



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:36 pm BST

PDB ID : 1SJC
Title : x-ray structure of o-succinylbenzoate synthase complexed with N-succinyl methionine
Authors : Thoden, J.B.; Taylor-Ringia, E.A.; Garrett, J.B.; Gerlt, J.A.; Holden, H.M.; Rayment, I.
Deposited on : 2004-03-03
Resolution : 2.10 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

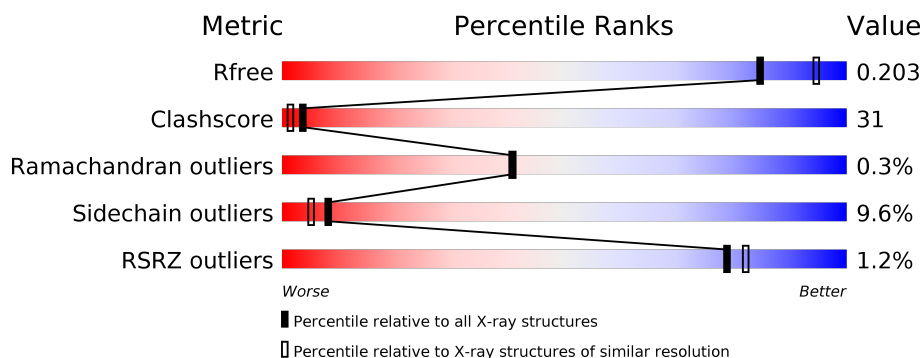
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 respectively. 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	368	<div> <div>2%</div> <div>52%</div> <div>38%</div> <div>9%</div> <div>•</div> </div>
1	B	368	<div> <div>2%</div> <div>56%</div> <div>35%</div> <div>8%</div> <div>•</div> </div>
1	C	368	<div> <div>2%</div> <div>56%</div> <div>34%</div> <div>9%</div> <div>•</div> </div>
1	D	368	<div> <div>2%</div> <div>41%</div> <div>44%</div> <div>14%</div> <div>•</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SMG	A	1000	-	-	X	-
3	SMG	B	1100	-	-	X	-
3	SMG	C	1200	-	-	X	-
3	SMG	D	1300	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12098 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.

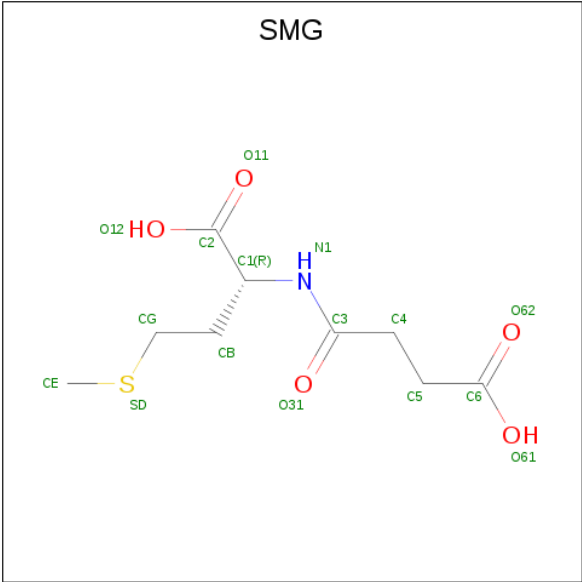
- Molecule 1 is a protein called N-acylamino acid racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	5	0
			2795	1776	490	517	12			
1	B	368	Total	C	N	O	S	0	3	0
			2786	1769	481	524	12			
1	C	367	Total	C	N	O	S	0	2	0
			2775	1764	480	519	12			
1	D	368	Total	C	N	O	S	0	1	0
			2779	1765	484	518	12			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

- Molecule 3 is N-SUCCINYLMETHIONINE (three-letter code: SMG) (formula: C₉H₁₅NO₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			16	9	1	5	1		
3	B	1	Total	C	N	O	S	0	0
			16	9	1	5	1		
3	C	1	Total	C	N	O	S	0	0
			16	9	1	5	1		
3	D	1	Total	C	N	O	S	0	0
			16	9	1	5	1		

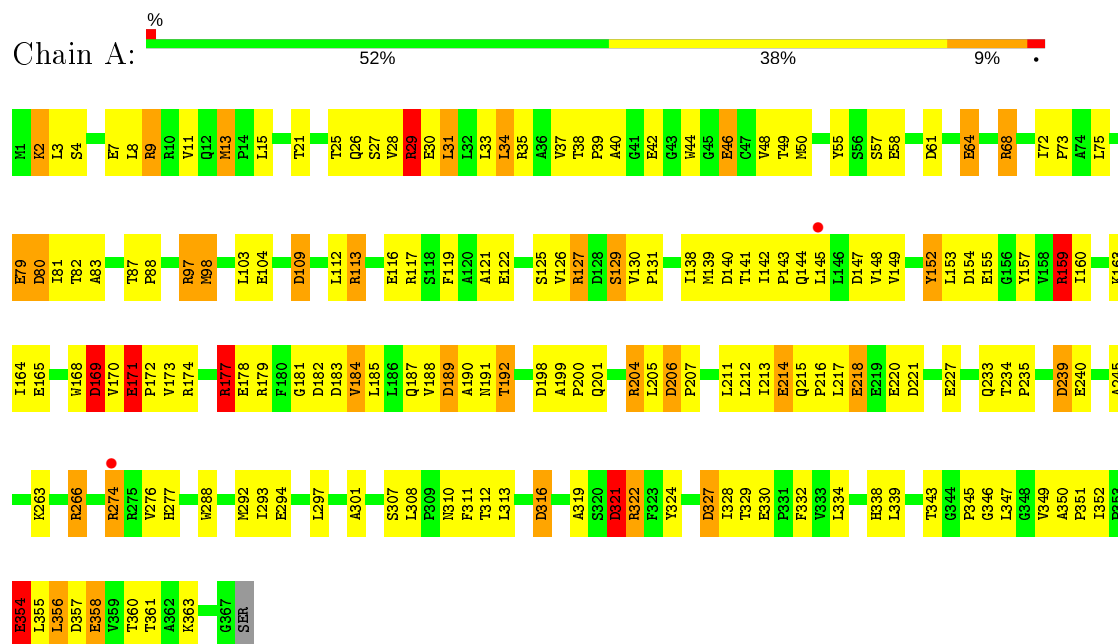
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	216	Total	O	0	0
			216	216		
4	B	295	Total	O	0	0
			295	295		
4	C	237	Total	O	0	0
			237	237		
4	D	147	Total	O	0	0
			147	147		

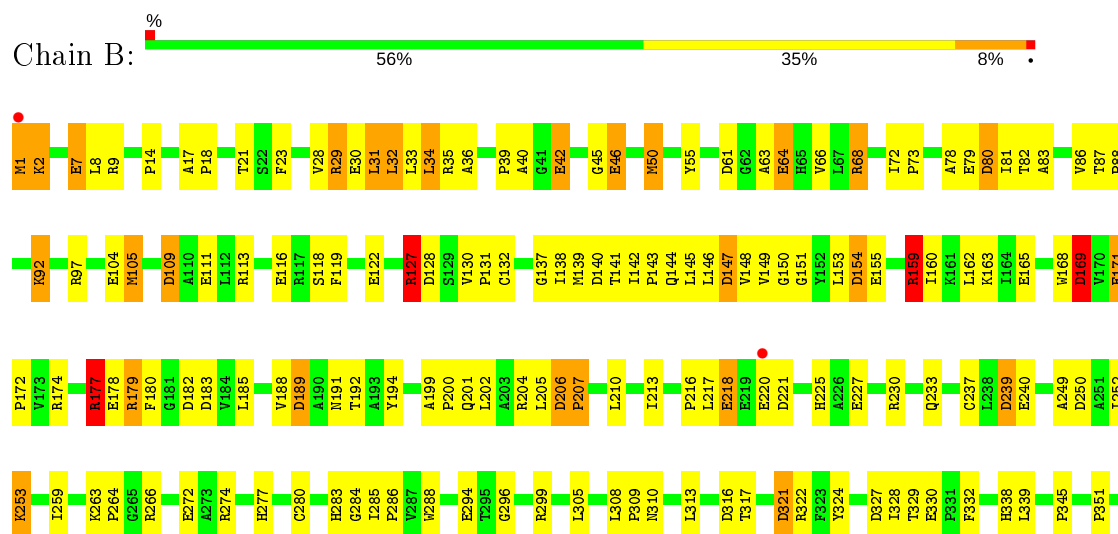
3 Residue-property plots

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: N-acylamino acid racemase

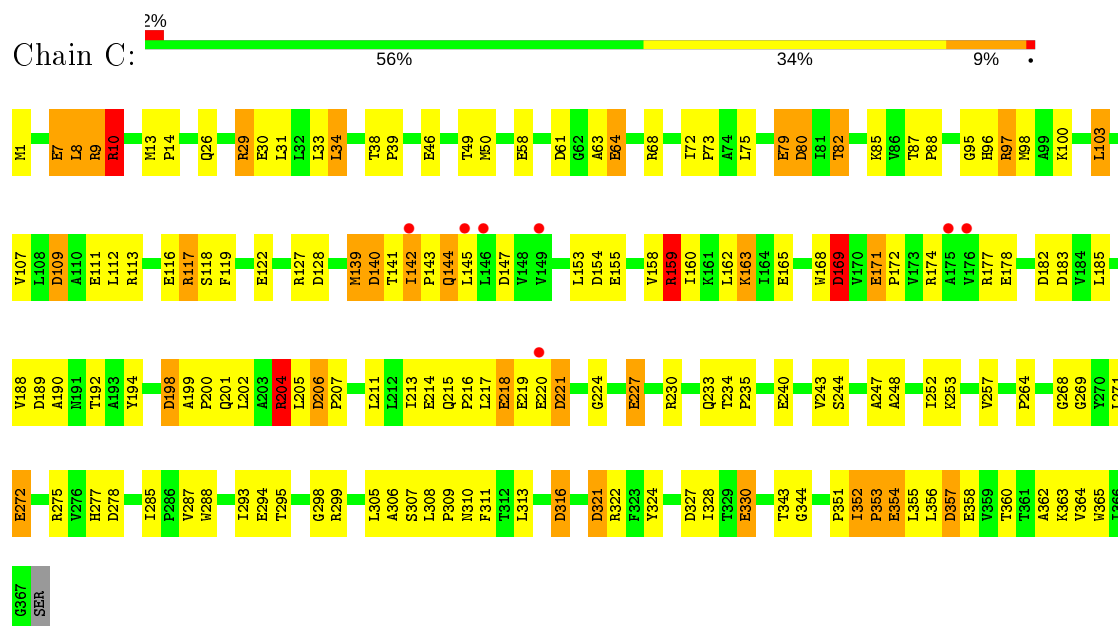


• Molecule 1: N-acylamino acid racemase

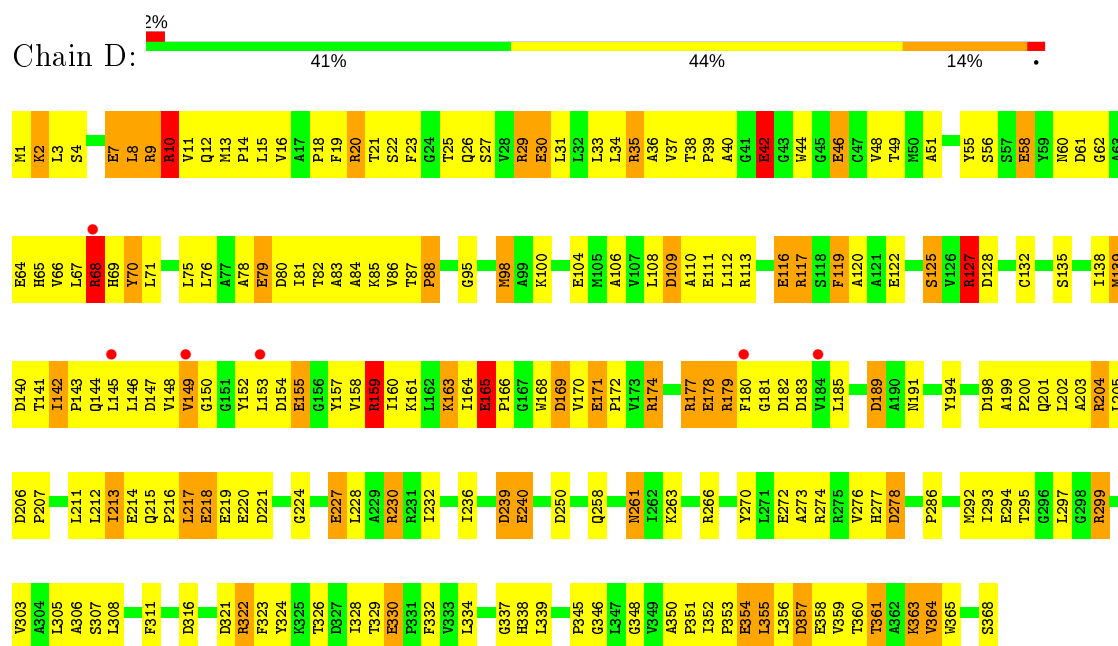




• Molecule 1: N-acylamino acid racemase



• Molecule 1: N-acylamino acid racemase



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	215.70Å 215.70Å 259.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10 49.92 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.10) 99.6 (49.92-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.83 (at 2.00Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.208 , 0.274 0.203 , 0.203	Depositor DCC
R_{free} test set	15319 reflections (9.93%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 126.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.015 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l 0.010 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l 0.004 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12098	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SMG, 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	1.02	20/2871 (0.7%)	1.50	57/3906 (1.5%)
1	B	1.05	22/2854 (0.8%)	1.48	48/3885 (1.2%)
1	C	1.08	25/2839 (0.9%)	1.42	42/3866 (1.1%)
1	D	1.05	23/2839 (0.8%)	1.48	51/3864 (1.3%)
All	All	1.05	90/11403 (0.8%)	1.47	198/15521 (1.3%)

