2	1:A:152:TYR:N	1.95	0.82
1:A:587:ARG:O	1:A:591:ARG:N	2.13	0.81
1:A:755:GLU:CD	1:A:755:GLU:H	1.83	0.81
1:B:767:GLN:HA	1:B:770:LYS:HG2	1.59	0.81
1:B:208:MSE:HA	1:B:210:LYS:HE3	1.62	0.81
1:B:340:TYR:OH	1:B:948:THR:HA	1.79	0.81
1:B:520:ARG:NH1	1:B:523:GLN:O	2.14	0.81
1:A:332:VAL:HG22	1:A:336:PHE:HB2	1.61	0.81
1:B:1008:PRO:HA	1:B:1033:TYR:HA	1.61	0.81
1:B:752:LEU:C	1:B:754:THR:H	1.82	0.81
1:A:808:LEU:HD21	1:A:831:LEU:HD23	1.63	0.80
1:A:208:MSE:H	1:A:210:LYS:HZ2	1.27	0.80
1:A:521:TYR:CE1	1:A:568:SER:HB3	2.16	0.80
1:A:672:ASN:C	1:A:675:GLN:HE22	1.84	0.80
1:A:385:GLN:O	1:A:388:LYS:HG2	1.80	0.80
1:A:446:SER:HA	1:A:463:VAL:HG13	1.62	0.80
1:A:747:GLN:NE2	1:A:750:GLN:O	2.14	0.80
1:B:536:GLN:OE1	1:B:537:ARG:NH1	2.14	0.80
1:B:836:SER:OG	1:B:837:LYS:N	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:860:GLU:HA	1:A:863:LYS:HD2	1.64	0.80
1:B:209:ALA:N	1:B:210:LYS:HD2	1.96	0.80
1:A:98:ASP:OD1	1:A:101:ASP:N	2.16	0.79
1:A:396:ALA:O	1:A:399:LEU:HB3	1.82	0.79
1:A:80:LYS:NZ	1:A:84:ASP:OD2	2.14	0.79
1:B:65:LEU:HD12	1:B:68:ILE:HD11	1.63	0.79
1:A:721:PHE:CZ	1:A:828:GLU:HB3	2.18	0.79
1:B:561:VAL:HG13	1:B:562:LEU:HD13	1.65	0.79
1:A:98:ASP:CG	1:A:101:ASP:H	1.86	0.78
1:B:453:GLN:HA	1:B:453:GLN:NE2	1.92	0.78
1:A:242:LEU:HD23	1:A:245:THR:HG21	1.64	0.78
1:A:549:GLN:HE22	1:A:571:GLU:HA	1.49	0.78
1:B:672:ASN:OD1	1:B:673:LEU:N	2.16	0.78
1:B:511:PRO:O	1:B:515:GLN:N	2.17	0.78
1:A:546:ARG:NH1	1:B:119:GLU:OE2	2.18	0.77
1:A:748:LEU:HA	1:A:751:LEU:HD21	1.66	0.77
1:A:471:VAL:HB	1:A:602:LEU:HB2	1.66	0.77
1:B:292:VAL:HA	1:B:295:LEU:HB2	1.67	0.77
1:B:295:LEU:HD11	1:B:324:SER:HB2	1.67	0.77
1:A:388:LYS:HG3	1:A:389:LEU:H	1.49	0.77
1:A:48:GLU:HG3	1:A:114:ALA:HB3	1.66	0.77
1:B:208:MSE:HA	1:B:210:LYS:CE	2.14	0.77
1:A:560:ARG:HH21	1:A:561:VAL:HG13	1.48	0.77
1:B:787:TRP:O	1:B:789:GLN:N	2.17	0.77
1:B:846:MSE:O	1:B:849:LEU:HG	1.85	0.76
1:A:335:GLU:HA	1:A:338:ASP:OD1	1.85	0.76
1:B:655:THR:OG1	1:B:656:ARG:NH1	2.19	0.76
1:A:151:GLN:CG	1:A:152:TYR:H	1.96	0.76
1:A:336:PHE:CD2	1:A:337:LEU:HD13	2.19	0.76
1:B:453:GLN:CA	1:B:453:GLN:HE21	1.99	0.76
1:B:858:SER:HA	1:B:861:PHE:HB3	1.67	0.76
1:B:917:THR:HB	1:B:948:THR:HG21	1.68	0.76
1:A:847:LYS:HE3	1:A:853:HIS:CD2	2.22	0.75
1:B:249:MSE:HB2	1:B:956:LEU:HD22	1.66	0.75
1:B:310:PHE:HB2	1:B:902:ILE:HG21	1.69	0.75
1:B:190:TYR:OH	1:B:219:ARG:NH1	2.18	0.74
1:B:710:ALA:O	1:B:712:LEU:N	2.19	0.74
1:A:104:SER:HB3	1:A:377:ARG:HH21	1.51	0.74
1:A:104:SER:HB3	1:A:377:ARG:NH2	2.02	0.74
1:A:803:THR:HB	1:A:815:PRO:HG3	1.69	0.74
1:B:210:LYS:HB2	1:B:211:GLU:CG	2.06	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:672:ASN:OD1	1:B:863:LYS:NZ	2.14	0.74
1:A:580:GLU:OE1	1:A:584:LYS:N	2.21	0.74
1:B:244:ARG:HB3	1:B:993:LEU:HB2	1.69	0.74
1:B:428:VAL:HG13	1:B:585:THR:HG22	1.70	0.74
1:B:387:ARG:HA	1:B:391:LEU:H	1.52	0.74
1:B:722:ARG:NH1	1:B:728:ILE:O	2.21	0.74
1:B:893:LYS:HE3	1:B:895:TRP:CD1	2.23	0.73
1:A:788:ALA:O	1:A:792:GLN:NE2	2.21	0.73
1:A:401:LEU:HD21	1:A:893:LYS:HD3	1.69	0.73
1:A:94:GLY:HA2	1:A:97:ASN:OD1	1.89	0.73
1:B:144:TRP:CE3	1:B:151:GLN:HG3	2.22	0.73
1:A:336:PHE:CE2	1:A:337:LEU:HD13	2.24	0.73
1:A:342:ALA:O	1:A:896:ASN:ND2	2.22	0.73
1:A:465:ARG:HE	1:A:644:LEU:HD11	1.54	0.73
1:A:654:LEU:HB2	1:A:656:ARG:HH22	1.53	0.73
1:B:589:ILE:HG23	1:B:594:LEU:HB2	1.71	0.73
1:A:698:LEU:HD13	1:A:839:LEU:HD21	1.71	0.72
1:B:209:ALA:HB2	1:B:216:TYR:HB3	1.70	0.72
1:B:474:ILE:HD11	1:B:485:VAL:HG21	1.71	0.72
1:B:817:PRO:HD2	1:B:821:THR:HG21	1.69	0.72
1:B:33:ASN:N	1:B:1029:VAL:O	2.23	0.72
1:B:146:HIS:HB3	1:B:188:ILE:HB	1.71	0.72
1:B:632:SER:OG	1:B:633:ILE:N	2.23	0.72
1:B:767:GLN:N	1:B:767:GLN:OE1	2.21	0.72
1:B:204:LYS:O	1:B:208:MSE:N	2.23	0.72
1:B:376:LEU:HG	1:B:912:ILE:HD13	1.72	0.72
1:B:210:LYS:HD3	1:B:211:GLU:HG2	1.70	0.72
1:B:349:PRO:HB2	1:B:352:ARG:HE	1.54	0.72
1:A:170:ALA:HB1	1:A:186:LEU:HD23	1.71	0.72
1:A:791:LYS:HE3	1:A:801:SER:HA	1.71	0.71
1:A:209:ALA:HB3	1:A:210:LYS:HE3	1.70	0.71
1:B:473:PRO:HA	1:B:504:VAL:HG22	1.72	0.71
1:B:76:ALA:HB2	1:B:85:ARG:HD2	1.72	0.71
1:B:1003:SER:HA	1:B:1039:LEU:HG	1.72	0.71
1:A:433:ASN:HB3	1:A:500:ARG:HG3	1.73	0.71
1:B:420:ARG:NE	1:B:649:LEU:HD21	2.03	0.71
1:A:667:LYS:HE3	1:A:669:ARG:HD3	1.72	0.71
1:B:853:HIS:NE2	1:B:855:VAL:O	2.24	0.71
1:A:80:LYS:HA	1:A:83:TYR:HB3	1.71	0.71
1:A:695:THR:OG1	1:A:696:ASN:N	2.24	0.71
1:A:111:ILE:HG23	1:A:112:ARG:NH1	2.05	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:GLN:NE2	1:A:527:GLY:O	2.23	0.70
1:B:289:SER:OG	1:B:290:SER:N	2.21	0.70
1:B:483:TYR:O	1:B:487:GLN:N	2.22	0.70
1:B:179:LEU:HG	1:B:209:ALA:CB	2.21	0.70
1:A:315:LYS:H	1:A:315:LYS:HD2	1.56	0.70
1:B:393:ASN:ND2	1:B:909:ASP:OD1	2.24	0.70
1:A:209:ALA:H	1:A:210:LYS:HZ1	1.37	0.70
1:A:582:MSE:O	1:A:586:GLY:N	2.18	0.70
1:A:473:PRO:O	1:A:610:ARG:NH2	2.25	0.70
1:B:751:LEU:CD1	1:B:752:LEU:H	2.05	0.70
1:A:245:THR:HA	1:A:285:LYS:HD3	1.74	0.70
1:B:558:SER:O	1:B:561:VAL:HG12	1.92	0.70
1:B:734:HIS:CD2	1:B:735:THR:H	2.10	0.70
1:A:800:PRO:O	1:A:803:THR:OG1	2.08	0.70
1:B:629:ILE:HD13	1:B:644:LEU:HD22	1.73	0.70
1:B:660:ILE:HG21	1:B:829:ILE:HG23	1.74	0.70
1:A:287:LEU:HD12	1:A:288:SER:H	1.57	0.69
1:A:156:THR:O	1:A:157:LEU:HG	1.91	0.69
1:B:293:ALA:HA	1:B:953:LEU:H	1.57	0.69
1:A:428:VAL:HG13	1:A:585:THR:HG22	1.72	0.69
1:A:208:MSE:HG3	1:A:213:GLN:HB2	1.73	0.69
1:A:591:ARG:HH21	1:A:655:THR:HB	1.57	0.69
1:A:292:VAL:HA	1:A:295:LEU:HB2	1.74	0.69
1:A:185:PRO:HB2	1:A:214:VAL:HA	1.75	0.69
1:A:638:VAL:HG21	1:A:642:THR:HG21	1.75	0.69
1:A:346:ALA:CB	1:A:895:TRP:HB2	2.23	0.69
1:A:750:GLN:HG3	1:A:753:ARG:HD3	1.74	0.69
1:A:367:VAL:O	1:A:927:ARG:NH2	2.26	0.69
1:A:529:ALA:O	1:A:533:LYS:HG2	1.92	0.68
1:A:399:LEU:O	1:A:401:LEU:N	2.24	0.68
1:A:526:HIS:O	1:A:562:LEU:HD21	1.93	0.68
1:A:539:LEU:HA	1:A:544:LEU:HD11	1.74	0.68
1:B:208:MSE:HG2	1:B:210:LYS:HE3	1.75	0.68
1:A:974:GLU:HB3	1:A:976:GLY:H	1.59	0.68
1:A:546:ARG:HD3	1:B:228:PHE:HE2	1.58	0.68
1:A:562:LEU:O	1:A:563:ARG:HD3	1.92	0.68
1:A:632:SER:O	1:A:637:ALA:HB2	1.94	0.68
1:A:385:GLN:NE2	1:A:673:LEU:HB3	2.08	0.68
1:B:36:LEU:HD23	1:B:233:LEU:HB2	1.76	0.68
1:A:30:SER:OG	1:A:31:SER:N	2.22	0.68
1:A:735:THR:N	1:A:804:ARG:HH22	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:752:LEU:CD2	1:A:760:SER:HB3	2.24	0.68
1:A:388:LYS:HG3	1:A:389:LEU:N	2.05	0.68
1:B:452:LEU:C	1:B:453:GLN:HE21	1.97	0.68
1:A:703:VAL:HG22	1:A:804:ARG:NH1	2.00	0.68
1:B:250:ILE:HD12	1:B:289:SER:HB2	1.75	0.67
1:B:510:GLU:O	1:B:514:SER:OG	2.05	0.67
1:B:520:ARG:HA	1:B:520:ARG:HH11	1.60	0.67
1:B:644:LEU:O	1:B:647:TYR:N	2.27	0.67
1:A:91:GLN:HG2	1:A:102:LEU:HD21	1.76	0.67
1:A:205:LEU:O	1:A:210:LYS:NZ	2.26	0.67
1:A:523:GLN:HG3	1:A:528:LEU:HA	1.76	0.67
1:A:703:VAL:HG13	1:A:804:ARG:NE	2.07	0.67
1:A:836:SER:OG	1:A:837:LYS:N	2.27	0.67
1:A:433:ASN:ND2	1:A:500:ARG:HA	2.03	0.67
1:B:517:LYS:NZ	1:B:578:LEU:HD12	2.10	0.67
1:A:82:LEU:O	1:A:86:PHE:HB2	1.95	0.67
1:B:210:LYS:CB	1:B:211:GLU:HG2	2.07	0.67
1:B:612:ASP:CG	1:B:616:GLN:HE22	1.97	0.67
1:B:83:TYR:CZ	1:B:87:LEU:HD11	2.30	0.67