All (90) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	GLU	CD-OE2	9.55	1.36	1.25
1	C	220[A]	GLU	CD-OE2	8.58	1.35	1.25
1	C	220[B]	GLU	CD-OE2	8.58	1.35	1.25
1	B	220[A]	GLU	CD-OE2	8.40	1.34	1.25
1	B	220[B]	GLU	CD-OE2	8.40	1.34	1.25
1	C	79[A]	GLU	CD-OE2	8.39	1.34	1.25
1	C	79[B]	GLU	CD-OE2	8.39	1.34	1.25
1	A	79	GLU	CD-OE2	7.98	1.34	1.25
1	D	354	GLU	CD-OE2	7.94	1.34	1.25
1	D	79	GLU	CD-OE2	7.91	1.34	1.25
1	B	358	GLU	CD-OE2	7.90	1.34	1.25
1	C	358	GLU	CD-OE2	7.85	1.34	1.25
1	C	354	GLU	CD-OE2	7.75	1.34	1.25
1	D	42	GLU	CD-OE2	7.73	1.34	1.25
1	A	220	GLU	CD-OE2	7.71	1.34	1.25
1	D	122	GLU	CD-OE2	7.66	1.34	1.25
1	C	178	GLU	CD-OE2	7.41	1.33	1.25
1	C	165	GLU	CD-OE2	7.41	1.33	1.25
1	D	358	GLU	CD-OE2	7.31	1.33	1.25
1	C	30	GLU	CD-OE2	7.27	1.33	1.25
1	D	46	GLU	CD-OE2	7.21	1.33	1.25
1	D	171	GLU	CD-OE2	7.16	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	178	GLU	CD-OE2	7.09	1.33	1.25
1	A	354	GLU	CD-OE2	7.08	1.33	1.25
1	D	155	GLU	CD-OE2	7.00	1.33	1.25
1	B	79[A]	GLU	CD-OE2	6.99	1.33	1.25
1	B	79[B]	GLU	CD-OE2	6.99	1.33	1.25
1	A	64	GLU	CD-OE2	6.96	1.33	1.25
1	C	155	GLU	CD-OE2	6.95	1.33	1.25
1	C	64	GLU	CD-OE2	6.94	1.33	1.25
1	B	171	GLU	CD-OE2	6.81	1.33	1.25
1	C	122	GLU	CD-OE2	6.77	1.33	1.25
1	A	358	GLU	CD-OE2	6.74	1.33	1.25
1	D	240	GLU	CD-OE2	6.73	1.33	1.25
1	B	330	GLU	CD-OE2	6.69	1.33	1.25
1	B	178	GLU	CD-OE2	6.65	1.32	1.25
1	D	165	GLU	CD-OE2	6.64	1.32	1.25
1	C	330	GLU	CD-OE2	6.63	1.32	1.25
1	C	219	GLU	CD-OE2	6.62	1.32	1.25
1	D	111	GLU	CD-OE2	6.59	1.32	1.25
1	D	104	GLU	CD-OE2	6.52	1.32	1.25
1	D	214	GLU	CD-OE2	6.50	1.32	1.25
1	C	218	GLU	CD-OE2	6.50	1.32	1.25
1	D	116	GLU	CD-OE2	6.49	1.32	1.25
1	D	227	GLU	CD-OE2	6.46	1.32	1.25
1	A	155	GLU	CD-OE2	6.42	1.32	1.25
1	C	111	GLU	CD-OE2	6.42	1.32	1.25
1	D	30	GLU	CD-OE2	6.37	1.32	1.25
1	A	178	GLU	CD-OE2	6.33	1.32	1.25
1	A	214	GLU	CD-OE2	6.24	1.32	1.25
1	D	220	GLU	CD-OE2	6.15	1.32	1.25
1	A	240	GLU	CD-OE2	6.12	1.32	1.25
1	A	171	GLU	CD-OE2	6.11	1.32	1.25
1	C	272	GLU	CD-OE2	6.09	1.32	1.25
1	A	218	GLU	CD-OE2	6.08	1.32	1.25
1	D	330	GLU	CD-OE2	6.06	1.32	1.25
1	B	104	GLU	CD-OE2	6.06	1.32	1.25
1	B	111	GLU	CD-OE2	6.00	1.32	1.25
1	B	155	GLU	CD-OE2	5.96	1.32	1.25
1	C	46	GLU	CD-OE2	5.94	1.32	1.25
1	C	227	GLU	CD-OE2	5.91	1.32	1.25
1	B	122	GLU	CD-OE2	5.89	1.32	1.25
1	A	104	GLU	CD-OE2	5.85	1.32	1.25
1	B	30	GLU	CD-OE2	5.80	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	218	GLU	CD-OE2	5.79	1.32	1.25
1	A	30	GLU	CD-OE2	5.76	1.31	1.25
1	A	122	GLU	CD-OE2	5.76	1.31	1.25
1	C	171	GLU	CD-OE2	5.74	1.31	1.25
1	A	42	GLU	CD-OE2	5.58	1.31	1.25
1	D	58	GLU	CD-OE2	5.51	1.31	1.25
1	B	165	GLU	CD-OE2	5.51	1.31	1.25
1	D	219	GLU	CD-OE2	5.47	1.31	1.25
1	C	116	GLU	CD-OE2	5.45	1.31	1.25
1	B	272	GLU	CD-OE2	5.44	1.31	1.25
1	A	330	GLU	CD-OE2	5.41	1.31	1.25
1	B	116	GLU	CD-OE2	5.39	1.31	1.25
1	C	7	GLU	CD-OE2	5.39	1.31	1.25
1	D	218	GLU	CD-OE2	5.37	1.31	1.25
1	B	7	GLU	CD-OE2	5.34	1.31	1.25
1	D	294	GLU	CD-OE2	5.32	1.31	1.25
1	B	46	GLU	CD-OE2	5.29	1.31	1.25
1	A	46	GLU	CD-OE2	5.26	1.31	1.25
1	C	214	GLU	CD-OE2	5.25	1.31	1.25
1	B	240	GLU	CD-OE2	5.24	1.31	1.25
1	B	294	GLU	CD-OE2	5.23	1.31	1.25
1	C	294	GLU	CD-OE2	5.22	1.31	1.25
1	B	64	GLU	CD-OE2	5.18	1.31	1.25
1	A	165	GLU	CD-OE2	5.12	1.31	1.25
1	C	240	GLU	CD-OE2	5.10	1.31	1.25
1	A	227	GLU	CD-OE2	5.08	1.31	1.25

All (198) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	159	ARG	NE-CZ-NH2	-11.46	114.57	120.30
1	A	274[A]	ARG	NE-CZ-NH2	-11.33	114.64	120.30
1	A	274[B]	ARG	NE-CZ-NH2	-11.33	114.64	120.30
1	A	274[A]	ARG	NE-CZ-NH1	10.96	125.78	120.30
1	A	274[B]	ARG	NE-CZ-NH1	10.96	125.78	120.30
1	D	10	ARG	NE-CZ-NH1	10.94	125.77	120.30
1	A	322	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	B	299	ARG	NE-CZ-NH1	-9.06	115.77	120.30
1	D	299	ARG	NE-CZ-NH1	9.05	124.83	120.30
1	D	68[A]	ARG	NE-CZ-NH1	8.86	124.73	120.30
1	D	68[B]	ARG	NE-CZ-NH1	8.86	124.73	120.30
1	B	221	ASP	CB-CG-OD2	-8.81	110.37	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	206	ASP	CB-CG-OD2	-8.79	110.39	118.30
1	C	117	ARG	NE-CZ-NH1	8.71	124.65	120.30
1	A	183	ASP	CB-CG-OD2	-8.67	110.50	118.30
1	B	154	ASP	CB-CG-OD2	-8.56	110.59	118.30
1	A	68[A]	ARG	NE-CZ-NH1	8.56	124.58	120.30
1	A	68[B]	ARG	NE-CZ-NH1	8.56	124.58	120.30
1	B	239	ASP	CB-CG-OD2	-8.49	110.66	118.30
1	B	239	ASP	CB-CG-OD1	8.48	125.93	118.30
1	D	159	ARG	NE-CZ-NH2	-8.44	116.08	120.30
1	D	239	ASP	CB-CG-OD1	8.44	125.90	118.30
1	B	154	ASP	CB-CG-OD1	8.43	125.89	118.30
1	A	316	ASP	CB-CG-OD2	-8.38	110.76	118.30
1	B	140	ASP	CB-CG-OD2	-8.30	110.83	118.30
1	B	206	ASP	CB-CG-OD2	-8.26	110.86	118.30
1	B	80	ASP	CB-CG-OD2	-8.22	110.90	118.30
1	B	128	ASP	CB-CG-OD1	8.22	125.70	118.30
1	A	177	ARG	NE-CZ-NH1	8.21	124.41	120.30
1	C	140	ASP	CB-CG-OD2	-8.16	110.96	118.30
1	D	159	ARG	NE-CZ-NH1	8.13	124.37	120.30
1	B	159	ARG	NE-CZ-NH1	8.13	124.36	120.30
1	A	97	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	D	278	ASP	CB-CG-OD1	8.07	125.56	118.30
1	C	109	ASP	CB-CG-OD2	-7.97	111.12	118.30
1	A	206	ASP	CB-CG-OD2	-7.95	111.14	118.30
1	A	189	ASP	CB-CG-OD2	-7.95	111.15	118.30
1	C	169	ASP	CB-CG-OD2	-7.79	111.29	118.30
1	D	204	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	A	221	ASP	CB-CG-OD2	-7.61	111.45	118.30
1	C	147	ASP	CB-CG-OD2	-7.60	111.46	118.30
1	A	321	ASP	CB-CG-OD1	7.60	125.14	118.30
1	C	182	ASP	CB-CG-OD2	-7.53	111.52	118.30
1	A	68[A]	ARG	NE-CZ-NH2	-7.50	116.55	120.30
1	A	68[B]	ARG	NE-CZ-NH2	-7.50	116.55	120.30
1	D	109	ASP	CB-CG-OD2	-7.41	111.63	118.30
1	A	198	ASP	CB-CG-OD2	-7.29	111.73	118.30
1	C	357	ASP	CB-CG-OD2	-7.28	111.75	118.30
1	D	61	ASP	CB-CG-OD2	-7.21	111.81	118.30
1	B	109	ASP	CB-CG-OD1	7.20	124.78	118.30
1	B	182	ASP	CB-CG-OD2	-7.17	111.85	118.30
1	A	189	ASP	CB-CG-OD1	7.16	124.75	118.30
1	A	239	ASP	CB-CG-OD1	7.13	124.72	118.30
1	C	327	ASP	CB-CG-OD2	-7.13	111.88	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	327	ASP	CB-CG-OD2	-7.11	111.90	118.30
1	C	275	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	B	316	ASP	CB-CG-OD2	-7.03	111.97	118.30
1	A	316	ASP	CB-CG-OD1	7.02	124.62	118.30
1	D	198	ASP	CB-CG-OD2	-7.02	111.98	118.30
1	D	321	ASP	CB-CG-OD1	7.01	124.61	118.30
1	C	159	ARG	NE-CZ-NH2	-6.98	116.81	120.30
1	C	316	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	C	198	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	A	109	ASP	CB-CG-OD2	-6.87	112.12	118.30
1	D	61	ASP	CB-CG-OD1	6.82	124.44	118.30
1	D	189	ASP	CB-CG-OD2	-6.81	112.17	118.30
1	B	316	ASP	CB-CG-OD1	6.77	124.40	118.30
1	A	61	ASP	CB-CG-OD2	-6.74	112.24	118.30
1	A	169	ASP	CB-CG-OD1	6.73	124.36	118.30
1	A	159	ARG	NE-CZ-NH1	6.71	123.66	120.30
1	B	183[A]	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	B	183[B]	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	A	140	ASP	CB-CG-OD2	-6.66	112.31	118.30
1	B	169	ASP	CB-CG-OD2	-6.64	112.33	118.30
1	B	357	ASP	CB-CG-OD1	6.64	124.27	118.30
1	D	128	ASP	CB-CG-OD2	-6.64	112.33	118.30
1	A	159	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	B	109	ASP	CB-CG-OD2	-6.60	112.36	118.30
1	C	357	ASP	CB-CG-OD1	6.59	124.23	118.30
1	B	221	ASP	CB-CG-OD1	6.56	124.20	118.30
1	B	97	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	B	147	ASP	CB-CG-OD2	-6.56	112.40	118.30
1	B	189	ASP	CB-CG-OD2	-6.55	112.40	118.30
1	B	189	ASP	CB-CG-OD1	6.54	124.19	118.30
1	D	128	ASP	CB-CG-OD1	6.51	124.16	118.30
1	D	278	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	A	239	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	D	321	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	A	147	ASP	CB-CG-OD2	-6.43	112.51	118.30
1	A	198	ASP	CB-CG-OD1	6.40	124.06	118.30
1	A	140	ASP	CB-CG-OD1	6.38	124.04	118.30
1	D	189	ASP	CB-CG-OD1	6.36	124.02	118.30
1	A	154	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	A	183	ASP	CB-CG-OD1	6.29	123.96	118.30
1	C	117	ARG	NE-CZ-NH2	-6.29	117.16	120.30
1	A	154	ASP	CB-CG-OD1	6.28	123.96	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	C	327	ASP	CB-CG-OD1	6.28	123.95	118.30
1	A	327	ASP	CB-CG-OD1	6.24	123.91	118.30
1	C	128	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	D	182	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	D	183	ASP	CB-CG-OD2	-6.22	112.71	118.30
1	C	169	ASP	CB-CG-OD1	6.21	123.89	118.30
1	B	357	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	B	182	ASP	CB-CG-OD1	6.19	123.87	118.30
1	A	204[A]	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	A	204[B]	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	D	183	ASP	CB-CG-OD1	6.10	123.79	118.30
1	D	117	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	D	147	ASP	CB-CG-OD2	-6.06	112.85	118.30
1	C	352	ILE	C-N-CD	-6.01	107.39	120.60
1	A	357	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	B	128	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	C	189	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	A	182	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	B	174	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	B	253	LYS	N-CA-CB	5.96	121.33	110.60
1	C	109	ASP	CB-CG-OD1	5.96	123.66	118.30
1	C	97	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	D	157	TYR	CB-CG-CD2	5.91	124.54	121.00
1	A	109	ASP	CB-CG-OD1	5.91	123.61	118.30
1	C	68	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	A	177	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	D	198	ASP	CB-CG-OD1	5.88	123.60	118.30
1	B	61	ASP	CB-CG-OD1	5.85	123.57	118.30
1	A	321	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	D	140	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	29	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	C	221	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	B	80	ASP	CB-CG-OD1	5.79	123.52	118.30
1	D	147	ASP	CB-CG-OD1	5.78	123.50	118.30
1	C	278	ASP	CB-CG-OD2	-5.76	113.11	118.30
1	A	80	ASP	CB-CG-OD1	5.76	123.48	118.30
1	C	147	ASP	CB-CG-OD1	5.75	123.48	118.30
1	C	183	ASP	CB-CG-OD2	-5.74	113.14	118.30
1	B	183[A]	ASP	CB-CG-OD1	5.73	123.46	118.30
1	B	183[B]	ASP	CB-CG-OD1	5.73	123.46	118.30
1	B	327	ASP	CB-CG-OD1	5.69	123.42	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	357	ASP	CB-CG-OD2	-5.68	113.19	118.30
1	A	152	TYR	CA-CB-CG	-5.63	102.70	113.40
1	C	189	ASP	CB-CG-OD1	5.61	123.35	118.30
1	D	10	ARG	CD-NE-CZ	5.61	131.45	123.60
1	C	165	GLU	CB-CA-C	-5.61	99.19	110.40
1	A	361	THR	CA-CB-CG2	-5.59	104.58	112.40
1	B	140	ASP	CB-CG-OD1	5.58	123.32	118.30
1	D	70	TYR	CB-CG-CD1	-5.58	117.66	121.00
1	B	147	ASP	CB-CG-OD1	5.57	123.31	118.30
1	C	80	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	A	61	ASP	CB-CG-OD1	5.55	123.30	118.30
1	D	239	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	D	80	ASP	CB-CG-OD2	-5.54	113.31	118.30
1	D	68[A]	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	D	68[B]	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	D	182	ASP	CB-CG-OD1	5.51	123.26	118.30
1	C	182	ASP	CB-CG-OD1	5.47	123.22	118.30
1	D	174	ARG	NE-CZ-NH2	-5.45	117.58	120.30
1	D	154	ASP	CB-CG-OD1	5.43	123.19	118.30
1	D	117	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	D	179	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	C	206	ASP	CB-CG-OD1	5.39	123.15	118.30
1	D	80	ASP	CB-CG-OD1	5.39	123.15	118.30
1	C	321	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	D	127	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	266	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	D	250	ASP	CB-CG-OD2	-5.34	113.49	118.30
1	A	116	GLU	CB-CA-C	5.33	121.06	110.40
1	A	182	ASP	CB-CG-OD1	5.33	123.09	118.30
1	C	97	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	B	177	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	C	10	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	C	154	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	B	127	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	C	183	ASP	CB-CG-OD1	5.28	123.05	118.30
1	A	357	ASP	CB-CG-OD1	5.27	123.05	118.30
1	B	321	ASP	CB-CG-OD2	-5.27	113.56	118.30
1	D	357	ASP	CB-CG-OD1	5.25	123.02	118.30
1	B	61	ASP	CB-CG-OD2	-5.25	113.58	118.30
1	A	169	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	D	154	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	A	113	ARG	NE-CZ-NH1	5.21	122.91	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	250	ASP	CB-CG-OD2	-5.19	113.63	118.30
1	D	230	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	D	250	ASP	CB-CG-OD1	5.16	122.94	118.30
1	D	157	TYR	CB-CG-CD1	-5.13	117.92	121.00
1	C	159	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	C	321	ASP	CB-CG-OD1	5.11	122.90	118.30
1	B	327	ASP	CB-CG-OD2	-5.11	113.71	118.30
1	C	61	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	C	140	ASP	CB-CG-OD1	5.11	122.89	118.30
1	B	165	GLU	N-CA-CB	-5.09	101.44	110.60
1	B	250	ASP	CB-CG-OD1	5.08	122.87	118.30
1	C	204	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	B	50	MET	CA-CB-CG	-5.06	104.69	113.30
1	B	169	ASP	CB-CG-OD1	5.06	122.86	118.30
1	D	230	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	D	140	ASP	CB-CG-OD2	-5.04	113.76	118.30
1	A	220	GLU	OE1-CD-OE2	5.01	129.31	123.30
1	A	113	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2795	0	2841	176	1
1	B	2786	0	2814	129	0
1	C	2775	0	2809	160	0
1	D	2779	0	2819	243	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	16	0	13	8	0
3	B	16	0	13	8	0
3	C	16	0	13	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	16	0	13	12	0
4	A	216	0	0	11	0
4	B	295	0	0	4	0
4	C	237	0	0	11	0
4	D	147	0	0	15	0
All	All	12098	0	11335	708	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 31.