1:B:293:ALA:HA	1:B:953:LEU:N	2.09	0.67
1:B:1019:ARG:HG2	1:B:1021:SER:HB3	1.76	0.66
1:A:752:LEU:HD23	1:A:760:SER:HB3	1.77	0.66
1:B:78:THR:CG2	1:B:81:GLU:HG3	2.25	0.66
1:A:721:PHE:CE1	1:A:828:GLU:HB3	2.30	0.66
1:A:846:MSE:HG2	1:A:847:LYS:H	1.61	0.66
1:A:681:ASP:OD2	1:A:683:THR:HG23	1.95	0.66
1:A:974:GLU:HG2	1:A:976:GLY:N	2.09	0.66
1:B:559:ALA:HA	1:B:562:LEU:HB2	1.77	0.66
1:B:398:ASP:O	1:B:401:LEU:HG	1.96	0.66
1:B:589:ILE:HA	1:B:594:LEU:HD12	1.78	0.66
1:B:672:ASN:HD22	1:B:866:SER:CB	2.09	0.66
1:B:179:LEU:HG	1:B:209:ALA:HB3	1.78	0.65
1:A:455:THR:OG1	1:A:457:PRO:HD2	1.96	0.65
1:A:435:LEU:HA	1:A:441:TYR:HD2	1.59	0.65
1:A:381:GLN:O	1:A:385:GLN:N	2.28	0.65
1:A:208:MSE:H	1:A:210:LYS:NZ	1.95	0.65
1:A:237:GLY:N	1:A:999:ASP:O	2.27	0.65
1:B:148:ASP:OD1	1:B:149:GLY:N	2.29	0.65
1:B:580:GLU:O	1:B:584:LYS:HD3	1.96	0.65
1:B:853:HIS:CE1	1:B:855:VAL:HG22	2.32	0.65
1:A:847:LYS:HZ2	1:A:854:LYS:H	1.43	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:VAL:CG2	1:A:584:LYS:HG2	2.26	0.65
1:B:817:PRO:O	1:B:818:SER:OG	2.12	0.65
1:A:698:LEU:HB2	1:A:728:ILE:HD11	1.78	0.65
1:B:439:LYS:O	1:B:442:SER:OG	2.10	0.65
1:B:91:GLN:HG2	1:B:97:ASN:OD1	1.97	0.65
1:A:734:HIS:CE1	1:A:749:TYR:OH	2.50	0.65
1:A:289:SER:OG	1:A:290:SER:N	2.30	0.64
1:A:665:PRO:O	1:A:667:LYS:N	2.25	0.64
1:B:536:GLN:HB2	1:B:537:ARG:HD2	1.79	0.64
1:B:243:LYS:HB3	1:B:993:LEU:HB3	1.80	0.64
1:A:635:GLN:HG2	1:A:636:ASP:H	1.61	0.64
1:A:816:VAL:HB	1:A:817:PRO:HD3	1.77	0.64
1:B:737:ASP:CG	1:B:791:LYS:HZ3	2.00	0.64
1:A:797:LEU:HD22	1:A:807:LEU:HD11	1.79	0.64
1:B:241:THR:OG1	1:B:995:THR:HB	1.97	0.64
1:A:113:SER:O	1:A:116:PRO:HD2	1.98	0.64
1:A:247:TYR:HB2	1:A:286:PRO:HG2	1.78	0.64
1:B:492:PHE:HB3	1:B:497:ILE:HD12	1.79	0.64
1:B:534:TYR:HA	1:B:555:THR:HG21	1.79	0.64
1:B:956:LEU:HD12	1:B:957:PRO:HD2	1.79	0.64
1:A:523:GLN:HE22	1:A:531:MSE:H	1.43	0.64
1:B:208:MSE:HA	1:B:210:LYS:CD	2.28	0.64
1:A:294:ARG:NH1	1:A:328:ALA:O	2.31	0.64
1:A:767:GLN:N	1:A:767:GLN:OE1	2.28	0.64
1:B:523:GLN:O	1:B:524:MSE:HG3	1.96	0.64
1:B:68:ILE:HG22	1:B:73:LEU:HD13	1.79	0.64
1:A:418:ASP:HA	1:A:649:LEU:HD11	1.80	0.64
1:A:702:VAL:O	1:A:732:PRO:HA	1.98	0.64
1:A:831:LEU:O	1:A:835:PHE:N	2.26	0.64
1:A:431:TRP:CE3	1:A:500:ARG:HG2	2.33	0.64
1:A:84:ASP:HA	1:A:87:LEU:HD12	1.79	0.64
1:B:44:PRO:HG2	1:B:47:LEU:HD12	1.80	0.64
1:B:100:ALA:O	1:B:104:SER:N	2.25	0.63
1:B:751:LEU:HD12	1:B:752:LEU:H	1.62	0.63
1:A:358:ASN:N	1:A:913:ASN:O	2.16	0.63
1:A:606:VAL:HG11	1:A:621:ARG:HG2	1.80	0.63
1:A:672:ASN:OD1	1:A:673:LEU:N	2.31	0.63
1:B:48:GLU:OE2	1:B:112:ARG:HD3	1.99	0.63
1:B:787:TRP:HD1	1:B:790:THR:HG1	1.47	0.63
1:A:432:LEU:HD11	1:A:503:LEU:HD11	1.81	0.63
1:A:721:PHE:HZ	1:A:828:GLU:HB3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:GLU:HG2	1:A:960:ARG:NH2	2.12	0.63
1:A:301:SER:HB3	1:A:333:THR:HG23	1.81	0.63
1:A:335:GLU:HB2	1:A:900:SER:HB3	1.81	0.63
1:A:702:VAL:HG11	1:A:718:ALA:HB1	1.80	0.63
1:B:30:SER:OG	1:B:31:SER:N	2.31	0.63
1:A:76:ALA:HB3	1:A:81:GLU:OE1	1.98	0.63
1:A:827:LEU:O	1:A:830:LEU:HB3	1.99	0.63
1:B:606:VAL:HG11	1:B:621:ARG:HD3	1.81	0.63
1:B:973:ASP:O	1:B:974:GLU:HB2	1.98	0.63
1:A:580:GLU:OE2	1:A:583:ASP:HB2	1.99	0.62
1:B:698:LEU:HB2	1:B:728:ILE:HG12	1.81	0.62
1:A:546:ARG:HD3	1:B:228:PHE:CE2	2.33	0.62
1:B:418:ASP:OD1	1:B:655:THR:HG22	1.98	0.62
1:B:849:LEU:O	1:B:851:LEU:N	2.31	0.62
1:B:905:SER:HB2	1:B:942:ASN:HA	1.81	0.62
1:A:428:VAL:HG22	1:A:584:LYS:HG2	1.80	0.62
1:A:108:SER:HA	1:A:111:ILE:HB	1.82	0.62
1:A:532:MSE:O	1:A:536:GLN:N	2.29	0.62
1:A:246:ASP:N	1:A:285:LYS:HD2	2.13	0.62
1:B:221:ARG:NH1	1:B:222:PRO:O	2.33	0.62
1:B:293:ALA:HB1	1:B:952:ILE:HG13	1.81	0.62
1:A:147:MSE:O	1:A:149:GLY:N	2.33	0.62
1:A:207:ALA:CA	1:A:210:LYS:HG3	2.29	0.62
1:A:675:GLN:C	1:A:677:ALA:H	2.03	0.62
1:B:586:GLY:O	1:B:590:LYS:HD3	2.00	0.62
1:A:249:MSE:CE	1:A:292:VAL:HG21	2.29	0.62
1:A:804:ARG:H	1:A:815:PRO:HB3	1.65	0.62
1:A:817:PRO:CD	1:A:818:SER:H	2.12	0.62
1:B:1004:TRP:CD1	1:B:1038:ILE:HD11	2.35	0.62
1:B:533:LYS:HA	1:B:536:GLN:HG3	1.82	0.62
1:B:78:THR:OG1	1:B:976:GLY:O	2.16	0.62
1:A:173:LEU:N	1:A:176:ASP:OD2	2.33	0.62
1:B:249:MSE:SE	1:B:292:VAL:HG11	2.50	0.62
1:B:449:ASP:O	1:B:452:LEU:HD21	2.00	0.62
1:B:33:ASN:O	1:B:1031:ALA:N	2.26	0.61
1:A:466:ASP:O	1:A:645:PRO:HD3	2.01	0.61
1:A:85:ARG:O	1:A:89:ILE:HD13	2.00	0.61
1:A:676:VAL:HA	1:A:680:HIS:CE1	2.35	0.61
1:B:210:LYS:HD3	1:B:211:GLU:CG	2.30	0.61
1:B:923:GLU:HG3	1:B:958:ILE:HA	1.80	0.61
1:B:239:GLU:O	1:B:240:LEU:HD23	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:LYS:N	1:A:315:LYS:HD2	2.16	0.61
1:B:339:GLU:HA	1:B:342:ALA:HB3	1.81	0.61
1:B:770:LYS:O	1:B:773:SER:OG	2.19	0.61
1:A:106:LYS:HD3	1:A:106:LYS:H	1.65	0.61
1:A:381:GLN:OE1	1:A:382:PHE:N	2.34	0.61
1:A:817:PRO:HD2	1:A:818:SER:H	1.66	0.61
1:A:635:GLN:O	1:A:637:ALA:N	2.33	0.61
1:A:794:ALA:O	1:A:797:LEU:HD12	2.01	0.61
1:B:736:SER:O	1:B:791:LYS:HD3	2.00	0.61
1:A:153:CYS:O	1:A:201:TYR:OH	2.17	0.60
1:B:748:LEU:O	1:B:751:LEU:N	2.34	0.60
1:A:387:ARG:CZ	1:A:393:ASN:HD21	2.13	0.60
1:B:205:LEU:HA	1:B:208:MSE:HB2	1.82	0.60
1:A:444:PHE:HD2	1:A:462:ALA:HB3	1.66	0.60
1:A:74:ASP:OD2	1:A:196:PRO:HB3	2.01	0.60
1:B:737:ASP:OD2	1:B:801:SER:HB3	2.01	0.60
1:A:521:TYR:CE1	1:A:525:THR:HG21	2.36	0.60
1:A:249:MSE:HE2	1:A:292:VAL:HG21	1.83	0.60
1:A:709:GLU:O	1:A:711:GLY:N	2.33	0.60
1:B:34:VAL:HG22	1:B:1031:ALA:HB3	1.83	0.60
1:B:555:THR:HA	1:B:558:SER:HB3	1.82	0.60
1:A:209:ALA:H	1:A:210:LYS:NZ	1.98	0.60
1:A:517:LYS:HG2	1:A:582:MSE:HE2	1.83	0.60
1:B:143:VAL:HG23	1:B:191:ALA:HB2	1.84	0.60
1:B:764:GLU:O	1:B:767:GLN:NE2	2.31	0.60
1:A:293:ALA:HA	1:A:953:LEU:H	1.66	0.60
1:A:393:ASN:HA	1:A:396:ALA:H	1.67	0.60
1:A:83:TYR:O	1:A:87:LEU:HD12	2.01	0.60
1:B:672:ASN:CG	1:B:673:LEU:H	2.01	0.60
1:A:102:LEU:HG	1:A:106:LYS:HZ1	1.66	0.60
1:A:560:ARG:NH2	1:A:561:VAL:HG13	2.15	0.60
1:B:250:ILE:H	1:B:289:SER:HA	1.65	0.59
1:B:250:ILE:HG13	1:B:288:SER:O	2.01	0.59
1:B:420:ARG:HE	1:B:649:LEU:CD2	2.04	0.59
1:B:917:THR:HB	1:B:948:THR:CG2	2.31	0.59
1:A:846:MSE:HG2	1:A:847:LYS:N	2.17	0.59
1:B:80:LYS:HB2	1:B:972:PHE:CB	2.31	0.59
1:A:698:LEU:HB2	1:A:728:ILE:CD1	2.32	0.59
1:A:130:GLU:HA	1:A:133:LEU:HD12	1.83	0.59
1:A:589:ILE:O	1:A:593:ASP:N	2.36	0.59
1:B:29:ASP:OD1	1:B:30:SER:N	2.30	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:GLN:NE2	1:A:547:PRO:HB3	2.17	0.59
1:B:294:ARG:HD2	1:B:298:ASN:HD21	1.68	0.59
1:A:542:ASP:O	1:A:543:LYS:HD3	2.03	0.59
1:A:351:GLY:H	1:A:951:ARG:HH12	1.50	0.59
1:A:567:GLN:OE1	1:A:568:SER:N	2.35	0.59
1:B:1019:ARG:O	1:B:1022:SER:N	2.27	0.59
1:B:906:HIS:NE2	1:B:910:ALA:HB2	2.17	0.59
1:A:799:TYR:N	1:A:800:PRO:HD3	2.18	0.59
1:A:83:TYR:CE1	1:A:87:LEU:HD11	2.37	0.59
1:B:705:ASP:O	1:B:707:ASP:N	2.36	0.59
1:B:709:GLU:H	1:B:709:GLU:CD	1.99	0.59
1:B:848:ASP:O	1:B:850:ASN:N	2.36	0.59
1:A:706:PHE:CD2	1:A:734:HIS:HB3	2.37	0.59
1:A:816:VAL:HB	1:A:817:PRO:CD	2.31	0.59
1:B:156:THR:O	1:B:157:LEU:HG	2.03	0.59
1:B:431:TRP:CZ3	1:B:500:ARG:HG2	2.38	0.59
1:A:179:LEU:N	1:A:216:TYR:O	2.34	0.58
1:A:523:GLN:CG	1:A:528:LEU:HA	2.32	0.58
1:A:244:ARG:O	1:A:992:ALA:HB1	2.04	0.58
1:A:847:LYS:HZ1	1:A:854:LYS:H	1.50	0.58
1:B:100:ALA:HB2	1:B:939:ASN:OD1	2.03	0.58
1:B:234:ALA:O	1:B:370:TYR:OH	2.20	0.58
1:B:762:ILE:O	1:B:766:ILE:HG23	2.04	0.58
1:A:621:ARG:HA	1:A:624:ILE:HD12	1.84	0.58
1:B:185:PRO:HG2	1:B:214:VAL:HG22	1.85	0.58
1:A:813:VAL:HG23	1:A:814:GLY:N	2.14	0.58
1:B:56:GLU:OE1	1:B:56:GLU:N	2.37	0.58
1:B:597:ARG:HG3	1:B:598:SER:N	2.19	0.58
1:B:346:ALA:HB3	1:B:893:LYS:HE2	1.84	0.58
1:A:1003:SER:O	1:A:1038:ILE:HB	2.03	0.58
1:A:385:GLN:HE22	1:A:673:LEU:HB3	1.67	0.58
1:A:845:VAL:HA	1:A:848:ASP:HB2	1.85	0.58
1:A:905:SER:CB	1:A:942:ASN:HA	2.34	0.58
1:A:972:PHE:O	1:A:979:ASN:ND2	2.30	0.58
1:B:393:ASN:ND2	1:B:911:SER:HB2	2.18	0.58
1:A:453:GLN:HG2	1:A:453:GLN:O	2.04	0.58
1:A:716:ILE:O	1:A:720:LYS:HG2	2.04	0.58
1:A:851:LEU:HG	1:A:852:GLY:N	2.19	0.58
1:B:342:ALA:HB1	1:B:895:TRP:CH2	2.39	0.58
1:B:927:ARG:HH12	1:B:999:ASP:CG	2.08	0.58
1:A:142:PRO:O	1:A:221:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:ASP:N	1:A:825:ASP:OD1	2.35	0.57
1:B:639:GLU:H	1:B:639:GLU:CD	2.07	0.57
1:B:723:LEU:HD11	1:B:761:GLU:HB3	1.86	0.57
1:A:639:GLU:H	1:A:639:GLU:CD	2.07	0.57
1:B:309:PRO:HB2	1:B:902:ILE:HD12	1.86	0.57
1:B:483:TYR:CZ	1:B:487:GLN:HG2	2.38	0.57
1:B:797:LEU:HD22	1:B:807:LEU:HD11	1.87	0.57
1:B:986:SER:O	1:B:987:ARG:HB3	2.04	0.57
1:B:661:MSE:O	1:B:661:MSE:HG3	2.05	0.57
1:A:644:LEU:HD12	1:A:644:LEU:H	1.68	0.57
1:B:548:ASP:OD1	1:B:551:LEU:HB2	2.05	0.57
1:A:65:LEU:HA	1:A:68:ILE:HG12	1.85	0.57
1:A:377:ARG:NH2	1:A:380:ARG:NH2	2.52	0.57
1:A:392:SER:O	1:A:395:GLU:HG2	2.03	0.57
1:A:492:PHE:HB3	1:A:497:ILE:HD12	1.85	0.57
1:A:707:ASP:OD2	1:A:745:SER:HB3	2.03	0.57
1:B:211:GLU:OE2	1:B:213:GLN:HB2	2.05	0.57
1:A:704:GLY:O	1:A:804:ARG:NH2	2.38	0.57
1:A:482:VAL:HG12	1:A:539:LEU:HD22	1.87	0.57
1:A:703:VAL:HG12	1:A:805:GLY:O	2.05	0.57
1:A:790:THR:O	1:A:794:ALA:N	2.38	0.57
1:A:839:LEU:HD12	1:A:865:THR:HB	1.87	0.57
1:B:107:PHE:HD2	1:B:373:LEU:HD13	1.69	0.57
1:A:111:ILE:C	1:A:112:ARG:HG3	2.25	0.57
1:A:358:ASN:OD1	1:A:913:ASN:N	2.31	0.56
1:A:431:TRP:CZ3	1:A:500:ARG:HG2	2.39	0.56
1:A:672:ASN:CG	1:A:673:LEU:H	2.07	0.56
1:A:990:GLU:HG2	1:A:1020:LEU:HB2	1.87	0.56
1:A:245:THR:HG22	1:A:247:TYR:H	1.70	0.56
1:B:463:VAL:C	1:B:465:ARG:H	2.08	0.56
1:A:629:ILE:HG12	1:A:647:TYR:CD2	2.40	0.56
1:B:185:PRO:O	1:B:215:SER:OG	2.23	0.56
1:A:1037:HIS:CG	1:A:1038:ILE:H	2.24	0.56
1:A:918:ILE:HD13	1:A:945:ILE:HG23	1.86	0.56
1:B:799:TYR:HA	1:B:803:THR:HG21	1.87	0.56
1:B:929:VAL:HB	1:B:930:PRO:HD3	1.87	0.56
1:A:130:GLU:OE1	1:B:510:GLU:N	2.37	0.56
1:A:207:ALA:HA	1:A:210:LYS:HG3	1.86	0.56
1:B:298:ASN:HD22	1:B:330:TYR:H	1.52	0.56
1:B:558:SER:C	1:B:560:ARG:HG2	2.26	0.56
1:B:733:LEU:HD23	1:B:794:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:TRP:HH2	1:A:469:ASN:HB3	1.70	0.56
1:A:64:LEU:O	1:A:68:ILE:HG23	2.05	0.56
1:A:751:LEU:HD22	1:A:763:LEU:HD11	1.87	0.56
1:A:627:GLN:O	1:A:631:GLN:N	2.30	0.56
1:A:676:VAL:HA	1:A:680:HIS:NE2	2.21	0.56
1:A:704:GLY:C	1:A:804:ARG:HD3	2.26	0.56
1:A:803:THR:HB	1:A:815:PRO:CG	2.35	0.56
1:B:712:LEU:O	1:B:716:ILE:N	2.24	0.56
1:A:927:ARG:HD2	1:A:999:ASP:OD1	2.06	0.56
1:B:847:LYS:NZ	1:B:853:HIS:HB3	2.21	0.56
1:A:735:THR:HG23	1:A:791:LYS:HD2	1.86	0.56
1:A:804:ARG:O	1:A:815:PRO:HA	2.06	0.56
1:A:614:PHE:O	1:A:618:LEU:N	2.29	0.56
1:A:927:ARG:O	1:A:930:PRO:HD2	2.05	0.56
1:B:787:TRP:HB2	1:B:790:THR:CG2	2.36	0.56
1:A:528:LEU:N	1:A:562:LEU:HD11	2.22	0.55
1:B:927:ARG:O	1:B:930:PRO:HD2	2.06	0.55
1:B:117:ARG:CZ	1:B:177:ARG:NH2	2.69	0.55
1:B:46:LEU:O	1:B:50:LEU:N	2.32	0.55
1:B:533:LYS:O	1:B:533:LYS:HG3	2.05	0.55
1:A:559:ALA:HB1	1:A:563:ARG:HG3	1.88	0.55
1:B:476:LEU:HD11	1:B:505:PRO:HB3	1.88	0.55
1:A:387:ARG:NH1	1:A:393:ASN:ND2	2.54	0.55
1:A:847:LYS:HD2	1:A:851:LEU:HB3	1.87	0.55
1:B:645:PRO:O	1:B:649:LEU:N	2.35	0.55
1:B:825:ASP:OD1	1:B:825:ASP:N	2.40	0.55
1:A:393:ASN:HB3	1:A:396:ALA:HB3	1.89	0.55
1:A:674:VAL:HG23	1:A:674:VAL:O	2.07	0.55
1:A:734:HIS:CE1	1:A:749:TYR:HH	2.22	0.55
1:A:910:ALA:C	1:A:912:ILE:H	2.09	0.55
1:B:721:PHE:O	1:B:725:HIS:N	2.37	0.55
1:B:125:TYR:CZ	1:B:221:ARG:HG3	2.40	0.55
1:B:705:ASP:HA	1:B:734:HIS:HD2	1.71	0.55
1:A:635:GLN:HB3	1:A:636:ASP:OD1	2.06	0.55
1:A:665:PRO:C	1:A:667:LYS:H	2.10	0.55
1:A:765:LYS:HD2	1:A:765:LYS:N	2.22	0.55
1:A:247:TYR:CE2	1:A:321:PRO:HB3	2.42	0.55
1:A:751:LEU:HD22	1:A:763:LEU:CD1	2.37	0.55
1:A:660:ILE:O	1:A:811:ARG:NH2	2.40	0.55
1:B:558:SER:HA	1:B:560:ARG:HD2	1.87	0.55
1:A:579:GLU:O	1:A:583:ASP:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:643:TRP:CZ2	1:A:645:PRO:HB2	2.42	0.55
1:B:623:ALA:O	1:B:626:LEU:HB3	2.07	0.55
1:A:1038:ILE:HG13	1:A:1039:LEU:H	1.71	0.55
1:A:57:ASN:CG	1:A:95:HIS:HB3	2.27	0.55
1:A:301:SER:OG	1:A:333:THR:N	2.30	0.54
1:A:387:ARG:NH1	1:A:393:ASN:HD21	2.05	0.54
1:A:560:ARG:HG2	1:A:561:VAL:N	2.21	0.54
1:A:718:ALA:O	1:A:721:PHE:HB3	2.06	0.54
1:B:291:GLU:HA	1:B:294:ARG:HH11	1.72	0.54
1:A:247:TYR:CD2	1:A:321:PRO:HB3	2.42	0.54
1:A:401:LEU:HD21	1:A:893:LYS:CD	2.35	0.54
1:B:188:ILE:HG23	1:B:217:VAL:HG22	1.88	0.54
1:B:41:ASP:HA	1:B:231:LEU:HB2	1.89	0.54
1:A:1001:PRO:HB2	1:A:1004:TRP:CD1	2.42	0.54
1:B:84:ASP:HA	1:B:87:LEU:HD12	1.88	0.54
1:B:85:ARG:O	1:B:89:ILE:HD13	2.07	0.54
1:A:655:THR:H	1:A:656:ARG:NH1	2.06	0.54
1:A:750:GLN:OE1	1:A:750:GLN:N	2.40	0.54
1:B:789:GLN:C	1:B:793:LEU:HG	2.28	0.54
1:B:853:HIS:CE1	1:B:855:VAL:H	2.24	0.54
1:A:513:LYS:O	1:A:517:LYS:N	2.36	0.54
1:B:186:LEU:HD11	1:B:217:VAL:CG1	2.37	0.54
1:A:111:ILE:HG22	1:A:111:ILE:O	2.07	0.54
1:A:132:ARG:HD2	1:A:168:LEU:HD22	1.88	0.54
1:A:990:GLU:O	1:A:992:ALA:N	2.40	0.54
1:B:209:ALA:CA	1:B:210:LYS:HD2	2.38	0.54
1:B:243:LYS:N	1:B:993:LEU:O	2.35	0.54
1:B:420:ARG:NH2	1:B:650:SER:HB3	2.22	0.54
1:A:444:PHE:CD2	1:A:462:ALA:HB3	2.42	0.54
1:B:520:ARG:NH1	1:B:523:GLN:HG3	2.23	0.54
1:A:151:GLN:CG	1:A:152:TYR:N	2.64	0.54
1:A:444:PHE:O	1:A:464:ARG:HG3	2.08	0.54
1:B:536:GLN:O	1:B:539:LEU:HB3	2.08	0.54
1:B:922:SER:O	1:B:925:SER:OG	2.26	0.54
1:A:734:HIS:HA	1:A:804:ARG:NH1	2.23	0.54
1:A:734:HIS:HE1	1:A:749:TYR:CE1	2.25	0.54
1:B:179:LEU:HG	1:B:209:ALA:HB1	1.90	0.54
1:B:334:GLN:HA	1:B:337:LEU:HD13	1.90	0.54
1:A:106:LYS:HD3	1:A:106:LYS:N	2.19	0.54
1:A:510:GLU:HB3	1:A:511:PRO:HD3	1.89	0.54
1:A:672:ASN:ND2	1:A:863:LYS:HA	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:ALA:HB1	1:A:952:ILE:HA	1.90	0.53
1:B:476:LEU:HB3	1:B:535:PHE:CE1	2.43	0.53
1:A:1037:HIS:CD2	1:A:1038:ILE:H	2.26	0.53
1:A:48:GLU:CG	1:A:114:ALA:HB3	2.37	0.53
1:A:523:GLN:OE1	1:A:531:MSE:HB2	2.07	0.53
1:A:733:LEU:HG	1:A:790:THR:HB	1.90	0.53
1:A:846:MSE:SE	1:A:848:ASP:HA	2.59	0.53
1:A:918:ILE:O	1:A:947:LEU:HA	2.07	0.53
1:A:283:ASP:O	1:A:989:PRO:HA	2.07	0.53
1:B:752:LEU:C	1:B:754:THR:N	2.55	0.53
1:A:107:PHE:O	1:A:111:ILE:HB	2.08	0.53
1:A:735:THR:CB	1:A:804:ARG:HH22	2.22	0.53
1:B:558:SER:HA	1:B:560:ARG:HG2	1.90	0.53
1:B:244:ARG:O	1:B:992:ALA:HA	2.09	0.53
1:B:703:VAL:HG23	1:B:733:LEU:HB3	1.91	0.53
1:A:1038:ILE:HD12	1:A:1039:LEU:HB2	1.90	0.53