All (708) 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:B:46:GLU:H	1:B:105:MET:CE	1.52	1.21
1:A:144:GLN:O	1:A:148:VAL:HG23	1.47	1.12
1:C:10:ARG:HD3	1:C:362:ALA:HB3	1.17	1.08
1:D:141:THR:HG22	1:D:143:PRO:HD2	1.30	1.06
1:D:38:THR:HB	1:D:39:PRO:HD2	1.31	1.05
1:B:78:ALA:HB3	1:B:81:ILE:HD11	1.38	1.03
1:D:141:THR:CG2	1:D:143:PRO:HD2	1.88	1.03
1:B:45:GLY:HA2	1:B:105:MET:HE3	1.37	1.01
1:C:38:THR:HB	1:C:39:PRO:HD2	1.39	1.01
1:B:46:GLU:N	1:B:105:MET:HE1	1.73	1.01
1:B:46:GLU:H	1:B:105:MET:HE1	0.89	1.00
1:A:199:ALA:HB3	1:A:200:PRO:HD3	1.44	1.00
1:D:9:ARG:HH12	1:D:363:LYS:HZ2	0.99	0.98
1:C:269:GLY:C	4:C:1237:HOH:O	2.03	0.97
1:D:322:ARG:NH1	1:D:323:PHE:CE2	2.34	0.96
1:D:21:THR:HG21	1:D:23:PHE:CE2	2.01	0.95
1:C:141:THR:HG22	1:C:144:GLN:H	1.34	0.93
1:B:45:GLY:CA	1:B:105:MET:HE3	1.97	0.93
1:C:141:THR:HG23	1:C:143:PRO:HD2	1.49	0.93
1:C:58:GLU:HB2	1:C:98:MET:CE	2.00	0.91
1:C:87:THR:HB	1:C:88:PRO:HD3	1.52	0.89
1:D:110:ALA:HA	4:D:1395:HOH:O	1.73	0.88
1:B:142:ILE:N	1:B:143:PRO:HD2	1.89	0.88
1:C:29:ARG:NH2	1:C:50:MET:HE2	1.90	0.86
1:D:159:ARG:HD2	4:D:1403:HOH:O	1.75	0.86
1:C:139:MET:HB2	1:C:168:TRP:CH2	2.11	0.85
1:D:9:ARG:HH12	1:D:363:LYS:NZ	1.73	0.85
1:A:35:ARG:HD3	1:A:44:TRP:CZ2	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:GLU:OE1	1:D:98:MET:HG3	1.76	0.84
1:D:1:MET:SD	1:D:38:THR:HG21	2.17	0.83
1:B:46:GLU:N	1:B:105:MET:CE	2.34	0.83
1:D:353:PRO:HA	1:D:356:LEU:HB3	1.60	0.83
1:D:206:ASP:N	1:D:207:PRO:HD2	1.92	0.83
1:A:263:LYS:HZ3	3:A:1000:SMG:C2	1.92	0.82
1:D:328:ILE:O	1:D:351:PRO:HA	1.78	0.82
1:A:7:GLU:OE2	1:A:9:ARG:NH1	2.13	0.82
1:D:9:ARG:NH1	1:D:363:LYS:HZ2	1.76	0.81
1:D:125:SER:HB2	1:D:307:SER:OG	1.79	0.81
1:D:352:ILE:O	1:D:355:LEU:HB2	1.79	0.81
1:D:21:THR:HG22	1:D:22:SER:N	1.95	0.81
1:C:58:GLU:HB2	1:C:98:MET:HE1	1.61	0.81
1:A:29:ARG:NE	1:A:31:LEU:HD23	1.94	0.81
1:D:20:ARG:HG2	1:D:138:ILE:HB	1.63	0.81
1:D:263:LYS:NZ	3:D:1300:SMG:O11	2.12	0.81
1:D:199:ALA:HB3	1:D:200:PRO:HD3	1.63	0.81
1:D:206:ASP:HB2	1:D:207:PRO:HD3	1.62	0.80
1:A:127:ARG:NH2	1:A:308:LEU:O	2.14	0.80
1:B:29:ARG:HD2	1:B:31:LEU:HD21	1.64	0.80
1:D:38:THR:HB	1:D:39:PRO:CD	2.10	0.80
1:C:109:ASP:O	1:C:113:ARG:HG3	1.82	0.80
1:A:144:GLN:O	1:A:148:VAL:CG2	2.28	0.79
1:A:58:GLU:HB2	1:A:98:MET:HE2	1.64	0.79
1:D:169:ASP:OD1	1:D:194:TYR:OH	1.99	0.79
1:A:169:ASP:O	1:A:173:VAL:HG23	1.83	0.79
1:C:159:ARG:NH2	1:C:316:ASP:OD1	2.14	0.79
1:C:33:LEU:C	1:C:34:LEU:HD12	2.03	0.79
1:C:75:LEU:CD1	1:C:103:LEU:HD13	2.12	0.79
1:C:169:ASP:OD1	1:C:194:TYR:OH	2.01	0.79
1:D:221:ASP:OD2	1:D:224:GLY:HA3	1.82	0.78
1:D:141:THR:HG22	1:D:143:PRO:CD	2.13	0.78
1:D:263:LYS:HZ1	3:D:1300:SMG:C2	1.95	0.78
1:C:201:GLN:O	1:C:204:ARG:HB2	1.84	0.78
1:B:142:ILE:N	1:B:143:PRO:CD	2.47	0.78
1:A:329:THR:HB	1:A:349:VAL:HG13	1.65	0.78
1:C:34:LEU:HD12	1:C:34:LEU:N	1.98	0.78
1:B:1:MET:SD	1:B:39:PRO:HB2	2.24	0.78
1:B:78:ALA:HB3	1:B:81:ILE:CD1	2.13	0.77
1:A:40:ALA:HB3	4:A:1066:HOH:O	1.84	0.77
1:D:159:ARG:HG2	1:D:160:ILE:N	1.98	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:THR:CB	1:C:39:PRO:HD2	2.14	0.77
1:D:132:CYS:O	1:D:158:VAL:HG22	1.84	0.77
1:B:50:MET:SD	3:B:1100:SMG:CE	2.73	0.77
1:D:2:LYS:HD2	1:D:3:LEU:N	2.00	0.77
1:A:98:MET:CE	4:A:1065:HOH:O	2.33	0.76
1:B:163:LYS:NZ	1:B:189:ASP:OD2	2.18	0.76
1:C:10:ARG:CD	1:C:362:ALA:HB3	2.09	0.76
1:D:163:LYS:NZ	3:D:1300:SMG:H1	2.00	0.76
1:C:141:THR:CG2	1:C:143:PRO:HD2	2.15	0.76
1:D:169:ASP:HB2	1:D:170:VAL:HG23	1.67	0.76
1:C:87:THR:HB	1:C:88:PRO:CD	2.16	0.75
1:A:201:GLN:O	1:A:204[A]:ARG:HB2	1.86	0.75
1:D:205:LEU:C	1:D:207:PRO:HD2	2.06	0.75
1:A:149:VAL:HG13	1:A:160:ILE:HD13	1.68	0.75
1:D:62:GLY:O	4:D:1387:HOH:O	2.05	0.75
1:B:50:MET:SD	3:B:1100:SMG:HE2	2.27	0.74
1:D:148:VAL:HG12	1:D:152:TYR:CE1	2.21	0.74
1:D:18:PRO:HA	1:D:26:GLN:O	1.86	0.74
1:B:29:ARG:HD2	1:B:31:LEU:CD2	2.18	0.74
1:A:206:ASP:HB2	1:A:207:PRO:HD3	1.67	0.74
1:D:206:ASP:N	1:D:207:PRO:CD	2.50	0.73
1:C:141:THR:HB	1:C:144:GLN:HB3	1.71	0.73
1:A:159:ARG:HG2	1:A:160:ILE:N	2.03	0.72
1:C:49:THR:HG22	1:C:98:MET:CE	2.20	0.72
1:B:8:LEU:CD2	1:B:34:LEU:HD22	2.19	0.72
1:C:127:ARG:HH11	1:C:307:SER:HA	1.52	0.72
1:A:201:GLN:O	1:A:204[B]:ARG:HB2	1.89	0.71
1:C:58:GLU:CB	1:C:98:MET:CE	2.67	0.71
1:A:117:ARG:HE	1:A:121:ALA:HB1	1.54	0.71
1:C:58:GLU:HB2	1:C:98:MET:HE2	1.72	0.71
1:C:7:GLU:OE1	1:C:9:ARG:NH1	2.22	0.71
1:D:75:LEU:O	1:D:81:ILE:HD11	1.89	0.71
1:D:9:ARG:HG3	1:D:9:ARG:HH11	1.56	0.71
1:A:21:THR:HG21	3:A:1000:SMG:HE1	1.73	0.71
1:D:142:ILE:HB	1:D:143:PRO:HD3	1.72	0.70
1:D:9:ARG:CG	1:D:9:ARG:HH11	2.04	0.70
1:C:248:ALA:O	1:C:252:ILE:HG13	1.91	0.70
1:A:329:THR:HG21	1:A:349:VAL:CG1	2.22	0.70
1:C:204:ARG:HH11	1:C:204:ARG:HG2	1.57	0.70
1:C:49:THR:HG22	1:C:98:MET:HE1	1.72	0.70
1:A:206:ASP:N	1:A:207:PRO:HD2	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:LEU:HB2	1:B:225:HIS:CE1	2.27	0.70
1:D:21:THR:HG22	1:D:22:SER:H	1.55	0.70
1:D:363:LYS:O	1:D:364:VAL:HG22	1.91	0.70
1:D:171:GLU:HB2	1:D:172:PRO:HD3	1.72	0.70
1:A:35:ARG:HD3	1:A:44:TRP:CH2	2.27	0.69
1:C:194:TYR:CE2	1:C:202:LEU:HD21	2.28	0.69
1:A:87:THR:HB	1:A:88:PRO:HD3	1.73	0.69
1:B:206:ASP:HB2	1:B:207:PRO:HD3	1.74	0.69
1:C:141:THR:CG2	1:C:144:GLN:H	2.04	0.69
1:C:75:LEU:HD11	1:C:103:LEU:HD13	1.72	0.69
1:D:293:ILE:HD11	3:D:1300:SMG:HE2	1.74	0.69
1:A:112:LEU:HB3	1:A:117:ARG:O	1.92	0.69
1:D:363:LYS:HG2	1:D:364:VAL:N	2.08	0.68
1:A:356:LEU:HD22	1:A:360:THR:OG1	1.93	0.68
1:B:201:GLN:O	1:B:204:ARG:HB2	1.94	0.68
1:B:159:ARG:HB2	1:B:185:LEU:HB2	1.74	0.68
1:C:159:ARG:HD2	4:C:1296:HOH:O	1.92	0.68
1:A:163:LYS:HZ3	3:A:1000:SMG:H1	1.58	0.68
1:A:293:ILE:O	1:A:293:ILE:HG22	1.91	0.68
3:C:1200:SMG:O62	4:C:1373:HOH:O	2.12	0.68
1:B:199:ALA:HB3	1:B:200:PRO:HD3	1.77	0.67
1:C:206:ASP:N	1:C:207:PRO:CD	2.57	0.67
1:C:353:PRO:HA	4:C:1285:HOH:O	1.94	0.67
1:D:297:LEU:HD23	1:D:329:THR:HG21	1.76	0.67
1:D:334:LEU:HD12	1:D:339:LEU:HD13	1.75	0.67
1:B:205:LEU:C	1:B:207:PRO:HD2	2.15	0.67
1:D:227:GLU:O	1:D:230:ARG:HB2	1.95	0.67
1:A:329:THR:HB	1:A:349:VAL:CG1	2.24	0.67
1:C:205:LEU:C	1:C:207:PRO:HD2	2.15	0.67
1:D:33:LEU:O	1:D:34:LEU:HD23	1.94	0.67
1:D:81:ILE:HD12	4:D:1361:HOH:O	1.95	0.67
1:D:8:LEU:CD1	1:D:34:LEU:HD22	2.25	0.66
1:A:206:ASP:N	1:A:207:PRO:CD	2.58	0.66
1:C:293:ILE:CD1	3:C:1200:SMG:CE	2.73	0.66
1:C:271:LEU:N	4:C:1237:HOH:O	2.29	0.66
1:D:44:TRP:O	1:D:106:ALA:HA	1.95	0.66
1:A:163:LYS:NZ	3:A:1000:SMG:H1	2.11	0.66
1:A:75:LEU:O	1:A:81:ILE:HD11	1.95	0.66
1:D:199:ALA:N	1:D:200:PRO:HD2	2.11	0.66
1:D:355:LEU:O	1:D:359:VAL:HG22	1.95	0.66
1:A:33:LEU:C	1:A:34:LEU:HD23	2.16	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:LEU:CD2	1:B:46:GLU:HG3	2.26	0.65
1:C:8:LEU:CD2	1:C:64:GLU:HG3	2.26	0.65
1:A:73:PRO:O	4:A:1175:HOH:O	2.13	0.65
1:D:35:ARG:HG3	1:D:44:TRP:CH2	2.31	0.65
1:D:201:GLN:O	1:D:204:ARG:HB2	1.97	0.65
1:B:163:LYS:HE3	1:B:191:ASN:OD1	1.96	0.65
1:B:92:LYS:HE3	4:B:1146:HOH:O	1.95	0.65
1:C:141:THR:HG23	1:C:143:PRO:CD	2.24	0.65
1:C:141:THR:CG2	1:C:143:PRO:CD	2.74	0.65
1:C:293:ILE:HD12	3:C:1200:SMG:HE1	1.79	0.65
1:D:213:ILE:HG12	1:D:216:PRO:HG3	1.78	0.64
1:D:29:ARG:NH1	1:D:49:THR:O	2.30	0.64
1:D:30:GLU:O	1:D:60:ASN:ND2	2.29	0.64
1:D:216:PRO:C	1:D:217:LEU:HD23	2.18	0.64
1:D:194:TYR:CE2	1:D:202:LEU:HD21	2.32	0.64
1:B:72:ILE:HB	1:B:73:PRO:HD3	1.80	0.64
1:C:58:GLU:CD	1:C:98:MET:HE2	2.19	0.63
1:C:75:LEU:HD12	1:C:103:LEU:HD13	1.79	0.63
1:A:4:SER:HB2	1:A:37:VAL:HG12	1.80	0.63
1:B:87:THR:HB	1:B:88:PRO:HD3	1.79	0.63
1:C:352:ILE:HB	1:C:355:LEU:HD12	1.81	0.63
1:C:288:TRP:HB3	1:C:313:LEU:HB2	1.79	0.63
1:D:95:GLY:O	1:D:100:LYS:HE3	1.97	0.63
1:A:329:THR:CG2	1:A:349:VAL:CG1	2.77	0.63