1:A:102:LEU:O	1:A:106:LYS:HD3	2.09	0.53
1:B:669:ARG:NH2	1:B:797:LEU:O	2.42	0.53
1:A:150:MSE:O	1:A:151:GLN:HB2	2.06	0.53
1:A:905:SER:HB3	1:A:942:ASN:HB2	1.91	0.53
1:A:119:GLU:O	1:A:123:GLN:HG3	2.09	0.53
1:A:474:ILE:O	1:A:506:LEU:N	2.34	0.53
1:A:533:LYS:HA	1:A:536:GLN:HG3	1.91	0.53
1:A:583:ASP:O	1:A:587:ARG:N	2.34	0.53
1:A:643:TRP:CD1	1:A:645:PRO:HD2	2.44	0.53
1:A:926:GLN:HE22	1:A:958:ILE:HD11	1.73	0.53
1:B:292:VAL:HG23	1:B:293:ALA:H	1.73	0.53
1:A:581:VAL:O	1:A:585:THR:HG23	2.09	0.53
1:A:944:LYS:HE2	1:A:946:PHE:CZ	2.44	0.53
1:B:107:PHE:CD2	1:B:373:LEU:HD13	2.43	0.53
1:B:607:LEU:O	1:B:608:LEU:HD23	2.09	0.53
1:A:36:LEU:HD11	1:A:1006:VAL:HG21	1.91	0.53
1:A:527:GLY:C	1:A:562:LEU:HD11	2.29	0.53
1:B:558:SER:CA	1:B:560:ARG:HG2	2.39	0.53
1:B:380:ARG:HB2	1:B:912:ILE:HD11	1.91	0.53
1:B:705:ASP:HA	1:B:734:HIS:CD2	2.45	0.52
1:B:763:LEU:O	1:B:766:ILE:HG12	2.09	0.52
1:A:247:TYR:CE2	1:A:956:LEU:HD21	2.44	0.52
1:B:100:ALA:HA	1:B:103:SER:HB3	1.90	0.52
1:B:125:TYR:CD2	1:B:222:PRO:HD3	2.44	0.52
1:B:249:MSE:HE2	1:B:956:LEU:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:VAL:HG21	1:B:794:ALA:CB	2.40	0.52
1:B:147:MSE:O	1:B:149:GLY:N	2.37	0.52
1:B:581:VAL:O	1:B:585:THR:HG23	2.09	0.52
1:B:711:GLY:O	1:B:714:LEU:HB3	2.09	0.52
1:B:824:GLU:H	1:B:824:GLU:CD	2.13	0.52
1:A:990:GLU:HG2	1:A:1020:LEU:CB	2.40	0.52
1:B:130:GLU:HA	1:B:133:LEU:HD12	1.91	0.52
1:A:314:THR:O	1:A:318:GLN:HG3	2.09	0.52
1:A:974:GLU:CB	1:A:976:GLY:H	2.23	0.52
1:A:378:HIS:HA	1:A:381:GLN:NE2	2.15	0.52
1:A:32:VAL:HB	1:A:985:PHE:HB2	1.90	0.52
1:B:250:ILE:N	1:B:289:SER:HA	2.24	0.52
1:B:432:LEU:CD1	1:B:503:LEU:HD13	2.40	0.52
1:A:292:VAL:HG23	1:A:293:ALA:H	1.74	0.52
1:B:240:LEU:HD12	1:B:988:LEU:HD21	1.91	0.52
1:B:1008:PRO:HB3	1:B:1033:TYR:CE1	2.45	0.52
1:B:434:ASP:N	1:B:438:ASP:OD2	2.39	0.52
1:B:339:GLU:HG3	1:B:900:SER:OG	2.10	0.52
1:A:247:TYR:CZ	1:A:956:LEU:HD21	2.45	0.52
1:A:247:TYR:OH	1:A:956:LEU:HD11	2.10	0.52
1:B:290:SER:HA	1:B:292:VAL:HG22	1.91	0.52
1:B:672:ASN:ND2	1:B:866:SER:OG	2.39	0.52
1:A:1000:VAL:HG22	1:A:1001:PRO:HD2	1.92	0.51
1:A:52:ALA:HB2	1:A:114:ALA:HB2	1.91	0.51
1:A:763:LEU:HA	1:A:766:ILE:HD12	1.91	0.51
1:A:239:GLU:HG2	1:A:960:ARG:HH21	1.74	0.51
1:A:93:GLU:HB2	1:A:96:ILE:HG22	1.92	0.51
1:B:56:GLU:OE2	1:B:105:PHE:HA	2.10	0.51
1:B:200:GLU:HB3	1:B:203:ARG:HD3	1.92	0.51
1:B:597:ARG:NH1	1:B:658:GLU:OE1	2.42	0.51
1:A:337:LEU:HG	1:A:340:TYR:HB3	1.92	0.51
1:A:390:GLY:O	1:A:854:LYS:HD3	2.10	0.51
1:B:347:SER:O	1:B:348:LEU:HB2	2.09	0.51
1:B:490:GLN:O	1:B:493:ILE:HB	2.10	0.51
1:A:208:MSE:CG	1:A:213:GLN:HB2	2.40	0.51
1:A:673:LEU:N	1:A:675:GLN:HE22	2.07	0.51
1:A:346:ALA:HB1	1:A:895:TRP:HB2	1.93	0.51
1:A:951:ARG:HD3	1:A:951:ARG:H	1.75	0.51
1:B:764:GLU:OE1	1:B:767:GLN:NE2	2.44	0.51
1:B:789:GLN:HB2	1:B:793:LEU:HD21	1.91	0.51
1:B:393:ASN:HD22	1:B:911:SER:HB2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:ALA:HA	1:A:1035:LEU:HB3	1.93	0.51
1:A:111:ILE:CG2	1:A:111:ILE:O	2.58	0.51
1:A:465:ARG:HE	1:A:644:LEU:CD1	2.22	0.51
1:B:203:ARG:O	1:B:207:ALA:N	2.36	0.51
1:B:917:THR:C	1:B:918:ILE:HD12	2.31	0.51
1:A:638:VAL:HG21	1:A:642:THR:CG2	2.39	0.51
1:A:734:HIS:NE2	1:A:749:TYR:OH	2.41	0.51
1:B:465:ARG:NH1	1:B:642:THR:O	2.44	0.51
1:B:244:ARG:CB	1:B:993:LEU:HB2	2.40	0.51
1:A:305:ASP:OD2	1:A:330:TYR:OH	2.13	0.51
1:A:562:LEU:C	1:A:563:ARG:HD3	2.30	0.51
1:B:124:TYR:CZ	1:B:173:LEU:HD11	2.45	0.51
1:B:32:VAL:HG22	1:B:1029:VAL:HB	1.91	0.51
1:B:432:LEU:HD11	1:B:503:LEU:HD13	1.92	0.51
1:B:449:ASP:OD1	1:B:633:ILE:HD13	2.11	0.51
1:B:78:THR:HG22	1:B:81:GLU:HG3	1.92	0.51
1:B:735:THR:HG21	1:B:802:GLY:N	2.24	0.51
1:A:370:TYR:HH	1:A:1004:TRP:HZ2	1.58	0.51
1:A:709:GLU:C	1:A:711:GLY:H	2.14	0.51
1:B:200:GLU:OE1	1:B:203:ARG:HD3	2.11	0.51
1:B:206:SER:O	1:B:210:LYS:N	2.43	0.51
1:B:493:ILE:O	1:B:496:LEU:N	2.42	0.51
1:B:647:TYR:HA	1:B:651:GLN:NE2	2.25	0.51
1:A:31:SER:O	1:A:1028:ASP:HB2	2.10	0.51
1:A:435:LEU:HA	1:A:441:TYR:CD2	2.44	0.51
1:A:459:GLN:O	1:A:460:LEU:HB2	2.10	0.51
1:B:63:PRO:O	1:B:66:ASP:HB2	2.10	0.51
1:B:353:ASN:OD1	1:B:918:ILE:HA	2.10	0.51
1:A:791:LYS:O	1:A:794:ALA:HB3	2.11	0.51
1:B:339:GLU:OE2	1:B:898:ALA:HB3	2.11	0.51
1:B:578:LEU:HA	1:B:582:MSE:HB2	1.93	0.51
1:B:347:SER:OG	1:B:893:LYS:HG3	2.11	0.51
1:B:911:SER:O	1:B:912:ILE:HG13	2.10	0.51
1:A:532:MSE:O	1:A:535:PHE:N	2.44	0.50
1:B:334:GLN:O	1:B:337:LEU:HB2	2.11	0.50
1:A:284:LEU:O	1:A:285:LYS:HB2	2.09	0.50
1:A:569:PHE:CD1	1:A:570:GLU:HB3	2.45	0.50
1:A:804:ARG:N	1:A:815:PRO:HB3	2.24	0.50
1:B:418:ASP:CG	1:B:655:THR:HG22	2.32	0.50
1:B:106:LYS:O	1:B:970:PRO:HD3	2.10	0.50
1:A:427:ASP:OD1	1:A:584:LYS:NZ	2.35	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:521:TYR:HE2	1:B:556:ILE:HD11	1.76	0.50
1:B:612:ASP:OD1	1:B:616:GLN:NE2	2.42	0.50
1:A:533:LYS:HE2	1:A:561:VAL:CG2	2.41	0.50
1:B:48:GLU:OE2	1:B:112:ARG:NH2	2.44	0.50
1:B:866:SER:O	1:B:870:LEU:HD13	2.11	0.50
1:A:481:ASP:CG	1:A:610:ARG:HH12	2.15	0.50
1:B:497:ILE:HG22	1:B:499:VAL:HG23	1.93	0.50
1:A:427:ASP:O	1:A:520:ARG:NH2	2.45	0.50
1:A:565:LYS:HG2	1:A:566:ALA:H	1.76	0.50
1:A:427:ASP:H	1:A:584:LYS:NZ	2.09	0.50
1:A:587:ARG:NH2	1:A:590:LYS:HE3	2.26	0.50
1:B:488:HIS:N	1:B:488:HIS:CD2	2.79	0.50
1:B:517:LYS:HZ3	1:B:578:LEU:HD12	1.76	0.50
1:B:71:GLY:C	1:B:73:LEU:H	2.15	0.50
1:B:834:GLU:O	1:B:838:ARG:HB3	2.12	0.50
1:A:1006:VAL:HA	1:A:1034:GLU:O	2.12	0.50
1:A:705:ASP:OD1	1:A:736:SER:OG	2.29	0.50
1:A:83:TYR:CZ	1:A:87:LEU:HD11	2.47	0.50
1:B:232:PHE:CD2	1:B:980:ARG:HB2	2.47	0.50
1:B:525:THR:O	1:B:564:GLY:HA2	2.12	0.50
1:A:433:ASN:CB	1:A:501:PHE:H	2.25	0.49
1:B:195:SER:O	1:B:198:PHE:HD2	1.95	0.49
1:B:200:GLU:HA	1:B:203:ARG:H	1.77	0.49
1:A:209:ALA:N	1:A:210:LYS:HG2	2.27	0.49
1:A:319:ASP:OD2	1:A:963:ARG:NH2	2.46	0.49
1:A:591:ARG:O	1:A:656:ARG:HA	2.13	0.49
1:B:47:LEU:O	1:B:51:GLU:N	2.34	0.49
1:A:679:SER:O	1:A:681:ASP:N	2.46	0.49
1:B:145:VAL:HG21	1:B:205:LEU:HD11	1.95	0.49
1:A:388:LYS:HE3	1:A:389:LEU:HD22	1.94	0.49
1:A:110:ALA:HB2	1:A:969:GLU:C	2.33	0.49
1:B:1028:ASP:N	1:B:1028:ASP:OD1	2.44	0.49
1:B:392:SER:HB3	1:B:395:GLU:HG3	1.94	0.49
1:A:100:ALA:HB1	1:A:380:ARG:NH2	2.17	0.49
1:A:202:HIS:CE1	1:A:206:SER:HB2	2.47	0.49
1:A:704:GLY:N	1:A:733:LEU:O	2.40	0.49
1:A:831:LEU:HA	1:A:834:GLU:HB3	1.93	0.49
1:B:713:ASN:HA	1:B:716:ILE:HG12	1.95	0.49
1:A:309:PRO:HG2	1:A:902:ILE:HG23	1.93	0.49
1:A:338:ASP:N	1:A:338:ASP:OD1	2.38	0.49
1:A:851:LEU:HD23	1:A:854:LYS:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ALA:CB	1:A:380:ARG:HH21	2.17	0.49
1:A:632:SER:OG	1:A:633:ILE:N	2.44	0.49
1:A:753:ARG:HG2	1:A:753:ARG:O	2.12	0.49
1:A:951:ARG:HB2	1:A:952:ILE:HG22	1.94	0.49
1:B:443:ASP:N	1:B:443:ASP:OD1	2.42	0.49
1:A:393:ASN:OD1	1:A:393:ASN:N	2.45	0.49
1:A:939:ASN:C	1:A:939:ASN:OD1	2.51	0.49
1:B:705:ASP:OD1	1:B:734:HIS:NE2	2.45	0.49
1:A:530:ALA:H	1:A:562:LEU:HD22	1.78	0.49
1:A:696:ASN:O	1:A:858:SER:HB3	2.11	0.49
1:A:785:ALA:HA	1:A:787:TRP:CE2	2.48	0.49
1:A:735:THR:HB	1:A:804:ARG:NH2	2.28	0.49
1:A:96:ILE:O	1:A:102:LEU:HB2	2.12	0.49
1:B:204:LYS:O	1:B:208:MSE:HB2	2.13	0.49
1:B:657:ASN:HB3	1:B:659:LEU:H	1.76	0.49
1:B:67:ARG:HG3	1:B:72:VAL:HG21	1.93	0.49
1:A:102:LEU:O	1:A:106:LYS:NZ	2.39	0.48
1:A:427:ASP:H	1:A:584:LYS:HZ1	1.60	0.48
1:B:292:VAL:HG23	1:B:293:ALA:N	2.28	0.48
1:B:349:PRO:HB3	1:B:352:ARG:HH11	1.77	0.48
1:B:360:LEU:HD12	1:B:890:SER:N	2.27	0.48
1:B:657:ASN:HB3	1:B:659:LEU:HB3	1.95	0.48
1:A:463:VAL:HG12	1:A:465:ARG:HG3	1.95	0.48
1:A:504:VAL:HG11	1:A:588:TYR:CE2	2.48	0.48
1:A:704:GLY:HA2	1:A:804:ARG:HG2	1.95	0.48
1:B:90:VAL:HB	1:B:95:HIS:HE1	1.78	0.48
1:A:849:LEU:HD23	1:A:849:LEU:N	2.29	0.48
1:A:849:LEU:O	1:A:850:ASN:HB2	2.12	0.48
1:B:555:THR:HA	1:B:558:SER:CB	2.43	0.48
1:A:487:GLN:O	1:A:491:THR:HG23	2.13	0.48
1:A:807:LEU:HD23	1:A:812:ALA:HA	1.95	0.48
1:B:476:LEU:O	1:B:515:GLN:HG2	2.14	0.48
1:B:857:GLY:O	1:B:861:PHE:N	2.46	0.48
1:B:974:GLU:HG2	1:B:977:ALA:HB3	1.96	0.48
1:B:35:ALA:N	1:B:1031:ALA:O	2.38	0.48
1:B:249:MSE:SE	1:B:292:VAL:CG2	3.07	0.48
1:B:353:ASN:HA	1:B:917:THR:O	2.13	0.48
1:B:485:VAL:HA	1:B:489:ILE:CG1	2.43	0.48
1:B:705:ASP:C	1:B:707:ASP:H	2.16	0.48
1:A:111:ILE:HG22	1:A:113:SER:OG	2.13	0.48
1:A:237:GLY:O	1:A:999:ASP:N	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:LYS:CE	1:A:389:LEU:HD22	2.44	0.48
1:A:449:ASP:HA	1:A:633:ILE:HD11	1.96	0.48
1:A:657:ASN:OD1	1:A:659:LEU:N	2.36	0.48
1:A:710:ALA:N	1:A:819:THR:OG1	2.47	0.48
1:B:749:TYR:CD1	1:B:749:TYR:N	2.79	0.48
1:A:485:VAL:HA	1:A:489:ILE:CG1	2.44	0.48
1:A:587:ARG:HG3	1:A:587:ARG:O	2.13	0.48
1:B:29:ASP:HA	1:B:1026:GLY:H	1.77	0.48
1:B:147:MSE:HG2	1:B:148:ASP:N	2.28	0.48
1:B:659:LEU:HD22	1:B:821:THR:OG1	2.12	0.48
1:B:1025:GLU:C	1:B:1027:SER:H	2.16	0.48
1:A:152:TYR:OH	1:B:707:ASP:O	2.32	0.48
1:A:185:PRO:HB2	1:A:214:VAL:HG13	1.95	0.48
1:A:540:GLU:O	1:A:543:LYS:HE3	2.13	0.48
1:A:633:ILE:HA	1:A:637:ALA:CB	2.44	0.48
1:A:667:LYS:HE3	1:A:669:ARG:CD	2.43	0.48
1:A:705:ASP:O	1:A:708:SER:OG	2.27	0.48
1:A:712:LEU:O	1:A:716:ILE:N	2.26	0.48
1:B:355:LEU:HD21	1:B:357:ILE:HG13	1.95	0.48
1:A:107:PHE:CE2	1:A:111:ILE:HD11	2.49	0.48
1:B:712:LEU:HA	1:B:715:LEU:HB3	1.95	0.48
1:B:893:LYS:NZ	1:B:895:TRP:HB3	2.29	0.48
1:B:92:ASP:N	1:B:92:ASP:OD1	2.47	0.48
1:A:660:ILE:O	1:A:662:PRO:HD3	2.14	0.47
1:A:998:MSE:HE3	1:A:998:MSE:HB3	1.70	0.47
1:B:320:PHE:O	1:B:323:TYR:N	2.47	0.47
1:A:388:LYS:CD	1:A:389:LEU:HD13	2.37	0.47
1:A:527:GLY:HA3	1:A:562:LEU:HD11	1.96	0.47
1:A:707:ASP:CG	1:A:745:SER:HB3	2.33	0.47
1:A:108:SER:CA	1:A:111:ILE:HB	2.43	0.47
1:A:208:MSE:N	1:A:210:LYS:HZ2	2.05	0.47
1:A:226:ALA:O	1:A:229:ARG:NH1	2.47	0.47
1:A:333:THR:O	1:A:336:PHE:HB3	2.14	0.47
1:A:748:LEU:CA	1:A:751:LEU:HD21	2.42	0.47
1:A:309:PRO:HB2	1:A:902:ILE:HD12	1.96	0.47
1:B:110:ALA:HB2	1:B:970:PRO:HD3	1.95	0.47
1:B:54:ALA:HA	1:B:57:ASN:O	2.14	0.47
1:B:635:GLN:O	1:B:637:ALA:N	2.47	0.47
1:A:357:ILE:O	1:A:360:LEU:HB3	2.15	0.47
1:B:628:LEU:O	1:B:631:GLN:HB3	2.13	0.47
1:B:735:THR:HG22	1:B:791:LYS:HZ1	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:ARG:C	1:A:379:GLU:H	2.17	0.47
1:A:600:PRO:HB2	1:A:607:LEU:HD22	1.95	0.47
1:B:146:HIS:ND1	1:B:188:ILE:HD12	2.30	0.47
1:B:154:SER:O	1:B:156:THR:N	2.43	0.47
1:B:210:LYS:HD3	1:B:211:GLU:CD	2.34	0.47
1:B:439:LYS:N	1:B:439:LYS:HD3	2.29	0.47
1:B:558:SER:C	1:B:560:ARG:N	2.66	0.47
1:B:993:LEU:O	1:B:994:LEU:HD23	2.15	0.47
1:A:292:VAL:O	1:A:295:LEU:N	2.47	0.47
1:A:599:PRO:O	1:A:610:ARG:HD3	2.15	0.47
1:A:78:THR:HG23	1:A:81:GLU:HG3	1.96	0.47
1:A:926:GLN:OE1	1:A:958:ILE:HD13	2.15	0.47
1:A:380:ARG:HH12	1:A:941:VAL:CG2	2.28	0.47
1:A:918:ILE:N	1:A:946:PHE:O	2.46	0.47
1:B:669:ARG:NH1	1:B:813:VAL:O	2.47	0.47
1:B:735:THR:HG22	1:B:791:LYS:NZ	2.29	0.47
1:B:799:TYR:OH	1:B:813:VAL:N	2.30	0.47
1:A:355:LEU:O	1:A:362:ILE:N	2.36	0.47
1:A:672:ASN:CA	1:A:675:GLN:HE22	2.27	0.47
1:B:627:GLN:HA	1:B:630:GLN:HB2	1.97	0.47
1:B:340:TYR:HH	1:B:948:THR:HA	1.75	0.47
1:A:203:ARG:O	1:A:206:SER:HB3	2.15	0.47
1:A:289:SER:O	1:A:292:VAL:HG13	2.14	0.47
1:A:351:GLY:HA2	1:A:948:THR:O	2.13	0.47
1:A:349:PRO:HA	1:A:352:ARG:NH2	2.29	0.47
1:A:416:ARG:NH2	1:A:604:ASN:O	2.44	0.47
1:B:46:LEU:O	1:B:49:LEU:HB2	2.15	0.47
1:B:745:SER:O	1:B:749:TYR:CZ	2.68	0.47
1:A:210:LYS:H	1:A:210:LYS:CD	2.09	0.47
1:A:39:SER:HB3	1:A:1036:GLU:HA	1.96	0.47
1:A:77:VAL:HA	1:A:82:LEU:HD23	1.96	0.47
1:A:791:LYS:O	1:A:795:ALA:N	2.32	0.47
1:B:424:GLU:HG2	1:B:588:TYR:N	2.30	0.47
1:B:789:GLN:O	1:B:793:LEU:HG	2.14	0.47
1:A:303:ILE:HD13	1:A:313:LEU:CD1	2.45	0.47
1:A:804:ARG:HG3	1:A:805:GLY:H	1.80	0.47
1:B:55:ALA:HB1	1:B:377:ARG:HH22	1.79	0.47
1:B:401:LEU:O	1:B:402:HIS:CD2	2.68	0.47
1:B:460:LEU:HA	1:B:460:LEU:HD23	1.63	0.47
1:B:521:TYR:HE1	1:B:568:SER:HB3	1.79	0.47
1:B:109:LEU:HB2	1:B:970:PRO:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1028:ASP:N	1:A:1028:ASP:OD1	2.48	0.47
1:A:90:VAL:HB	1:A:96:ILE:HG21	1.96	0.47
1:B:353:ASN:HB3	1:B:928:TRP:CZ3	2.50	0.47
1:B:517:LYS:HZ1	1:B:578:LEU:HD12	1.80	0.47
1:A:797:LEU:HD22	1:A:807:LEU:CD1	2.44	0.46
1:A:293:ALA:HA	1:A:953:LEU:N	2.30	0.46
1:B:467:VAL:O	1:B:645:PRO:HG3	2.15	0.46
1:B:696:ASN:OD1	1:B:858:SER:OG	2.33	0.46
1:B:698:LEU:O	1:B:729:GLU:N	2.37	0.46
1:B:792:GLN:HG2	1:B:795:ALA:HB3	1.96	0.46
1:B:703:VAL:HG21	1:B:794:ALA:HB2	1.97	0.46
1:A:363:ASP:OD1	1:A:364:SER:N	2.48	0.46
1:B:211:GLU:OE2	1:B:213:GLN:N	2.49	0.46
1:B:826:ASP:O	1:B:829:ILE:HG22	2.16	0.46
1:A:152:TYR:HE1	1:B:709:GLU:OE2	1.99	0.46
1:A:934:THR:HG21	1:A:966:LEU:HG	1.97	0.46
1:B:484:MSE:SE	1:B:610:ARG:HH12	2.48	0.46
1:B:549:GLN:HA	1:B:552:PHE:HB3	1.98	0.46
1:A:435:LEU:H	1:A:500:ARG:HD2	1.81	0.46
1:A:763:LEU:HD12	1:A:766:ILE:HD12	1.98	0.46
1:B:1008:PRO:HB3	1:B:1033:TYR:CZ	2.50	0.46
1:B:291:GLU:HB3	1:B:328:ALA:HB1	1.97	0.46
1:B:298:ASN:N	1:B:298:ASN:OD1	2.49	0.46
1:B:111:ILE:HD11	1:B:369:ALA:HB1	1.97	0.46
1:B:483:TYR:O	1:B:484:MSE:C	2.54	0.46
1:B:562:LEU:HB3	1:B:563:ARG:H	1.29	0.46
1:A:236:TYR:HB3	1:A:1000:VAL:HG23	1.96	0.46
1:A:223:PRO:HB2	1:A:227:SER:OG	2.16	0.46
1:A:712:LEU:O	1:A:716:ILE:HG23	2.15	0.46
1:B:1037:HIS:CG	1:B:1038:ILE:H	2.34	0.46
1:B:135:THR:HG21	1:B:139:ALA:N	2.30	0.46
1:B:463:VAL:HG12	1:B:463:VAL:O	2.15	0.46
1:B:593:ASP:OD2	1:B:658:GLU:HG3	2.15	0.46
1:B:636:ASP:N	1:B:636:ASP:OD1	2.48	0.46
1:B:718:ALA:O	1:B:721:PHE:HB3	2.15	0.46
1:B:672:ASN:HB2	1:B:866:SER:HB3	1.96	0.46
1:B:237:GLY:HA3	1:B:962:TYR:OH	2.16	0.46
1:A:377:ARG:HD3	1:A:380:ARG:HB2	1.97	0.46
1:A:530:ALA:HA	1:A:533:LYS:HG3	1.95	0.46
1:A:481:ASP:OD1	1:A:610:ARG:NH1	2.48	0.46
1:A:951:ARG:HD3	1:A:951:ARG:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:996:LEU:HD13	1:B:1015:LEU:HD22	1.98	0.46
1:B:39:SER:OG	1:B:40:PHE:N	2.49	0.46
1:B:463:VAL:C	1:B:465:ARG:N	2.69	0.46
1:A:240:LEU:HA	1:A:240:LEU:HD23	1.62	0.46
1:B:712:LEU:H	1:B:712:LEU:HD12	1.79	0.46
1:A:291:GLU:O	1:A:294:ARG:HB3	2.15	0.46
1:A:487:GLN:OE1	1:A:488:HIS:HB3	2.16	0.46
1:B:522:LEU:HB3	1:B:531:MSE:HB2	1.98	0.46
1:B:84:ASP:HA	1:B:87:LEU:CD1	2.46	0.46
1:A:188:ILE:HD13	1:A:219:ARG:NH1	2.31	0.46
1:A:296:GLY:HA3	1:A:953:LEU:HD11	1.98	0.46
1:A:911:SER:O	1:A:912:ILE:HG13	2.16	0.46