1:A:319:ALA:HB1	1:A:332:PHE:O	1.99	0.63
1:A:113:ARG:HG2	1:A:113:ARG:HH11	1.63	0.63
1:A:199:ALA:HB3	1:A:200:PRO:CD	2.26	0.63
1:A:171:GLU:N	1:A:172:PRO:HD2	2.14	0.63
1:A:139:MET:HG3	1:A:145:LEU:HA	1.80	0.62
1:A:8:LEU:HD11	1:A:34:LEU:HD22	1.82	0.62
1:D:21:THR:CG2	1:D:22:SER:N	2.61	0.62
1:C:127:ARG:NH1	1:C:307:SER:HA	2.13	0.62
1:C:38:THR:HB	1:C:39:PRO:CD	2.23	0.62
1:A:98:MET:HE1	4:A:1065:HOH:O	1.97	0.62
1:C:204:ARG:NH1	1:C:204:ARG:HG2	2.13	0.62
1:D:21:THR:CG2	1:D:22:SER:H	2.12	0.62
1:D:15:LEU:HD23	1:D:324:TYR:HE1	1.64	0.62
1:D:109:ASP:OD1	1:D:346:GLY:HA3	2.00	0.62
1:D:352:ILE:CG2	1:D:355:LEU:HD22	2.29	0.62
1:B:358:GLU:HG2	1:B:358:GLU:O	1.99	0.62
1:A:75:LEU:HD12	1:A:103:LEU:HD21	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:ARG:HG2	1:B:160:ILE:N	2.14	0.61
1:D:274:ARG:O	1:D:277:HIS:HB3	1.99	0.61
1:D:112:LEU:HD12	1:D:119:PHE:CD1	2.35	0.61
1:B:179:ARG:HG3	1:B:179:ARG:O	1.99	0.61
1:A:15:LEU:HB2	1:A:27:SER:O	2.00	0.61
1:A:185:LEU:HD22	1:A:211:LEU:HD11	1.83	0.61
1:C:227:GLU:O	1:C:230:ARG:HB2	2.00	0.61
1:A:87:THR:N	1:A:88:PRO:HD2	2.14	0.61
1:B:288:TRP:HB3	1:B:313:LEU:HB2	1.83	0.60
1:C:243:VAL:O	1:C:244:SER:HB3	2.01	0.60
1:A:33:LEU:HD21	1:A:46:GLU:HG3	1.83	0.60
1:D:8:LEU:HD12	1:D:34:LEU:HD22	1.82	0.60
1:C:29:ARG:CZ	1:C:50:MET:HE2	2.31	0.60
1:D:352:ILE:HG21	1:D:355:LEU:HD22	1.83	0.60
1:D:163:LYS:HZ1	3:D:1300:SMG:H1	1.66	0.60
1:B:201:GLN:OE1	1:B:201:GLN:HA	2.01	0.60
1:B:252:ILE:HG12	1:B:285:ILE:HG13	1.82	0.60
1:A:8:LEU:CD1	1:A:34:LEU:HD22	2.31	0.60
1:C:142:ILE:N	1:C:143:PRO:HD2	2.17	0.60
1:B:280:CYS:HB3	1:B:285:ILE:O	2.01	0.60
1:C:34:LEU:CD1	1:C:34:LEU:N	2.65	0.60
1:A:263:LYS:NZ	3:A:1000:SMG:C2	2.63	0.60
1:B:227:GLU:OE1	1:B:230:ARG:NH1	2.35	0.59
1:C:139:MET:CG	1:C:145:LEU:HB2	2.31	0.59
1:D:338:HIS:O	1:D:339:LEU:HD12	2.03	0.59
1:B:29:ARG:CD	1:B:31:LEU:HD21	2.31	0.59
1:A:28:VAL:HG12	1:A:29:ARG:N	2.15	0.59
1:B:171:GLU:HB2	1:B:172:PRO:HD3	1.84	0.59
1:D:270:TYR:O	1:D:273:ALA:HB3	2.02	0.59
1:D:29:ARG:CZ	1:D:31:LEU:HD23	2.33	0.59
1:A:21:THR:HG22	1:A:163:LYS:HE3	1.85	0.59
1:A:8:LEU:CD2	1:A:64:GLU:HG3	2.33	0.59
3:D:1300:SMG:O11	4:D:1421:HOH:O	2.16	0.59
1:C:252:ILE:HD13	1:C:285:ILE:HG13	1.84	0.58
1:D:159:ARG:NH2	1:D:316:ASP:OD1	2.26	0.58
1:A:113:ARG:HA	1:A:345:PRO:HB2	1.84	0.58
1:D:164:ILE:HB	1:D:168:TRP:O	2.03	0.58
1:C:49:THR:CG2	1:C:98:MET:HE3	2.34	0.58
1:C:82:THR:CG2	1:C:85:LYS:HD2	2.33	0.58
1:A:199:ALA:N	1:A:200:PRO:HD2	2.18	0.58
1:A:332:PHE:HB3	1:A:339:LEU:HD21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:VAL:CG1	1:A:350:ALA:N	2.65	0.58
1:C:190:ALA:HB3	1:C:216:PRO:HA	1.84	0.58
1:D:141:THR:HG22	1:D:142:ILE:N	2.18	0.58
1:C:82:THR:HG23	1:C:85:LYS:HD2	1.85	0.58
1:C:364:VAL:HG23	4:C:1383:HOH:O	2.03	0.58
1:D:87:THR:HB	1:D:88:PRO:HD3	1.86	0.58
1:B:7:GLU:OE2	1:B:363:LYS:HD2	2.04	0.58
1:D:23:PHE:HZ	3:D:1300:SMG:HG1	1.68	0.58
1:D:199:ALA:HB3	1:D:200:PRO:CD	2.33	0.58
1:A:125:SER:HB2	1:A:307:SER:OG	2.04	0.57
1:D:119:PHE:HB2	4:D:1341:HOH:O	2.03	0.57
1:D:217:LEU:HD21	1:D:228:LEU:HD22	1.86	0.57
1:A:129:SER:OG	1:A:338:HIS:ND1	2.32	0.57
1:C:127:ARG:HB2	1:C:307:SER:HB2	1.85	0.57
1:D:21:THR:HG21	1:D:23:PHE:CD2	2.39	0.57
1:B:141:THR:CB	1:B:143:PRO:HD2	2.33	0.57
1:B:237:CYS:HA	1:B:259:ILE:O	2.04	0.57
1:D:68[B]:ARG:NH2	1:D:364:VAL:HG21	2.19	0.57
1:B:263:LYS:HB2	1:B:266:ARG:NH1	2.20	0.57
1:C:139:MET:HB2	1:C:168:TRP:HH2	1.69	0.57
1:C:38:THR:CB	1:C:39:PRO:CD	2.82	0.57
1:D:297:LEU:CD2	1:D:329:THR:HG21	2.33	0.57
1:A:57:SER:HB3	4:A:1090:HOH:O	2.05	0.57
1:B:33:LEU:HD21	1:B:46:GLU:HG3	1.86	0.57
1:C:293:ILE:HD12	3:C:1200:SMG:CE	2.35	0.57
1:D:62:GLY:CA	4:D:1387:HOH:O	2.52	0.57
1:C:87:THR:CB	1:C:88:PRO:HD3	2.30	0.56
1:A:329:THR:CB	1:A:349:VAL:CG1	2.82	0.56
1:C:141:THR:HG22	1:C:144:GLN:N	2.14	0.56
1:A:149:VAL:HG13	1:A:160:ILE:CD1	2.35	0.56
1:D:353:PRO:O	1:D:357:ASP:OD2	2.24	0.56
1:A:38:THR:HB	1:A:39:PRO:HD2	1.86	0.56
1:C:139:MET:HG2	1:C:145:LEU:HB2	1.86	0.56
1:A:199:ALA:N	1:A:200:PRO:CD	2.68	0.56
1:A:263:LYS:NZ	3:A:1000:SMG:O11	2.33	0.56
1:B:50:MET:HE1	3:B:1100:SMG:CE	2.36	0.56
1:B:46:GLU:N	1:B:105:MET:HE3	2.18	0.56
1:D:135:SER:HB2	1:D:161:LYS:HD3	1.88	0.56
1:D:148:VAL:CG1	1:D:152:TYR:CE1	2.88	0.56
1:D:363:LYS:HG2	1:D:364:VAL:H	1.70	0.56
1:B:283:HIS:CE1	1:C:253:LYS:HE2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:58:GLU:CB	1:C:98:MET:HE2	2.35	0.56
1:D:82:THR:HG22	1:D:84:ALA:H	1.69	0.56
1:A:21:THR:HG21	3:A:1000:SMG:CE	2.36	0.55
1:A:72:ILE:N	1:A:73:PRO:HD2	2.22	0.55
1:C:58:GLU:CB	1:C:98:MET:HE1	2.33	0.55
1:D:142:ILE:O	1:D:145:LEU:N	2.39	0.55
1:A:321:ASP:HA	1:A:324:TYR:O	2.05	0.55
1:A:138:ILE:HG23	1:A:168:TRP:CD1	2.40	0.55
1:C:95:GLY:O	1:C:100:LYS:HE3	2.07	0.55
1:D:217:LEU:HD21	1:D:228:LEU:CD2	2.37	0.55
1:A:205:LEU:C	1:A:207:PRO:HD2	2.26	0.55
1:A:187:GLN:HB2	1:A:212:LEU:CD1	2.36	0.55
1:C:206:ASP:N	1:C:207:PRO:HD2	2.22	0.55
1:C:87:THR:CB	1:C:88:PRO:CD	2.83	0.55
1:D:141:THR:CG2	1:D:142:ILE:N	2.69	0.55
1:C:269:GLY:O	4:C:1237:HOH:O	2.17	0.55
1:D:334:LEU:HD12	1:D:339:LEU:CD1	2.36	0.55
1:A:8:LEU:HD23	1:A:64:GLU:HG3	1.86	0.55
1:C:127:ARG:NH1	1:C:306:ALA:O	2.40	0.55
1:C:328:ILE:O	1:C:351:PRO:HA	2.07	0.55
1:D:3:LEU:HD23	1:D:76:LEU:HD23	1.89	0.55
1:A:11:VAL:HB	1:A:31:LEU:HD12	1.90	0.54
1:D:2:LYS:O	1:D:39:PRO:HD3	2.07	0.54
1:C:58:GLU:OE1	1:C:98:MET:HE2	2.07	0.54
1:D:87:THR:N	1:D:88:PRO:HD2	2.21	0.54
1:A:352:ILE:HG22	1:A:355:LEU:HG	1.90	0.54
1:C:194:TYR:CD2	1:C:202:LEU:HD21	2.42	0.54
1:C:352:ILE:O	1:C:355:LEU:HB2	2.06	0.54
1:A:192:THR:HB	1:A:218:GLU:HA	1.90	0.54
1:D:363:LYS:C	1:D:364:VAL:HG22	2.27	0.54
1:C:139:MET:HB2	1:C:168:TRP:CZ2	2.43	0.53
1:C:362:ALA:O	1:C:363:LYS:HB2	2.07	0.53
1:B:139:MET:HG3	1:B:145:LEU:HA	1.90	0.53
1:D:194:TYR:CD2	1:D:202:LEU:HD21	2.43	0.53
1:D:218:GLU:HG2	4:D:1357:HOH:O	2.09	0.53
1:B:249:ALA:O	1:B:253:LYS:HG3	2.08	0.53
1:C:118:SER:HB3	1:C:344:GLY:O	2.08	0.53
1:C:162:LEU:O	1:C:188:VAL:HA	2.08	0.53
1:A:191:ASN:C	1:A:192:THR:HG23	2.28	0.53
1:B:206:ASP:N	1:B:207:PRO:CD	2.71	0.53
1:A:277:HIS:CD2	1:A:311:PHE:CE1	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4:SER:HB2	1:D:37:VAL:O	2.09	0.53
1:A:356:LEU:CD2	1:A:360:THR:OG1	2.57	0.53
1:A:72:ILE:N	1:A:73:PRO:CD	2.72	0.53
1:C:169:ASP:OD2	1:C:201:GLN:NE2	2.38	0.53
1:D:62:GLY:HA2	4:D:1387:HOH:O	2.06	0.53
1:B:35:ARG:HD2	1:B:42:GLU:OE2	2.09	0.53
1:C:142:ILE:N	1:C:143:PRO:CD	2.72	0.53
1:D:159:ARG:HH21	1:D:161:LYS:HB3	1.74	0.53
1:D:215:GLN:HG3	1:D:240:GLU:OE1	2.08	0.53
1:A:329:THR:HG21	1:A:349:VAL:HG11	1.90	0.52
1:C:264:PRO:HG3	1:C:305:LEU:HD22	1.90	0.52
1:D:58:GLU:HB2	1:D:98:MET:CE	2.39	0.52
1:D:142:ILE:HB	1:D:143:PRO:CD	2.37	0.52
1:A:87:THR:CB	1:A:88:PRO:HD3	2.37	0.52
1:C:287:VAL:O	1:C:311:PHE:HA	2.09	0.52
1:D:148:VAL:O	1:D:149:VAL:C	2.46	0.52
1:A:33:LEU:CD2	1:A:46:GLU:HG3	2.39	0.52
1:B:283:HIS:ND1	1:C:253:LYS:HE2	2.24	0.52
1:B:179:ARG:HG2	1:B:180:PHE:CE1	2.45	0.52
1:D:60:ASN:HB2	4:D:1352:HOH:O	2.09	0.52
1:B:332:PHE:HB3	1:B:339:LEU:HD21	1.92	0.52
1:C:293:ILE:O	1:C:293:ILE:HG22	2.10	0.52
1:D:120:ALA:HB1	1:D:125:SER:HB3	1.92	0.52
1:D:163:LYS:NZ	3:D:1300:SMG:O31	2.37	0.52
1:D:363:LYS:C	1:D:364:VAL:CG2	2.79	0.52
1:D:56:SER:OG	1:D:98:MET:CE	2.58	0.52
1:D:10:ARG:HH11	1:D:10:ARG:HG3	1.75	0.52
1:D:199:ALA:N	1:D:200:PRO:CD	2.73	0.51
1:A:352:ILE:CG2	1:A:355:LEU:HG	2.40	0.51
1:A:87:THR:N	1:A:88:PRO:CD	2.73	0.51
1:D:261:ASN:C	1:D:261:ASN:OD1	2.49	0.51
1:A:87:THR:CB	1:A:88:PRO:CD	2.88	0.51
1:B:8:LEU:HD23	1:B:34:LEU:HD22	1.92	0.51
1:D:22:SER:OG	1:D:191:ASN:HB2	2.11	0.51
1:A:192:THR:HG22	1:A:215:GLN:HG2	1.91	0.51
1:B:162:LEU:O	1:B:188:VAL:HA	2.11	0.51