1:B:80:LYS:HB2	1:B:972:PHE:CG	2.50	0.46
1:A:336:PHE:CG	1:A:337:LEU:HD13	2.50	0.46
1:A:530:ALA:H	1:A:562:LEU:CD2	2.28	0.46
1:B:211:GLU:HG3	1:B:212:GLY:H	1.78	0.46
1:B:608:LEU:HD13	1:B:617:GLU:HB2	1.98	0.46
1:B:716:ILE:O	1:B:720:LYS:HG3	2.16	0.46
1:A:460:LEU:HD21	1:A:626:LEU:HD11	1.98	0.45
1:A:709:GLU:C	1:A:711:GLY:N	2.69	0.45
1:B:349:PRO:CB	1:B:352:ARG:HE	2.25	0.45
1:B:487:GLN:HB3	1:B:488:HIS:HD2	1.81	0.45
1:B:766:ILE:O	1:B:769:ILE:HG12	2.17	0.45
1:B:836:SER:HG	1:B:837:LYS:H	1.57	0.45
1:A:630:GLN:O	1:A:634:VAL:HG22	2.16	0.45
1:A:655:THR:H	1:A:656:ARG:CZ	2.29	0.45
1:B:987:ARG:O	1:B:987:ARG:CG	2.65	0.45
1:A:292:VAL:HG23	1:A:293:ALA:N	2.30	0.45
1:A:793:LEU:O	1:A:797:LEU:HD11	2.17	0.45
1:B:632:SER:O	1:B:637:ALA:HB2	2.15	0.45
1:B:733:LEU:HD11	1:B:790:THR:HA	1.97	0.45
1:B:903:THR:HG22	1:B:944:LYS:HD3	1.97	0.45
1:A:447:ASP:HB2	1:A:450:ALA:HB3	1.97	0.45
1:A:699:LEU:O	1:A:809:ASN:N	2.49	0.45
1:A:735:THR:HG23	1:A:791:LYS:CD	2.46	0.45
1:B:342:ALA:HB1	1:B:895:TRP:HH2	1.80	0.45
1:A:290:SER:HA	1:A:292:VAL:HG22	1.98	0.45
1:A:380:ARG:O	1:A:384:GLY:N	2.48	0.45
1:A:766:ILE:O	1:A:769:ILE:HG12	2.17	0.45
1:B:1010:GLU:H	1:B:1010:GLU:CD	2.19	0.45
1:B:1023:LEU:HD11	1:B:1029:VAL:HG23	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:ARG:O	1:B:173:LEU:HG	2.17	0.45
1:B:204:LYS:HD2	1:B:208:MSE:HG3	1.97	0.45
1:B:29:ASP:HA	1:B:1025:GLU:HG2	1.98	0.45
1:B:463:VAL:HB	1:B:498:PRO:HB2	1.98	0.45
1:B:672:ASN:O	1:B:674:VAL:N	2.50	0.45
1:B:710:ALA:HA	1:B:713:ASN:OD1	2.16	0.45
1:B:78:THR:HG23	1:B:81:GLU:HG3	1.95	0.45
1:B:799:TYR:HE1	1:B:813:VAL:HG23	1.81	0.45
1:A:310:PHE:O	1:A:313:LEU:HB3	2.16	0.45
1:A:444:PHE:HB3	1:A:462:ALA:O	2.17	0.45
1:A:660:ILE:HA	1:A:660:ILE:HD13	1.85	0.45
1:A:772:THR:O	1:A:773:SER:OG	2.23	0.45
1:B:150:MSE:HB3	1:B:151:GLN:H	1.61	0.45
1:B:167:ASP:O	1:B:168:LEU:HD23	2.16	0.45
1:B:62:PHE:O	1:B:66:ASP:N	2.42	0.45
1:B:465:ARG:NH2	1:B:640:GLU:OE2	2.49	0.45
1:B:708:SER:OG	1:B:710:ALA:N	2.49	0.45
1:B:734:HIS:CD2	1:B:735:THR:N	2.82	0.45
1:B:786:TYR:HB2	1:B:787:TRP:HE3	1.82	0.45
1:A:187:ALA:N	1:A:215:SER:O	2.33	0.45
1:A:643:TRP:CE3	1:A:646:SER:HB3	2.51	0.45
1:A:675:GLN:C	1:A:677:ALA:N	2.69	0.45
1:A:761:GLU:C	1:A:765:LYS:HZ2	2.19	0.45
1:B:445:PRO:HG2	1:B:462:ALA:HB2	1.98	0.45
1:B:558:SER:O	1:B:560:ARG:HG2	2.17	0.45
1:A:516:ALA:O	1:A:520:ARG:HG2	2.16	0.45
1:A:530:ALA:HB2	1:A:562:LEU:CD2	2.47	0.45
1:A:569:PHE:HD1	1:A:570:GLU:HB3	1.82	0.45
1:A:855:VAL:HG13	1:A:860:GLU:HG3	1.99	0.45
1:B:123:GLN:O	1:B:127:THR:OG1	2.25	0.45
1:B:787:TRP:HE3	1:B:787:TRP:H	1.64	0.45
1:A:515:GLN:HG3	1:A:535:PHE:CZ	2.52	0.45
1:A:62:PHE:CD1	1:A:179:LEU:HD22	2.51	0.45
1:A:702:VAL:HG11	1:A:718:ALA:CB	2.47	0.45
1:A:725:HIS:CE1	1:A:828:GLU:CD	2.91	0.45
1:A:789:GLN:HB3	1:A:793:LEU:HD22	1.97	0.45
1:B:178:LYS:HE3	1:B:178:LYS:HB3	1.47	0.45
1:A:249:MSE:HE1	1:A:292:VAL:HG21	1.98	0.45
1:A:351:GLY:N	1:A:951:ARG:HH12	2.14	0.45
1:B:208:MSE:C	1:B:210:LYS:HD2	2.36	0.45
1:B:698:LEU:HD13	1:B:808:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1014:ASP:HB3	1:A:1017:ASN:HB2	2.00	0.44
1:A:616:GLN:O	1:A:620:MSE:N	2.47	0.44
1:B:202:HIS:CE1	1:B:206:SER:HB2	2.52	0.44
1:A:209:ALA:H	1:A:210:LYS:CE	2.31	0.44
1:A:292:VAL:C	1:A:294:ARG:N	2.70	0.44
1:A:460:LEU:HD23	1:A:460:LEU:HA	1.76	0.44
1:B:599:PRO:HA	1:B:600:PRO:HD3	1.76	0.44
1:A:401:LEU:O	1:A:402:HIS:HB3	2.17	0.44
1:A:733:LEU:HD21	1:A:790:THR:HA	1.99	0.44
1:A:78:THR:HG22	1:A:81:GLU:OE1	2.16	0.44
1:B:111:ILE:O	1:B:112:ARG:HB2	2.17	0.44
1:B:111:ILE:HG22	1:B:113:SER:HB3	1.99	0.44
1:B:147:MSE:HA	1:B:186:LEU:O	2.17	0.44
1:B:616:GLN:HG3	1:B:616:GLN:H	1.42	0.44
1:A:859:VAL:O	1:A:862:ALA:HB3	2.17	0.44
1:B:205:LEU:O	1:B:208:MSE:C	2.55	0.44
1:B:246:ASP:O	1:B:248:ILE:N	2.49	0.44
1:B:450:ALA:HA	1:B:452:LEU:HG	2.00	0.44
1:B:459:GLN:O	1:B:460:LEU:HB2	2.18	0.44
1:B:858:SER:HA	1:B:861:PHE:CB	2.41	0.44
1:B:293:ALA:CB	1:B:952:ILE:HG13	2.45	0.44
1:A:107:PHE:CD1	1:A:968:PRO:HA	2.53	0.44
1:A:169:GLU:OE1	1:A:171:ARG:HB2	2.18	0.44
1:A:207:ALA:C	1:A:210:LYS:HG3	2.38	0.44
1:A:334:GLN:HG3	1:A:335:GLU:OE1	2.17	0.44
1:A:402:HIS:CD2	1:A:402:HIS:C	2.90	0.44
1:A:530:ALA:HB2	1:A:562:LEU:HD23	1.99	0.44
1:A:616:GLN:O	1:A:620:MSE:HG3	2.17	0.44
1:A:936:SER:HB3	1:A:943:VAL:HB	1.99	0.44
1:A:110:ALA:HB2	1:A:970:PRO:N	2.32	0.44
1:B:602:LEU:HA	1:B:602:LEU:HD23	1.59	0.44
1:B:313:LEU:HD21	1:B:929:VAL:HG22	1.99	0.44
1:A:485:VAL:HA	1:A:489:ILE:HB	1.99	0.44
1:A:917:THR:C	1:A:918:ILE:HD12	2.37	0.44
1:B:190:TYR:CZ	1:B:219:ARG:HD2	2.51	0.44
1:B:188:ILE:HD13	1:B:219:ARG:CZ	2.47	0.44
1:B:666:SER:OG	1:B:668:ILE:HD11	2.18	0.44
1:B:83:TYR:O	1:B:87:LEU:HD12	2.18	0.44
1:A:448:ILE:HG22	1:A:465:ARG:CD	2.48	0.44
1:A:419:TRP:CZ3	1:A:649:LEU:HD13	2.53	0.44
1:A:672:ASN:C	1:A:675:GLN:NE2	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:VAL:HG23	1:A:733:LEU:HB3	1.99	0.44
1:B:298:ASN:ND2	1:B:327:VAL:O	2.50	0.44
1:B:746:SER:HA	1:B:749:TYR:CG	2.53	0.44
1:B:789:GLN:OE1	1:B:789:GLN:N	2.50	0.44
1:A:62:PHE:N	1:A:63:PRO:HD2	2.32	0.44
1:A:784:LEU:HB3	1:A:787:TRP:CH2	2.53	0.44
1:B:675:GLN:O	1:B:680:HIS:ND1	2.37	0.44
1:B:929:VAL:O	1:B:933:ARG:N	2.42	0.44
1:A:298:ASN:N	1:A:298:ASN:OD1	2.50	0.44
1:A:515:GLN:HE22	1:A:547:PRO:HB3	1.82	0.44
1:A:84:ASP:HA	1:A:87:LEU:CD1	2.48	0.44
1:B:105:PHE:O	1:B:109:LEU:HD12	2.18	0.44
1:B:113:SER:O	1:B:116:PRO:HD2	2.18	0.44
1:B:203:ARG:HG2	1:B:204:LYS:N	2.32	0.44
1:B:537:ARG:NH2	1:B:540:GLU:OE1	2.51	0.44
1:B:417:TYR:N	1:B:605:GLY:O	2.51	0.44
1:B:807:LEU:HD23	1:B:812:ALA:HA	1.99	0.44
1:A:351:GLY:N	1:A:951:ARG:HH22	2.16	0.43
1:A:836:SER:HB3	1:A:838:ARG:H	1.83	0.43
1:A:310:PHE:CZ	1:A:933:ARG:HB2	2.53	0.43
1:B:151:GLN:O	1:B:152:TYR:HD1	2.00	0.43
1:B:125:TYR:CE2	1:B:221:ARG:HG3	2.53	0.43
1:B:45:TYR:O	1:B:49:LEU:HG	2.18	0.43
1:B:467:VAL:O	1:B:648:PHE:HE2	2.01	0.43
1:B:513:LYS:O	1:B:516:ALA:N	2.50	0.43
1:A:188:ILE:HG21	1:A:219:ARG:NH1	2.32	0.43
1:A:532:MSE:O	1:A:536:GLN:HG3	2.18	0.43
1:A:974:GLU:OE1	1:A:977:ALA:O	2.36	0.43
1:B:371:SER:OG	1:B:372:LEU:N	2.49	0.43
1:B:842:VAL:O	1:B:846:MSE:HB2	2.18	0.43
1:B:847:LYS:HZ1	1:B:853:HIS:HB3	1.82	0.43
1:B:106:LYS:HB3	1:B:969:GLU:HB3	1.99	0.43
1:A:1000:VAL:HG21	1:A:1004:TRP:CE3	2.53	0.43
1:A:418:ASP:HB3	1:A:655:THR:HG22	1.99	0.43
1:A:950:VAL:HB	1:A:953:LEU:HG	1.99	0.43
1:B:1036:GLU:O	1:B:1037:HIS:HB2	2.19	0.43
1:B:250:ILE:N	1:B:288:SER:O	2.47	0.43
1:B:353:ASN:HB3	1:B:928:TRP:CE3	2.52	0.43
1:B:477:THR:HA	1:B:544:LEU:O	2.18	0.43
1:B:720:LYS:H	1:B:720:LYS:HG3	1.63	0.43
1:B:75:ASP:CG	1:B:85:ARG:HH21	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:ASN:HB3	1:A:501:PHE:H	1.84	0.43
1:A:527:GLY:CA	1:A:562:LEU:HD11	2.47	0.43
1:B:105:PHE:CE2	1:B:109:LEU:HD11	2.54	0.43
1:B:204:LYS:O	1:B:208:MSE:CB	2.66	0.43
1:B:349:PRO:CB	1:B:352:ARG:HH11	2.32	0.43
1:B:370:TYR:O	1:B:373:LEU:HB3	2.17	0.43
1:B:629:ILE:C	1:B:631:GLN:N	2.69	0.43
1:B:903:THR:HG22	1:B:944:LYS:CD	2.49	0.43
1:A:1037:HIS:CG	1:A:1038:ILE:N	2.85	0.43
1:A:567:GLN:OE1	1:A:569:PHE:N	2.52	0.43
1:A:672:ASN:HA	1:A:675:GLN:NE2	2.33	0.43