1:A:297:LEU:HD23	1:A:329:THR:HG21	1.93	0.51
1:A:354:GLU:O	1:A:358:GLU:HG3	2.11	0.51
1:C:8:LEU:HD22	1:C:64:GLU:HG3	1.92	0.51
1:B:141:THR:C	1:B:143:PRO:HD2	2.31	0.51
1:D:46:GLU:OE2	1:D:295:THR:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:56:SER:OG	1:D:98:MET:HE2	2.10	0.51
1:A:329:THR:HG21	1:A:349:VAL:HG12	1.92	0.51
1:A:352:ILE:O	1:A:355:LEU:N	2.43	0.51
1:B:139:MET:HG3	1:B:145:LEU:CA	2.41	0.51
1:B:142:ILE:HB	1:B:143:PRO:HD3	1.93	0.51
1:A:170:VAL:HG21	1:A:204[B]:ARG:HB3	1.93	0.51
1:A:46:GLU:OE2	1:A:294:GLU:HB3	2.11	0.51
1:B:8:LEU:O	1:B:363:LYS:HA	2.10	0.51
1:D:203:ALA:HA	1:D:232:ILE:HG22	1.92	0.51
1:A:213:ILE:HG22	1:A:234:THR:HG22	1.92	0.51
1:A:328:ILE:O	1:A:351:PRO:HA	2.10	0.51
1:D:142:ILE:HG22	1:D:146:LEU:HD12	1.93	0.51
1:D:206:ASP:CB	1:D:207:PRO:HD3	2.36	0.51
1:B:264:PRO:HG3	1:B:305:LEU:HD22	1.93	0.50
1:D:171:GLU:HB2	1:D:172:PRO:CD	2.39	0.50
1:D:272:GLU:O	1:D:276:VAL:HG23	2.11	0.50
1:B:145:LEU:O	1:B:149:VAL:HG23	2.11	0.50
1:D:85:LYS:C	1:D:88:PRO:HD2	2.31	0.50
1:A:139:MET:HG3	1:A:145:LEU:CA	2.41	0.50
1:A:310:ASN:O	1:A:312:THR:N	2.44	0.50
1:B:50:MET:HE1	3:B:1100:SMG:HE1	1.93	0.50
1:D:143:PRO:O	1:D:144:GLN:C	2.49	0.50
1:B:29:ARG:CD	1:B:31:LEU:CD2	2.88	0.50
1:C:257:VAL:HG13	1:C:257:VAL:O	2.10	0.50
1:D:348:GLY:HA2	4:D:1374:HOH:O	2.12	0.50
1:A:159:ARG:NH2	1:A:316:ASP:OD1	2.26	0.50
1:B:146:LEU:O	1:B:180:PHE:HZ	1.94	0.50
1:B:200:PRO:HA	4:B:1331:HOH:O	2.12	0.50
1:D:148:VAL:HG12	1:D:152:TYR:HE1	1.74	0.50
1:D:353:PRO:O	1:D:354:GLU:C	2.50	0.50
1:C:272:GLU:N	4:C:1237:HOH:O	2.13	0.49
1:D:194:TYR:N	1:D:194:TYR:CD1	2.79	0.49
1:D:215:GLN:HG2	1:D:239:ASP:H	1.77	0.49
1:D:25:THR:HG22	1:D:26:GLN:N	2.26	0.49
1:B:206:ASP:N	1:B:207:PRO:HD2	2.27	0.49
1:C:356:LEU:O	1:C:356:LEU:HD12	2.11	0.49
1:A:349:VAL:HG12	1:A:350:ALA:N	2.28	0.49
1:D:15:LEU:CD2	1:D:324:TYR:HE1	2.25	0.49
1:A:2:LYS:O	1:A:38:THR:HG22	2.12	0.49
1:D:55:TYR:OH	1:D:266:ARG:HD3	2.12	0.49
1:D:78:ALA:HB3	1:D:81:ILE:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:HIS:NE2	1:A:310:ASN:HB3	2.28	0.49
1:A:301:ALA:HB2	1:A:347:LEU:CD2	2.42	0.49
1:B:109:ASP:OD2	1:B:113:ARG:NH1	2.45	0.49
1:B:64:GLU:O	1:B:68:ARG:HB2	2.13	0.49
1:A:212:LEU:O	1:A:212:LEU:HD12	2.13	0.49
1:C:204:ARG:HH11	1:C:204:ARG:CG	2.25	0.49
1:D:19:PHE:HE2	3:D:1300:SMG:HE2	1.78	0.49
1:B:216:PRO:C	1:B:217:LEU:HD23	2.33	0.49
1:B:227:GLU:CD	1:B:230:ARG:HH11	2.15	0.49
1:D:293:ILE:HD11	3:D:1300:SMG:CE	2.43	0.49
1:C:72:ILE:HB	1:C:73:PRO:HD3	1.95	0.49
1:B:83:ALA:O	1:B:86:VAL:HB	2.13	0.48
1:C:141:THR:HG22	1:C:143:PRO:N	2.29	0.48
1:C:49:THR:HG22	1:C:98:MET:HE3	1.92	0.48
1:B:29:ARG:CZ	1:B:31:LEU:HD23	2.43	0.48
1:B:21:THR:HG22	1:B:163:LYS:HG2	1.96	0.48
1:D:55:TYR:OH	1:D:239:ASP:OD1	2.27	0.48
1:A:171:GLU:N	1:A:172:PRO:CD	2.76	0.48
1:C:96:HIS:O	1:C:100:LYS:HG3	2.14	0.48
1:A:206:ASP:OD1	4:A:1155:HOH:O	2.20	0.48
1:C:127:ARG:NH2	1:C:308:LEU:O	2.47	0.48
1:C:142:ILE:O	1:C:145:LEU:HB3	2.13	0.48
1:D:68[A]:ARG:HB3	1:D:69:HIS:CD2	2.49	0.48
1:D:16:VAL:HG23	1:D:323:PHE:O	2.14	0.47
1:A:113:ARG:HG2	1:A:113:ARG:NH1	2.26	0.47
1:A:9:ARG:HG3	1:A:9:ARG:HH11	1.79	0.47
1:C:213:ILE:HG22	1:C:234:THR:HG22	1.95	0.47
1:D:148:VAL:CG1	1:D:152:TYR:HE1	2.27	0.47
1:C:171:GLU:N	1:C:172:PRO:HD2	2.30	0.47
1:B:194:TYR:CD2	1:B:202:LEU:HD21	2.50	0.47
1:D:206:ASP:CB	1:D:207:PRO:CD	2.92	0.47
1:A:29:ARG:HD3	1:A:31:LEU:CD2	2.44	0.47
1:D:356:LEU:O	1:D:359:VAL:HG23	2.14	0.47
1:D:9:ARG:NH1	1:D:9:ARG:CG	2.70	0.47
1:B:118:SER:HB2	4:B:1159:HOH:O	2.14	0.47
1:C:198:ASP:O	1:C:201:GLN:HB3	2.14	0.47
1:D:169:ASP:O	1:D:172:PRO:HD2	2.14	0.47
1:D:36:ALA:O	1:D:42:GLU:HB3	2.15	0.47
1:A:171:GLU:HA	1:A:171:GLU:OE2	2.13	0.47
1:B:130:VAL:O	1:B:338:HIS:HA	2.15	0.47
1:D:46:GLU:OE1	1:D:297:LEU:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:113:ARG:HG2	1:D:345:PRO:HB2	1.96	0.47
1:C:174:ARG:HG2	4:C:1368:HOH:O	2.15	0.47
1:D:206:ASP:HB2	1:D:207:PRO:CD	2.39	0.47
1:C:199:ALA:N	1:C:200:PRO:CD	2.78	0.47
1:C:75:LEU:HD12	1:C:103:LEU:CD1	2.44	0.47
1:D:179:ARG:HG2	1:D:180:PHE:CE1	2.50	0.47
1:B:127:ARG:NH2	1:B:308:LEU:O	2.47	0.47
1:D:49:THR:HG22	1:D:98:MET:HE3	1.96	0.47
1:C:141:THR:HG22	1:C:143:PRO:CD	2.45	0.46
1:D:48:VAL:HB	1:D:292:MET:HG3	1.98	0.46
1:B:87:THR:HB	1:B:88:PRO:CD	2.45	0.46
1:D:19:PHE:CE2	3:D:1300:SMG:HE2	2.50	0.46
1:D:326:THR:HG22	1:D:326:THR:O	2.14	0.46
1:C:192:THR:HG22	1:C:215:GLN:HG2	1.96	0.46
1:D:51:ALA:HB3	4:D:1351:HOH:O	2.15	0.46
1:A:190:ALA:HB3	1:A:216:PRO:HA	1.97	0.46
1:B:227:GLU:CD	1:B:230:ARG:NH1	2.69	0.46
1:B:308:LEU:CB	1:B:309:PRO:HD2	2.45	0.46
1:D:360:THR:HG22	1:D:361:THR:N	2.29	0.46
1:A:159:ARG:CD	4:A:1077:HOH:O	2.62	0.46
1:B:82:THR:O	1:B:86:VAL:HG23	2.16	0.46
1:D:67:LEU:HD23	1:D:71:LEU:HB2	1.97	0.46
1:A:329:THR:CB	1:A:349:VAL:HG11	2.46	0.46
1:A:97:ARG:HD2	4:A:1027:HOH:O	2.14	0.46
1:C:293:ILE:CD1	3:C:1200:SMG:HE1	2.40	0.46
1:D:2:LYS:C	1:D:2:LYS:HD2	2.34	0.46
1:C:233:GLN:O	1:C:235:PRO:HD3	2.15	0.46
1:D:8:LEU:CD1	1:D:34:LEU:CD2	2.94	0.46
1:D:58:GLU:CD	1:D:98:MET:HG3	2.36	0.46
1:C:163:LYS:NZ	3:C:1200:SMG:H1	2.31	0.46
1:A:33:LEU:O	1:A:34:LEU:HD23	2.16	0.46
1:C:353:PRO:O	1:C:357:ASP:OD2	2.34	0.46
1:D:171:GLU:N	1:D:172:PRO:HD2	2.31	0.46
1:D:127:ARG:NH2	1:D:308:LEU:O	2.49	0.46
1:D:127:ARG:HH22	1:D:311:PHE:HB2	1.80	0.46
1:D:328:ILE:HG13	1:D:329:THR:HG23	1.98	0.46
1:A:29:ARG:HE	1:A:31:LEU:HD23	1.78	0.46
1:B:138:ILE:HG23	1:B:168:TRP:CD1	2.51	0.45
1:D:199:ALA:O	1:D:203:ALA:N	2.48	0.45
1:D:62:GLY:C	4:D:1387:HOH:O	2.52	0.45
1:A:164:ILE:HG12	1:A:188:VAL:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:THR:O	1:A:83:ALA:C	2.53	0.45
1:C:142:ILE:HD13	1:C:168:TRP:CZ3	2.52	0.45
1:C:31:LEU:HD22	1:C:295:THR:HG23	1.98	0.45
1:C:364:VAL:HG12	1:C:365:TRP:N	2.31	0.45
1:D:263:LYS:HB2	1:D:266:ARG:NH1	2.31	0.45
1:A:29:ARG:NH1	1:A:50:MET:CE	2.79	0.45
1:A:29:ARG:HD3	1:A:31:LEU:HD21	1.98	0.45
1:B:227:GLU:HA	1:B:230:ARG:NH1	2.32	0.45
1:C:159:ARG:HG2	1:C:160:ILE:N	2.32	0.45
1:C:50:MET:HE3	3:C:1200:SMG:CE	2.47	0.45
1:D:239:ASP:OD1	1:D:266:ARG:NH1	2.49	0.45
1:B:50:MET:CE	3:B:1100:SMG:CE	2.94	0.45
1:A:117:ARG:HE	1:A:121:ALA:CB	2.25	0.45
1:B:17:ALA:HA	1:B:18:PRO:HD3	1.83	0.45
1:C:72:ILE:HB	1:C:73:PRO:CD	2.47	0.45
1:D:356:LEU:O	1:D:356:LEU:HD12	2.16	0.45
1:A:28:VAL:HG12	1:A:29:ARG:H	1.81	0.45
1:D:216:PRO:HB2	1:D:217:LEU:HD23	1.98	0.45
1:D:3:LEU:HB3	4:D:1361:HOH:O	2.16	0.45
1:A:239:ASP:OD1	1:A:266:ARG:NH1	2.46	0.45
1:A:9:ARG:CG	1:A:9:ARG:HH11	2.30	0.45
1:B:148:VAL:O	1:B:149:VAL:C	2.54	0.45
1:B:113:ARG:HG2	1:B:345:PRO:HB2	1.97	0.45
1:D:334:LEU:CD2	1:D:337:GLY:HA2	2.47	0.45
1:A:350:ALA:HB1	1:A:351:PRO:HD2	1.98	0.45
1:C:97:ARG:O	1:C:268:GLY:HA2	2.15	0.45
1:C:49:THR:CG2	1:C:98:MET:CE	2.90	0.45
1:D:299:ARG:O	1:D:303:VAL:HG23	2.16	0.45
1:A:29:ARG:NH1	1:A:50:MET:HE2	2.31	0.45
1:B:32:LEU:HA	1:B:32:LEU:HD23	1.70	0.45
1:D:170:VAL:HG23	1:D:170:VAL:H	1.44	0.45
1:D:37:VAL:HG21	1:D:365:TRP:CH2	2.52	0.45
1:A:212:LEU:C	1:A:212:LEU:HD12	2.37	0.44
1:B:23:PHE:CE2	1:B:191:ASN:HB3	2.52	0.44
1:D:334:LEU:HD21	1:D:337:GLY:HA2	1.99	0.44
1:A:28:VAL:CG1	1:A:29:ARG:N	2.79	0.44
1:B:284:GLY:O	1:B:286:PRO:HD3	2.17	0.44
1:D:329:THR:O	1:D:330:GLU:C	2.56	0.44
1:D:350:ALA:HB1	1:D:351:PRO:HD2	1.99	0.44
1:D:2:LYS:CD	1:D:3:LEU:N	2.77	0.44
1:C:352:ILE:HA	1:C:353:PRO:HD3	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:GLN:OE1	1:D:201:GLN:HA	2.17	0.44
1:D:258:GLN:O	1:D:286:PRO:HD2	2.18	0.44
1:D:299:ARG:HG2	1:D:332:PHE:CD1	2.53	0.44
1:A:187:GLN:HB2	1:A:212:LEU:HD12	2.00	0.44
1:A:170:VAL:CG2	1:A:204[B]:ARG:HB3	2.47	0.44
1:B:23:PHE:HE2	1:B:191:ASN:CG	2.21	0.44
1:C:198:ASP:C	1:C:200:PRO:HD2	2.38	0.44