1:A:792:GLN:O	1:A:795:ALA:N	2.52	0.43
1:B:1023:LEU:HD13	1:B:1028:ASP:HA	2.01	0.43
1:B:399:LEU:O	1:B:401:LEU:HB2	2.18	0.43
1:B:550:ALA:O	1:B:554:GLU:HB2	2.19	0.43
1:A:56:GLU:CD	1:A:104:SER:OG	2.56	0.43
1:A:643:TRP:O	1:A:646:SER:OG	2.27	0.43
1:A:851:LEU:CD2	1:A:854:LYS:HG3	2.48	0.43
1:A:862:ALA:O	1:A:865:THR:OG1	2.36	0.43
1:A:244:ARG:HB2	1:A:993:LEU:HB2	2.01	0.43
1:B:31:SER:O	1:B:1028:ASP:HB2	2.18	0.43
1:B:455:THR:HB	1:B:456:TYR:H	1.62	0.43
1:B:551:LEU:HA	1:B:551:LEU:HD23	1.87	0.43
1:B:72:VAL:HG23	1:B:73:LEU:HD12	1.99	0.43
1:B:354:VAL:HG23	1:B:356:TRP:CH2	2.53	0.43
1:B:923:GLU:OE2	1:B:959:LYS:HG2	2.19	0.43
1:A:175:PHE:HE1	1:A:219:ARG:HG2	1.83	0.43
1:A:376:LEU:HG	1:A:912:ILE:CD1	2.49	0.43
1:A:63:PRO:O	1:A:66:ASP:HB2	2.19	0.43
1:B:205:LEU:O	1:B:216:TYR:CD2	2.71	0.43
1:B:377:ARG:HA	1:B:380:ARG:NH1	2.34	0.43
1:B:78:THR:HG22	1:B:81:GLU:OE2	2.19	0.43
1:A:107:PHE:O	1:A:111:ILE:N	2.52	0.43
1:A:706:PHE:CE2	1:A:734:HIS:HB3	2.54	0.43
1:A:811:ARG:HB2	1:A:834:GLU:OE2	2.18	0.43
1:B:244:ARG:N	1:B:993:LEU:HB2	2.34	0.43
1:B:355:LEU:HG	1:B:915:VAL:O	2.19	0.43
1:A:349:PRO:HA	1:A:352:ARG:HH22	1.83	0.43
1:A:388:LYS:HZ2	1:A:389:LEU:HD22	1.84	0.43
1:A:380:ARG:HH12	1:A:941:VAL:HG22	1.83	0.43
1:B:34:VAL:HA	1:B:1031:ALA:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:VAL:C	1:B:294:ARG:N	2.72	0.43
1:A:1000:VAL:CG2	1:A:1004:TRP:CE3	3.02	0.42
1:A:176:ASP:HB3	1:A:217:VAL:HG21	2.02	0.42
1:A:344:ARG:HA	1:A:348:LEU:HG	2.01	0.42
1:A:522:LEU:O	1:A:526:HIS:N	2.45	0.42
1:A:562:LEU:O	1:A:563:ARG:NH2	2.52	0.42
1:A:629:ILE:O	1:A:633:ILE:HG22	2.18	0.42
1:A:672:ASN:HD21	1:A:863:LYS:HA	1.84	0.42
1:B:209:ALA:HB2	1:B:216:TYR:CB	2.45	0.42
1:B:377:ARG:HG3	1:B:380:ARG:HH22	1.83	0.42
1:B:537:ARG:N	1:B:537:ARG:HD2	2.33	0.42
1:B:83:TYR:CE2	1:B:87:LEU:HD11	2.53	0.42
1:B:242:LEU:HD11	1:B:961:PHE:CE1	2.54	0.42
1:A:1005:LEU:HA	1:A:1005:LEU:HD23	1.85	0.42
1:A:169:GLU:HG2	1:A:170:ALA:H	1.84	0.42
1:A:635:GLN:HG2	1:A:636:ASP:N	2.31	0.42
1:A:897:GLY:O	1:A:898:ALA:C	2.57	0.42
1:B:712:LEU:HD12	1:B:712:LEU:N	2.34	0.42
1:B:913:ASN:HD22	1:B:942:ASN:HB3	1.84	0.42
1:B:958:ILE:CD1	1:B:960:ARG:HG2	2.49	0.42
1:A:177:ARG:H	1:A:217:VAL:HG23	1.83	0.42
1:A:242:LEU:HB3	1:A:245:THR:OG1	2.19	0.42
1:A:393:ASN:HB3	1:A:396:ALA:CB	2.48	0.42
1:A:603:ALA:O	1:A:606:VAL:HG12	2.18	0.42
1:B:298:ASN:ND2	1:B:330:TYR:H	2.16	0.42
1:B:41:ASP:CG	1:B:230:PRO:HA	2.40	0.42
1:B:57:ASN:O	1:B:60:SER:OG	2.36	0.42
1:A:191:ALA:N	1:A:221:ARG:HG2	2.34	0.42
1:A:703:VAL:HA	1:A:733:LEU:O	2.20	0.42
1:A:806:VAL:H	1:A:813:VAL:HG21	1.84	0.42
1:B:181:ASP:OD1	1:B:212:GLY:HA2	2.20	0.42
1:B:32:VAL:HG13	1:B:1029:VAL:HB	2.00	0.42
1:B:343:ASN:OD1	1:B:344:ARG:HG2	2.18	0.42
1:B:418:ASP:OD2	1:B:591:ARG:NH2	2.51	0.42
1:B:430:ILE:HD13	1:B:531:MSE:HE1	2.01	0.42
1:B:459:GLN:O	1:B:459:GLN:HG2	2.19	0.42
1:A:241:THR:HA	1:A:960:ARG:HA	2.01	0.42
1:A:433:ASN:HD22	1:A:500:ARG:CA	2.09	0.42
1:A:794:ALA:O	1:A:796:ASP:N	2.53	0.42
1:A:974:GLU:HG3	1:A:975:HIS:N	2.34	0.42
1:A:34:VAL:CG2	1:A:996:LEU:HD11	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:ASP:O	1:B:183:THR:N	2.52	0.42
1:B:700:MSE:SE	1:B:806:VAL:HG21	2.70	0.42
1:A:828:GLU:HG3	1:A:828:GLU:O	2.20	0.42
1:A:903:THR:HG22	1:A:944:LYS:HD2	2.01	0.42
1:A:320:PHE:HB3	1:A:958:ILE:HG13	2.01	0.42
1:A:320:PHE:CD2	1:A:958:ILE:HG23	2.54	0.42
1:B:338:ASP:CG	1:B:339:GLU:HG2	2.39	0.42
1:B:520:ARG:CZ	1:B:524:MSE:HE3	2.49	0.42
1:A:847:LYS:HB2	1:A:853:HIS:CD2	2.54	0.42
1:A:892:ILE:O	1:A:893:LYS:HD3	2.19	0.42
1:A:974:GLU:HG3	1:A:975:HIS:H	1.84	0.42
1:B:179:LEU:HD23	1:B:216:TYR:HD2	1.85	0.42
1:B:516:ALA:O	1:B:519:ALA:HB3	2.20	0.42
1:B:521:TYR:CE2	1:B:556:ILE:HD11	2.55	0.42
1:A:183:THR:OG1	1:A:185:PRO:HD2	2.20	0.42
1:A:192:ASP:OD2	1:A:194:ALA:HB3	2.20	0.42
1:A:451:LEU:HG	1:A:460:LEU:HD22	2.01	0.42
1:A:46:LEU:O	1:A:49:LEU:HB2	2.20	0.42
1:A:696:ASN:OD1	1:A:697:SER:N	2.41	0.42
1:A:792:GLN:HB2	1:A:793:LEU:H	1.54	0.42
1:A:823:ALA:O	1:A:826:ASP:HB2	2.19	0.42
1:A:931:ILE:HA	1:A:966:LEU:HD23	2.01	0.42
1:A:351:GLY:HA3	1:A:951:ARG:HH22	1.85	0.42
1:A:98:ASP:C	1:A:98:ASP:OD1	2.57	0.42
1:A:1038:ILE:CG1	1:A:1039:LEU:H	2.33	0.42
1:A:497:ILE:HG22	1:A:499:VAL:HG23	2.02	0.42
1:A:602:LEU:HD23	1:A:602:LEU:HA	1.75	0.42
1:A:707:ASP:OD1	1:A:745:SER:HB3	2.20	0.42
1:A:951:ARG:H	1:A:951:ARG:CD	2.31	0.42
1:B:292:VAL:O	1:B:295:LEU:N	2.53	0.42
1:B:37:GLN:O	1:B:1034:GLU:HG3	2.20	0.42
1:B:62:PHE:N	1:B:63:PRO:HD2	2.34	0.42
1:B:669:ARG:HH12	1:B:814:GLY:HA2	1.85	0.42
1:A:679:SER:C	1:A:681:ASP:H	2.24	0.42
1:A:89:ILE:HG22	1:A:90:VAL:N	2.35	0.42
1:A:905:SER:HB3	1:A:942:ASN:HA	2.02	0.42
1:B:300:ALA:O	1:B:303:ILE:N	2.53	0.42
1:B:430:ILE:HD11	1:B:520:ARG:HD3	2.02	0.42
1:B:672:ASN:HD21	1:B:863:LYS:HA	1.84	0.42
1:B:799:TYR:CE1	1:B:813:VAL:HG23	2.54	0.42
1:A:39:SER:OG	1:A:40:PHE:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:ALA:HB3	1:A:582:MSE:HE1	2.01	0.41
1:A:523:GLN:O	1:A:524:MSE:HB2	2.20	0.41
1:A:533:LYS:HE2	1:A:561:VAL:HG23	2.02	0.41
1:A:419:TRP:CE3	1:A:649:LEU:HD13	2.55	0.41
1:A:79:GLU:HA	1:A:82:LEU:HD11	2.02	0.41
1:A:806:VAL:O	1:A:813:VAL:HG22	2.20	0.41
1:A:851:LEU:O	1:A:853:HIS:HD2	2.03	0.41
1:A:974:GLU:CG	1:A:975:HIS:N	2.83	0.41
1:A:990:GLU:C	1:A:992:ALA:H	2.23	0.41
1:B:69:ALA:HB1	1:B:199:GLY:O	2.20	0.41
1:B:455:THR:HG22	1:B:456:TYR:CD2	2.55	0.41
1:B:847:LYS:HE3	1:B:852:GLY:C	2.39	0.41
1:A:620:MSE:O	1:A:624:ILE:HG13	2.20	0.41
1:A:654:LEU:HB3	1:A:655:THR:HG23	2.02	0.41
1:A:655:THR:H	1:A:656:ARG:NH2	2.18	0.41
1:A:240:LEU:HD23	1:A:995:THR:O	2.20	0.41
1:B:44:PRO:HG2	1:B:47:LEU:CD1	2.46	0.41
1:B:510:GLU:HB3	1:B:511:PRO:HD3	2.02	0.41
1:B:551:LEU:O	1:B:555:THR:N	2.42	0.41
1:B:572:ALA:C	1:B:574:SER:H	2.22	0.41
1:A:633:ILE:HA	1:A:637:ALA:HB3	2.02	0.41
1:A:847:LYS:HB2	1:A:847:LYS:HE3	1.62	0.41
1:A:953:LEU:HD12	1:A:953:LEU:H	1.85	0.41
1:B:75:ASP:OD1	1:B:76:ALA:N	2.51	0.41
1:B:786:TYR:HB2	1:B:787:TRP:CE3	2.55	0.41
1:B:991:ASP:OD1	1:B:991:ASP:N	2.52	0.41
1:A:102:LEU:C	1:A:106:LYS:HZ3	2.19	0.41
1:A:48:GLU:CD	1:A:115:VAL:HG23	2.41	0.41
1:A:351:GLY:CA	1:A:951:ARG:HH22	2.33	0.41
1:A:377:ARG:HD3	1:A:377:ARG:HA	1.80	0.41
1:A:433:ASN:ND2	1:A:499:VAL:O	2.54	0.41
1:A:622:VAL:O	1:A:626:LEU:N	2.38	0.41
1:A:828:GLU:HA	1:A:831:LEU:H	1.85	0.41
1:A:927:ARG:HD2	1:A:999:ASP:CG	2.41	0.41
1:A:240:LEU:HD12	1:A:985:PHE:CD2	2.55	0.41
1:B:66:ASP:OD1	1:B:202:HIS:NE2	2.43	0.41
1:B:347:SER:HB2	1:B:895:TRP:HE1	1.85	0.41
1:A:124:TYR:CE2	1:A:173:LEU:HD11	2.55	0.41
1:A:785:ALA:HA	1:A:787:TRP:CZ2	2.54	0.41
1:A:815:PRO:O	1:A:816:VAL:HG22	2.21	0.41
1:A:930:PRO:HG2	1:A:964:HIS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:GLU:OE1	1:B:213:GLN:NE2	2.54	0.41
1:B:934:THR:HG21	1:B:966:LEU:HG	2.03	0.41
1:A:247:TYR:CZ	1:A:321:PRO:HA	2.55	0.41
1:A:34:VAL:HG22	1:A:996:LEU:HD11	2.02	0.41
1:A:376:LEU:O	1:A:379:GLU:HB3	2.21	0.41
1:A:359:GLY:O	1:A:891:ALA:HB3	2.21	0.41
1:A:993:LEU:O	1:A:994:LEU:HD23	2.20	0.41
1:B:301:SER:O	1:B:305:ASP:N	2.51	0.41
1:B:451:LEU:N	1:B:452:LEU:HG	2.36	0.41