1:D:13:MET:HA	1:D:14:PRO:HD3	1.50	0.44
1:D:274:ARG:HD2	1:D:274:ARG:HH11	1.66	0.44
1:C:50:MET:CE	3:C:1200:SMG:CE	2.95	0.44
1:C:351:PRO:CB	1:C:356:LEU:HD22	2.48	0.44
1:D:142:ILE:N	4:D:1381:HOH:O	2.38	0.44
1:D:211:LEU:O	1:D:212:LEU:HB3	2.18	0.44
1:B:141:THR:HB	1:B:143:PRO:HD2	1.99	0.44
1:B:137:GLY:HA2	1:B:163:LYS:HB2	2.00	0.44
1:A:159:ARG:HD3	4:A:1077:HOH:O	2.18	0.44
1:B:45:GLY:HA2	1:B:105:MET:CE	2.26	0.44
1:D:212:LEU:HD12	1:D:212:LEU:C	2.37	0.44
1:A:293:ILE:N	3:A:1000:SMG:O62	2.44	0.43
1:A:152:TYR:CD2	1:A:157:TYR:CD1	3.06	0.43
1:A:49:THR:HG22	1:A:58:GLU:HB3	2.00	0.43
1:C:277:HIS:CD2	1:C:310:ASN:HB3	2.53	0.43
1:D:216:PRO:HB2	1:D:217:LEU:CD2	2.48	0.43
1:D:351:PRO:O	1:D:353:PRO:HD3	2.18	0.43
1:D:58:GLU:HB2	1:D:98:MET:HE2	1.99	0.43
1:A:245:ALA:HA	1:A:276:VAL:HG22	2.00	0.43
1:A:3:LEU:HA	1:A:3:LEU:HD12	1.79	0.43
1:B:151:GLY:O	1:B:154:ASP:HB2	2.19	0.43
1:C:118:SER:HB2	4:C:1203:HOH:O	2.17	0.43
1:D:149:VAL:O	1:D:150:GLY:C	2.57	0.43
1:D:363:LYS:NZ	1:D:363:LYS:CB	2.81	0.43
1:A:125:SER:OG	1:A:126:VAL:N	2.51	0.43
1:B:1:MET:SD	1:B:40:ALA:HB2	2.58	0.43
1:C:264:PRO:HG3	1:C:305:LEU:CD2	2.48	0.43
1:D:58:GLU:HB2	1:D:98:MET:HE3	1.99	0.43
1:A:35:ARG:CD	1:A:44:TRP:CZ2	2.93	0.43
1:B:277:HIS:CD2	1:B:310:ASN:HB3	2.54	0.43
1:D:112:LEU:HB3	1:D:117:ARG:O	2.19	0.43
1:D:8:LEU:HD11	1:D:34:LEU:HD22	1.98	0.43
1:D:356:LEU:O	1:D:359:VAL:CG2	2.66	0.43
1:A:189:ASP:HA	1:A:214:GLU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:GLN:O	1:A:235:PRO:HD3	2.18	0.43
1:A:38:THR:CB	1:A:39:PRO:HD2	2.48	0.43
1:B:2:LYS:O	1:B:2:LYS:HE3	2.19	0.43
1:D:141:THR:CG2	1:D:143:PRO:CD	2.79	0.43
1:D:142:ILE:O	1:D:143:PRO:C	2.56	0.43
1:D:166:PRO:HD3	1:D:194:TYR:CZ	2.53	0.43
1:A:190:ALA:O	1:A:191:ASN:C	2.57	0.43
1:B:153:LEU:HD23	1:B:153:LEU:HA	1.85	0.43
1:B:169:ASP:OD2	1:B:194:TYR:OH	2.21	0.43
1:B:239:ASP:OD1	1:B:266:ARG:NH1	2.49	0.43
1:B:29:ARG:NE	1:B:31:LEU:HD21	2.34	0.43
1:C:298:GLY:O	1:C:299:ARG:C	2.57	0.43
1:C:87:THR:N	1:C:88:PRO:HD2	2.34	0.43
1:D:139:MET:HG2	1:D:145:LEU:HB2	2.00	0.43
1:D:153:LEU:HD23	1:D:153:LEU:HA	1.73	0.43
1:D:227:GLU:HA	1:D:230:ARG:NH1	2.34	0.43
1:A:29:ARG:NH1	1:A:292:MET:O	2.52	0.43
1:A:13:MET:HB3	1:A:324:TYR:CE2	2.54	0.43
1:B:23:PHE:HE2	1:B:191:ASN:HB3	1.84	0.43
1:B:217:LEU:HD23	1:B:217:LEU:N	2.34	0.43
1:B:328:ILE:O	1:B:351:PRO:HA	2.18	0.43
1:C:192:THR:HB	1:C:218:GLU:HA	1.99	0.43
1:C:9:ARG:HG2	1:C:360:THR:HG23	2.01	0.43
1:D:11:VAL:HG13	1:D:359:VAL:HB	2.00	0.43
1:D:67:LEU:HA	1:D:67:LEU:HD23	1.90	0.43
1:B:63:ALA:O	1:B:66:VAL:HG12	2.19	0.43
1:C:112:LEU:HB3	1:C:117:ARG:O	2.19	0.43
1:C:1:MET:HE1	1:C:107:VAL:O	2.17	0.43
1:D:4:SER:N	1:D:37:VAL:O	2.49	0.43
1:A:4:SER:HB2	1:A:37:VAL:O	2.19	0.42
1:B:130:VAL:HA	1:B:131:PRO:HD3	1.91	0.42
1:B:194:TYR:CE2	1:B:202:LEU:HD21	2.54	0.42
1:A:288:TRP:HB3	1:A:313:LEU:HB2	2.00	0.42
1:A:355:LEU:HA	1:A:355:LEU:HD23	1.76	0.42
1:B:355:LEU:HA	1:B:355:LEU:HD12	1.67	0.42
1:C:293:ILE:HG13	3:C:1200:SMG:CE	2.50	0.42
1:C:98:MET:HB2	1:C:98:MET:HE3	1.50	0.42
1:D:159:ARG:HA	1:D:185:LEU:HB2	2.01	0.42
1:A:159:ARG:HD2	1:A:187:GLN:OE1	2.19	0.42
1:C:271:LEU:HA	1:C:271:LEU:HD23	1.81	0.42
1:D:148:VAL:HG12	1:D:152:TYR:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:GLU:OE1	1:D:98:MET:CG	2.60	0.42
1:A:129:SER:HA	1:A:339:LEU:O	2.19	0.42
1:A:277:HIS:CD2	1:A:310:ASN:HB3	2.54	0.42
1:B:142:ILE:HD12	1:B:172:PRO:HA	2.01	0.42
1:B:192:THR:HB	1:B:218:GLU:HA	2.00	0.42
1:C:321:ASP:HA	1:C:324:TYR:O	2.19	0.42
1:B:141:THR:O	1:B:144:GLN:HB3	2.20	0.42
1:B:14:PRO:HA	1:B:28:VAL:HG22	2.00	0.42
1:D:35:ARG:HG3	1:D:44:TRP:CZ2	2.53	0.42
1:D:85:LYS:O	1:D:88:PRO:HD2	2.19	0.42
1:B:50:MET:CE	3:B:1100:SMG:HE2	2.49	0.42
1:B:50:MET:HE1	3:B:1100:SMG:HE2	2.00	0.42
1:C:316:ASP:HB3	3:C:1200:SMG:H42	2.01	0.42
1:D:142:ILE:N	1:D:143:PRO:HD2	2.35	0.42
1:D:38:THR:CB	1:D:39:PRO:HD2	2.19	0.42
1:D:66:VAL:O	1:D:70:TYR:N	2.48	0.42
1:A:142:ILE:O	1:A:143:PRO:C	2.56	0.42
1:A:153:LEU:HD23	1:A:153:LEU:HA	1.67	0.42
1:A:171:GLU:O	1:A:174:ARG:HB3	2.20	0.42
1:B:358:GLU:CG	1:B:358:GLU:O	2.66	0.42
1:D:305:LEU:O	1:D:307:SER:N	2.52	0.42
1:B:132:CYS:SG	1:B:317:THR:O	2.78	0.42
1:C:63:ALA:O	1:C:64:GLU:C	2.57	0.42
1:D:145:LEU:O	1:D:146:LEU:C	2.59	0.42
1:A:25:THR:HG22	1:A:26:GLN:N	2.34	0.42
1:A:334:LEU:HD12	1:A:338:HIS:O	2.20	0.42
1:D:163:LYS:HE3	1:D:189:ASP:HB3	2.02	0.42
1:D:217:LEU:HD23	1:D:217:LEU:N	2.35	0.42
1:D:7:GLU:HB2	1:D:365:TRP:HE3	1.84	0.42
1:D:38:THR:CB	1:D:39:PRO:CD	2.82	0.42
1:A:277:HIS:NE2	1:A:310:ASN:N	2.61	0.41
1:A:321:ASP:C	1:A:321:ASP:OD1	2.58	0.41
1:A:352:ILE:HG22	1:A:355:LEU:H	1.84	0.41
1:C:75:LEU:CD1	1:C:103:LEU:CD1	2.93	0.41
1:D:23:PHE:CZ	3:D:1300:SMG:HG1	2.53	0.41
1:A:352:ILE:O	1:A:352:ILE:HG22	2.20	0.41
1:B:163:LYS:HZ1	3:B:1100:SMG:C2	2.33	0.41
1:C:153:LEU:HA	1:C:153:LEU:HD23	1.93	0.41
1:D:205:LEU:C	1:D:207:PRO:CD	2.84	0.41
1:D:65:HIS:O	1:D:69:HIS:HD2	2.02	0.41
1:A:141:THR:OG1	1:A:144:GLN:CB	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:TYR:HD2	1:A:157:TYR:CD1	2.38	0.41
1:C:127:ARG:NH2	1:C:311:PHE:O	2.53	0.41
1:C:171:GLU:O	1:C:172:PRO:C	2.57	0.41
1:C:221:ASP:OD2	1:C:224:GLY:HA3	2.20	0.41
1:D:356:LEU:C	1:D:356:LEU:HD12	2.39	0.41
1:D:8:LEU:O	1:D:363:LYS:HA	2.20	0.41
1:A:327:ASP:OD1	1:A:328:ILE:N	2.54	0.41
1:A:113:ARG:HG3	1:A:346:GLY:HA3	2.01	0.41
1:A:181:GLY:O	1:A:184:VAL:HG23	2.21	0.41
1:B:177:ARG:HD3	1:B:177:ARG:HA	1.69	0.41
1:B:296:GLY:HA3	1:B:329:THR:OG1	2.21	0.41
1:C:158:VAL:O	1:C:185:LEU:HD12	2.20	0.41
1:C:308:LEU:CB	1:C:309:PRO:CD	2.98	0.41
1:D:165:GLU:HG2	1:D:166:PRO:N	2.34	0.41
1:A:109:ASP:OD1	1:A:346:GLY:HA3	2.21	0.41
1:A:234:THR:HA	1:A:235:PRO:HD2	1.92	0.41
1:B:127:ARG:HG3	4:B:1387:HOH:O	2.20	0.41
1:B:147:ASP:O	1:B:150:GLY:N	2.54	0.41
1:C:244:SER:O	1:C:247:ALA:HB3	2.20	0.41
1:C:353:PRO:O	1:C:354:GLU:C	2.58	0.41
1:D:82:THR:HG22	1:D:84:ALA:N	2.35	0.41
1:D:85:LYS:O	1:D:86:VAL:C	2.57	0.41
1:A:130:VAL:HA	1:A:131:PRO:HD3	1.92	0.41
1:C:72:ILE:N	1:C:73:PRO:HD2	2.36	0.41
1:C:49:THR:HG23	1:C:98:MET:HE3	2.03	0.41
1:D:3:LEU:CD2	1:D:76:LEU:HD23	2.50	0.41
1:C:13:MET:HA	1:C:14:PRO:HD3	1.91	0.41
1:C:355:LEU:HD23	1:C:355:LEU:HA	1.81	0.41
1:D:354:GLU:HG3	1:D:355:LEU:HD13	2.03	0.41
1:D:37:VAL:HG21	1:D:365:TRP:CZ3	2.56	0.41
1:D:68[B]:ARG:NH2	1:D:364:VAL:HG11	2.36	0.41
1:B:308:LEU:HA	1:B:309:PRO:HD3	1.96	0.41
1:C:72:ILE:CB	1:C:73:PRO:CD	2.99	0.41
1:D:177:ARG:HA	1:D:177:ARG:HD3	1.51	0.41
1:D:21:THR:CG2	1:D:23:PHE:CD2	3.04	0.41
1:A:192:THR:HG22	1:A:215:GLN:CG	2.51	0.41
1:C:293:ILE:CD1	3:C:1200:SMG:HE2	2.50	0.41
1:D:200:PRO:O	1:D:203:ALA:HB3	2.21	0.41
1:A:177:ARG:HA	1:A:177:ARG:HD3	1.87	0.40
1:C:163:LYS:HD2	1:C:163:LYS:HA	1.50	0.40
1:D:83:ALA:CB	1:D:108:LEU:HD13	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:174:ARG:O	1:D:178:GLU:HB2	2.21	0.40
1:D:177:ARG:HD2	1:D:181:GLY:O	2.20	0.40
1:A:277:HIS:NE2	1:A:310:ASN:CB	2.84	0.40
1:B:210:LEU:HD23	1:B:210:LEU:HA	1.73	0.40
1:D:7:GLU:HA	1:D:364:VAL:O	2.22	0.40
1:A:159:ARG:HD2	4:A:1077:HOH:O	2.20	0.40
1:A:55:TYR:OH	1:A:266:ARG:HD3	2.21	0.40
1:A:48:VAL:HG22	4:A:1057:HOH:O	2.21	0.40
1:B:321:ASP:HA	1:B:324:TYR:O	2.22	0.40
1:B:36:ALA:O	1:B:42:GLU:HA	2.21	0.40
1:D:350:ALA:HB1	1:D:351:PRO:CD	2.51	0.40
1:A:201:GLN:OE1	1:A:204[A]:ARG:HD2	2.22	0.40
1:A:352:ILE:O	1:A:355:LEU:HB2	2.21	0.40
1:B:202:LEU:C	1:B:204:ARG:N	2.72	0.40
1:C:159:ARG:CD	4:C:1296:HOH:O	2.62	0.40
1:C:185:LEU:HB3	1:C:211:LEU:HD11	2.02	0.40
1:D:293:ILE:HG22	1:D:293:ILE:O	2.20	0.40
1:B:142:ILE:HG22	1:B:143:PRO:N	2.37	0.40
1:D:171:GLU:OE1	1:D:171:GLU:HA	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274[A]:ARG:NH2	1:D:278:ASP:OD2[17_555]	1.80	0.40

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	370/368 (100%)	348 (94%)	22 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	369/368 (100%)	353 (96%)	16 (4%)	0	100	100
1	C	367/368 (100%)	345 (94%)	21 (6%)	1 (0%)	41	41
1	D	367/368 (100%)	326 (89%)	37 (10%)	4 (1%)	14	9
All	All	1473/1472 (100%)	1372 (93%)	96 (6%)	5 (0%)	41	41

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	40	ALA
1	D	306	ALA
1	D	149	VAL
1	D	142	ILE
1	C	353	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	295/291 (101%)	267 (90%)	28 (10%)	8	5
1	B	294/291 (101%)	269 (92%)	25 (8%)	10	7
1	C	292/291 (100%)	269 (92%)	23 (8%)	12	9
1	D	292/291 (100%)	254 (87%)	38 (13%)	4	2
All	All	1173/1164 (101%)	1059 (90%)	114 (10%)	8	5

All (114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	9	ARG
1	A	13	MET
1	A	29	ARG
1	A	31	LEU
1	A	34	LEU

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Mol	Chain	Res	Type
1	A	68[A]	ARG
1	A	68[B]	ARG
1	A	79	GLU
1	A	80	ASP
1	A	98	MET
1	A	119	PHE
1	A	127	ARG
1	A	129	SER
1	A	159	ARG
1	A	169	ASP
1	A	171	GLU
1	A	177	ARG
1	A	179	ARG
1	A	184	VAL
1	A	192	THR
1	A	217	LEU
1	A	321	ASP
1	A	322	ARG
1	A	343	THR
1	A	354	GLU
1	A	356	LEU
1	A	363	LYS
1	B	1	MET
1	B	2	LYS
1	B	9	ARG
1	B	29	ARG
1	B	31	LEU
1	B	32	LEU
1	B	34	LEU
1	B	42	GLU
1	B	55	TYR
1	B	68	ARG
1	B	80	ASP
1	B	92	LYS
1	B	105	MET
1	B	119	PHE
1	B	127	ARG
1	B	159	ARG
1	B	169	ASP
1	B	177	ARG
1	B	179	ARG
1	B	207	PRO

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Mol	Chain	Res	Type
1	B	213	ILE
1	B	233	GLN
1	B	274	ARG
1	B	322	ARG
1	B	355	LEU
1	C	8	LEU
1	C	9	ARG
1	C	10	ARG
1	C	26	GLN
1	C	29	ARG
1	C	34	LEU
1	C	80	ASP
1	C	82	THR
1	C	103	LEU
1	C	119	PHE
1	C	139	MET
1	C	140	ASP
1	C	142	ILE
1	C	144	GLN
1	C	159	ARG
1	C	163	LYS
1	C	169	ASP
1	C	177	ARG
1	C	204	ARG
1	C	217	LEU
1	C	322	ARG
1	C	330	GLU
1	C	343	THR
1	D	2	LYS
1	D	7	GLU
1	D	8	LEU
1	D	9	ARG
1	D	10	ARG
1	D	12	GLN
1	D	20	ARG
1	D	27	SER
1	D	29	ARG
1	D	35	ARG
1	D	42	GLU
1	D	64	GLU
1	D	68[A]	ARG
1	D	68[B]	ARG

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Mol	Chain	Res	Type
1	D	79	GLU
1	D	88	PRO
1	D	98	MET
1	D	116	GLU
1	D	119	PHE
1	D	125	SER
1	D	127	ARG
1	D	139	MET
1	D	155	GLU
1	D	159	ARG
1	D	163	LYS
1	D	165	GLU
1	D	169	ASP
1	D	177	ARG
1	D	213	ILE
1	D	217	LEU
1	D	236	ILE
1	D	261	ASN
1	D	322	ARG
1	D	355	LEU
1	D	361	THR
1	D	363	LYS
1	D	364	VAL
1	D	368	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	HIS
1	A	258	GLN
1	B	12	GLN
1	B	69	HIS
1	B	233	GLN
1	C	26	GLN
1	D	69	HIS
1	D	115	HIS
1	D	258	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	SMG	B	1100	2	9,15,15	1.08	1 (11%)	10,18,18	2.60	4 (40%)
3	SMG	A	1000	2	9,15,15	1.07	1 (11%)	10,18,18	2.07	4 (40%)
3	SMG	D	1300	2	9,15,15	1.32	2 (22%)	10,18,18	3.26	3 (30%)
3	SMG	C	1200	2	9,15,15	1.33	2 (22%)	10,18,18	3.66	4 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SMG	B	1100	2	-	3/11/17/17	-
3	SMG	A	1000	2	-	4/11/17/17	-
3	SMG	D	1300	2	-	4/11/17/17	-
3	SMG	C	1200	2	-	2/11/17/17	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1200	SMG	C4-C3	-3.07	1.45	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1300	SMG	C4-C3	-2.99	1.45	1.51
3	A	1000	SMG	C4-C3	-2.80	1.46	1.51
3	B	1100	SMG	C4-C3	-2.79	1.46	1.51
3	D	1300	SMG	CB-C1	-2.18	1.50	1.53
3	C	1200	SMG	CB-C1	-2.14	1.50	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1200	SMG	CB-C1-N1	-9.60	96.21	110.19
3	D	1300	SMG	CB-C1-N1	-8.99	97.10	110.19
3	C	1200	SMG	C4-C5-C6	-5.22	103.92	112.67
3	B	1100	SMG	C1-N1-C3	-4.89	115.54	123.33
3	A	1000	SMG	CE-SD-CG	4.17	114.72	100.40
3	B	1100	SMG	C4-C3-N1	4.03	122.83	115.83
3	D	1300	SMG	C4-C5-C6	-3.67	106.52	112.67
3	B	1100	SMG	O31-C3-N1	-2.68	118.42	122.95
3	D	1300	SMG	CG-CB-C1	-2.65	105.61	112.96
3	A	1000	SMG	C4-C3-N1	2.62	120.37	115.83
3	A	1000	SMG	C1-N1-C3	-2.48	119.37	123.33
3	B	1100	SMG	C4-C5-C6	-2.44	108.58	112.67
3	C	1200	SMG	CB-CG-SD	-2.40	100.60	113.48
3	A	1000	SMG	C4-C5-C6	-2.11	109.13	112.67
3	C	1200	SMG	O31-C3-N1	-2.07	119.46	122.95

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1100	SMG	C1-CB-CG-SD
3	A	1000	SMG	N1-C1-CB-CG
3	A	1000	SMG	C2-C1-CB-CG
3	D	1300	SMG	N1-C1-CB-CG
3	D	1300	SMG	C2-C1-CB-CG
3	C	1200	SMG	N1-C1-CB-CG
3	C	1200	SMG	C2-C1-CB-CG
3	A	1000	SMG	C1-CB-CG-SD
3	D	1300	SMG	C1-CB-CG-SD
3	B	1100	SMG	CB-CG-SD-CE
3	A	1000	SMG	CB-CG-SD-CE
3	D	1300	SMG	CB-CG-SD-CE
3	B	1100	SMG	C3-C4-C5-C6

There are no ring outliers.

4 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1100	SMG	8	0
3	A	1000	SMG	8	0
3	D	1300	SMG	12	0
3	C	1200	SMG	11	0

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 ⓘ

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	367/368 (99%)	-0.32	2 (0%) 91 92	23, 51, 84, 98	0
1	B	368/368 (100%)	-0.43	2 (0%) 91 92	22, 38, 68, 100	0
1	C	367/368 (99%)	-0.33	7 (1%) 66 71	27, 47, 81, 100	0
1	D	368/368 (100%)	-0.18	6 (1%) 72 75	27, 58, 91, 100	0
All	All	1470/1472 (99%)	-0.32	17 (1%) 79 82	22, 48, 85, 100	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	220[A]	GLU	5.3
1	C	145	LEU	3.5
1	D	149	VAL	3.3
1	C	220[A]	GLU	3.2
1	D	68[A]	ARG	3.2
1	D	145	LEU	3.0
1	D	153	LEU	2.8
1	A	274[A]	ARG	2.7
1	D	184	VAL	2.7
1	C	149	VAL	2.7
1	D	180	PHE	2.6
1	C	176	VAL	2.4
1	B	1	MET	2.3
1	A	145	LEU	2.3
1	C	142	ILE	2.1
1	C	175	ALA	2.1
1	C	146	LEU	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 [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	D	1301	1/1	0.82	0.07	66,66,66,66	0
3	SMG	D	1300	16/16	0.88	0.17	37,78,100,100	0
3	SMG	C	1200	16/16	0.93	0.10	23,54,100,100	0
2	MG	A	1001	1/1	0.94	0.04	47,47,47,47	0
3	SMG	B	1100	16/16	0.95	0.11	31,50,100,100	0
3	SMG	A	1000	16/16	0.95	0.10	38,57,85,100	0
2	MG	C	1201	1/1	0.97	0.06	47,47,47,47	0
2	MG	B	1101	1/1	0.98	0.03	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.