1:A:1001:PRO:HA	1:A:1002:PRO:HD3	1.77	0.41
1:A:418:ASP:HA	1:A:649:LEU:CD1	2.49	0.41
1:A:764:GLU:OE1	1:A:764:GLU:HA	2.21	0.41
1:A:847:LYS:C	1:A:849:LEU:N	2.72	0.41
1:B:485:VAL:HA	1:B:489:ILE:HG12	2.02	0.41
1:B:419:TRP:CH2	1:B:649:LEU:HB2	2.56	0.41
1:B:77:VAL:HG23	1:B:78:THR:H	1.85	0.41
1:B:957:PRO:O	1:B:958:ILE:C	2.58	0.41
1:A:169:GLU:HG2	1:A:170:ALA:N	2.36	0.41
1:A:935:LEU:O	1:A:938:LEU:HB2	2.20	0.41
1:B:588:TYR:CZ	1:B:592:LEU:HD12	2.56	0.41
1:B:629:ILE:HG22	1:B:647:TYR:HD2	1.85	0.41
1:B:733:LEU:HD21	1:B:793:LEU:HB2	2.02	0.41
1:A:287:LEU:O	1:A:325:SER:HB2	2.21	0.41
1:A:463:VAL:CG1	1:A:465:ARG:HG3	2.51	0.41
1:A:521:TYR:HE1	1:A:568:SER:HB3	1.78	0.41
1:A:591:ARG:HG3	1:A:655:THR:O	2.21	0.41
1:A:957:PRO:O	1:A:958:ILE:C	2.59	0.41
1:B:384:GLY:HA2	1:B:387:ARG:NH2	2.36	0.41
1:B:669:ARG:NH1	1:B:814:GLY:HA2	2.36	0.41
1:A:141:CYS:HA	1:A:142:PRO:HD3	1.66	0.41
1:A:630:GLN:O	1:A:634:VAL:HG13	2.20	0.41
1:B:867:LEU:O	1:B:870:LEU:HB2	2.21	0.41
1:B:918:ILE:O	1:B:947:LEU:HA	2.20	0.41
1:A:388:LYS:NZ	1:A:389:LEU:HD22	2.36	0.41
1:A:491:THR:O	1:A:495:ARG:N	2.43	0.41
1:A:654:LEU:HB2	1:A:656:ARG:NH2	2.29	0.41
1:B:1009:LYS:HG3	1:B:1032:ILE:O	2.21	0.41
1:B:542:ASP:O	1:B:543:LYS:HD3	2.21	0.41
1:B:938:LEU:HB2	1:B:941:VAL:HB	2.02	0.41
1:B:80:LYS:HD2	1:B:972:PHE:HB2	2.03	0.41
1:A:113:SER:C	1:A:116:PRO:HD2	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:SER:C	1:A:210:LYS:HD2	2.41	0.40
1:A:207:ALA:N	1:A:210:LYS:HZ2	2.19	0.40
1:A:246:ASP:OD2	1:A:285:LYS:HE3	2.22	0.40
1:A:475:ASP:OD1	1:A:477:THR:HB	2.21	0.40
1:A:644:LEU:HB2	1:A:645:PRO:HD3	2.03	0.40
1:A:784:LEU:O	1:A:786:TYR:N	2.54	0.40
1:B:1039:LEU:O	1:B:1040:ILE:HD13	2.20	0.40
1:B:382:PHE:CE1	1:B:386:PHE:HE2	2.39	0.40
1:B:787:TRP:CE3	1:B:787:TRP:N	2.86	0.40
1:B:929:VAL:O	1:B:932:LEU:HB2	2.22	0.40
1:B:998:MSE:HB2	1:B:998:MSE:HE3	1.51	0.40
1:A:102:LEU:HG	1:A:106:LYS:NZ	2.35	0.40
1:A:132:ARG:HH11	1:A:168:LEU:HB3	1.86	0.40
1:A:433:ASN:HB2	1:A:501:PHE:H	1.86	0.40
1:A:720:LYS:HG3	1:A:824:GLU:HG2	2.03	0.40
1:A:969:GLU:HG2	1:A:970:PRO:HD2	2.03	0.40
1:B:400:LEU:H	1:B:400:LEU:HG	1.26	0.40
1:B:474:ILE:HD12	1:B:503:LEU:HG	2.03	0.40
1:B:624:ILE:O	1:B:627:GLN:N	2.55	0.40
1:B:817:PRO:CD	1:B:821:THR:HG21	2.46	0.40
1:A:1003:SER:HA	1:A:1039:LEU:HD12	2.04	0.40
1:A:353:ASN:HB3	1:A:928:TRP:CH2	2.55	0.40
1:A:45:TYR:HB2	1:A:79:GLU:OE2	2.21	0.40
1:A:492:PHE:HZ	1:A:615:LEU:HD11	1.86	0.40
1:A:761:GLU:O	1:A:765:LYS:NZ	2.38	0.40
1:A:846:MSE:HE2	1:A:847:LYS:O	2.21	0.40
1:B:714:LEU:HD12	1:B:714:LEU:HA	1.81	0.40
1:A:421:ASP:HB3	1:A:429:ILE:HG13	2.03	0.40
1:A:523:GLN:HG3	1:A:527:GLY:C	2.41	0.40
1:A:515:GLN:CD	1:A:547:PRO:HB3	2.42	0.40
1:A:712:LEU:HA	1:A:715:LEU:HB3	2.04	0.40
1:B:453:GLN:N	1:B:453:GLN:HE21	2.19	0.40
1:B:459:GLN:HE22	1:B:498:PRO:HG2	1.87	0.40
1:B:56:GLU:OE1	1:B:377:ARG:NH1	2.54	0.40
1:B:91:GLN:HG2	1:B:97:ASN:CG	2.42	0.40
1:A:179:LEU:HD23	1:A:216:TYR:CD2	2.56	0.40
1:A:188:ILE:HD13	1:A:219:ARG:CZ	2.51	0.40
1:A:241:THR:HG22	1:A:960:ARG:HB2	2.03	0.40
1:A:974:GLU:CG	1:A:976:GLY:H	2.35	0.40
1:B:1000:VAL:HG22	1:B:1001:PRO:HD2	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:456:TYR:OH	1:B:456:TYR:OH[5_554]	2.09	0.11

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	893/1130 (79%)	685 (77%)	155 (17%)	53 (6%)	2	12
1	B	893/1130 (79%)	696 (78%)	155 (17%)	42 (5%)	3	17
All	All	1786/2260 (79%)	1381 (77%)	310 (17%)	95 (5%)	2	14

All (95) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	GLU
1	A	61	TYR
1	A	148	ASP
1	A	348	LEU
1	A	524	MSE
1	A	527	GLY
1	A	544	LEU
1	A	560	ARG
1	A	563	ARG
1	A	636	ASP
1	A	652	ALA
1	A	674	VAL
1	A	680	HIS
1	A	710	ALA
1	A	785	ALA
1	A	816	VAL
1	A	850	ASN
1	A	851	LEU

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Mol	Chain	Res	Type
1	A	898	ALA
1	A	908	ASP
1	A	958	ILE
1	B	210	LYS
1	B	213	GLN
1	B	612	ASP
1	B	664	ASP
1	B	673	LEU
1	B	706	PHE
1	B	786	TYR
1	B	788	ALA
1	B	803	THR
1	B	811	ARG
1	B	850	ASN
1	B	906	HIS
1	B	958	ILE
1	B	974	GLU
1	B	990	GLU
1	A	75	ASP
1	A	400	LEU
1	A	707	ASP
1	A	991	ASP
1	B	56	GLU
1	B	524	MSE
1	B	636	ASP
1	B	711	GLY
1	B	751	LEU
1	B	815	PRO
1	B	818	SER
1	B	849	LEU
1	B	898	ALA
1	A	112	ARG
1	A	151	GLN
1	A	347	SER
1	A	442	SER
1	A	566	ALA
1	A	654	LEU
1	A	846	MSE
1	A	993	LEU
1	A	1021	SER
1	B	61	TYR
1	B	456	TYR

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Mol	Chain	Res	Type
1	B	459	GLN
1	B	597	ARG
1	B	652	ALA
1	B	677	ALA
1	A	210	LYS
1	A	297	MSE
1	A	460	LEU
1	A	673	LEU
1	A	697	SER
1	A	792	GLN
1	B	148	ASP
1	B	285	LYS
1	B	348	LEU
1	B	616	GLN
1	A	401	LEU
1	A	422	GLU
1	A	453	GLN
1	A	666	SER
1	A	966	LEU
1	B	632	SER
1	A	309	PRO
1	A	676	VAL
1	A	857	GLY
1	B	460	LEU
1	B	484	MSE
1	B	544	LEU
1	B	600	PRO
1	A	564	GLY
1	B	309	PRO
1	A	813	VAL
1	B	892	ILE
1	A	367	VAL
1	A	600	PRO
1	A	817	PRO
1	B	142	PRO

### 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	782/948 (82%)	737 (94%)	45 (6%)	23	59
1	B	782/948 (82%)	746 (95%)	36 (5%)	31	68
All	All	1564/1896 (82%)	1483 (95%)	81 (5%)	27	63

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	GLU
1	A	98	ASP
1	A	106	LYS
1	A	112	ARG
1	A	204	LYS
1	A	208	MSE
1	A	210	LYS
1	A	335	GLU
1	A	380	ARG
1	A	381	GLN
1	A	389	LEU
1	A	393	ASN
1	A	394	ILE
1	A	401	LEU
1	A	402	HIS
1	A	420	ARG
1	A	447	ASP
1	A	477	THR
1	A	544	LEU
1	A	561	VAL
1	A	563	ARG
1	A	573	LEU
1	A	580	GLU
1	A	582	MSE
1	A	587	ARG
1	A	657	ASN
1	A	674	VAL
1	A	703	VAL
1	A	712	LEU
1	A	742	THR
1	A	762	ILE
1	A	763	LEU
1	A	786	TYR
1	A	793	LEU

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Mol	Chain	Res	Type
1	A	804	ARG
1	A	816	VAL
1	A	821	THR
1	A	837	LYS
1	A	839	LEU
1	A	892	ILE
1	A	906	HIS
1	A	924	ARG
1	A	927	ARG
1	A	951	ARG
1	A	974	GLU
1	B	89	ILE
1	B	178	LYS
1	B	203	ARG
1	B	210	LYS
1	B	217	VAL
1	B	250	ILE
1	B	432	LEU
1	B	453	GLN
1	B	456	TYR
1	B	488	HIS
1	B	544	LEU
1	B	563	ARG
1	B	576	THR
1	B	579	GLU
1	B	590	LYS
1	B	629	ILE
1	B	638	VAL
1	B	639	GLU
1	B	676	VAL
1	B	679	SER
1	B	709	GLU
1	B	745	SER
1	B	746	SER
1	B	751	LEU
1	B	761	GLU
1	B	803	THR
1	B	804	ARG
1	B	816	VAL
1	B	820	SER
1	B	846	MSE
1	B	855	VAL

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Mol	Chain	Res	Type
1	B	866	SER
1	B	986	SER
1	B	998	MSE
1	B	1006	VAL
1	B	1010	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	213	GLN
1	A	378	HIS
1	A	433	ASN
1	A	549	GLN
1	A	675	GLN
1	A	853	HIS
1	B	453	GLN
1	B	469	ASN
1	B	488	HIS
1	B	913	ASN
1	B	1037	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	898/1130 (79%)	-0.34	9 (1%) 82 67	70, 117, 187, 345	0
1	B	898/1130 (79%)	-0.34	9 (1%) 82 67	76, 115, 181, 279	0
All	All	1796/2260 (79%)	-0.34	18 (1%) 82 67	70, 116, 185, 345	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	819	THR	6.7
1	B	820	SER	5.6
1	B	94	GLY	5.1
1	A	728	ILE	4.5
1	A	1039	LEU	4.3
1	A	561	VAL	4.2
1	A	694	GLY	4.1
1	A	611	GLY	4.0
1	B	458	GLY	2.9
1	A	819	THR	2.9
1	A	562	LEU	2.8
1	B	818	SER	2.7
1	A	1042	GLY	2.6
1	B	833	TYR	2.5
1	B	228	PHE	2.5
1	B	457	PRO	2.4
1	B	730	VAL	2.2
1	A	818	SER	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.