



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:38 PM UTC

PDB ID : 1OYP / pdb_00001oyp
Title : Crystal Structure of the phosphorolytic exoribonuclease RNase PH from *Bacillus subtilis*
Authors : Harlow, L.S.; Kadziola, A.; Jensen, K.F.; Larsen, S.
Deposited on : 2003-04-07
Resolution : 2.76 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

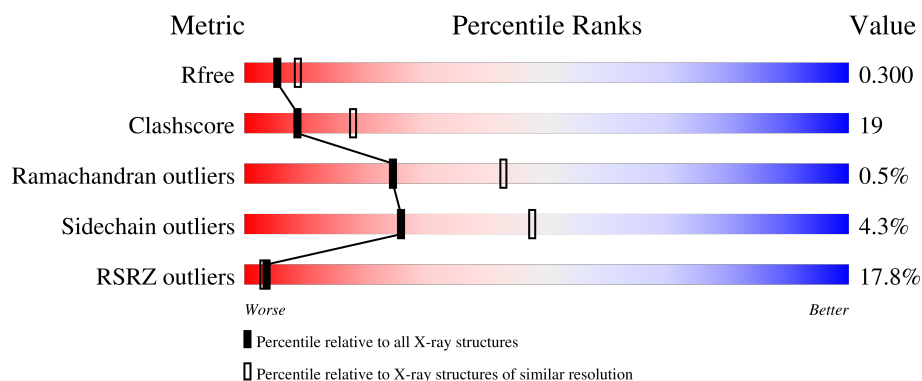
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 of 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	245	
1	B	245	
1	C	245	
1	D	245	
1	E	245	

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Mol	Chain	Length	Quality of chain
1	F	245	17% 61% 29% • 8%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 10368 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 Ribonuclease PH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			
1	B	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			
1	C	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			
1	D	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			
1	E	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			
1	F	226	Total	C	N	O	S	0	0	0
			1718	1074	296	340	8			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

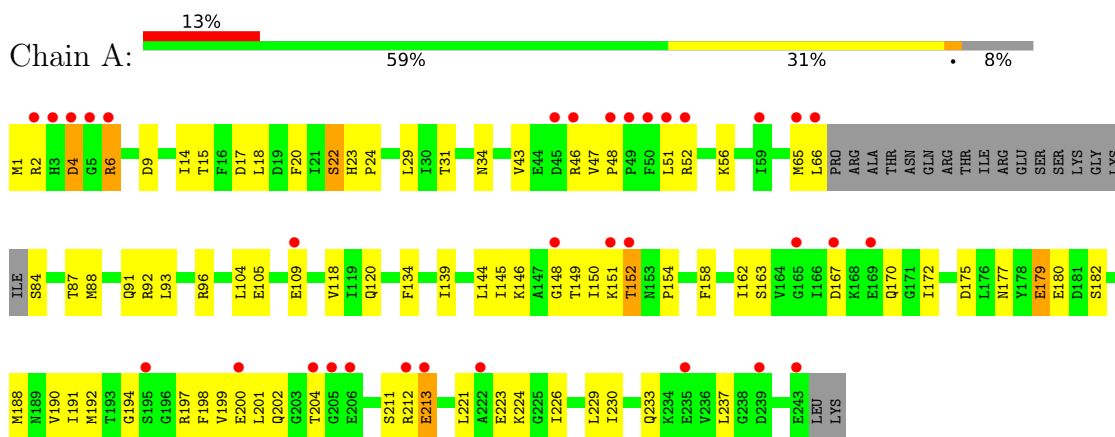


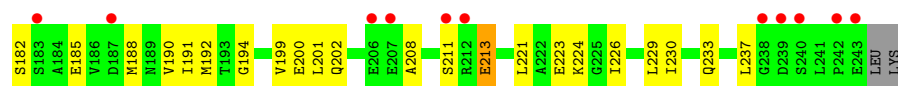
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

3 Residue-property plots

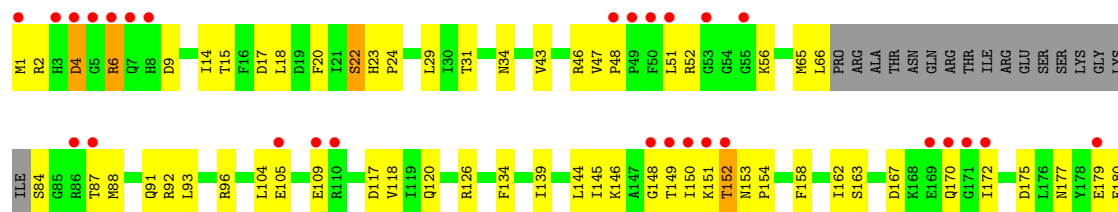
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Ribonuclease PH

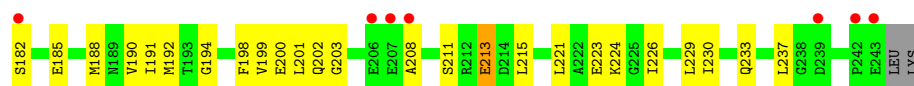
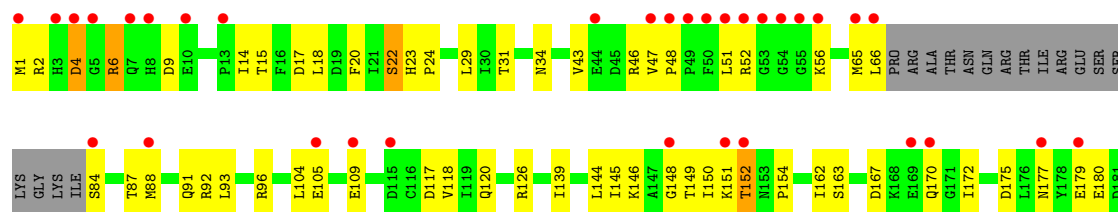




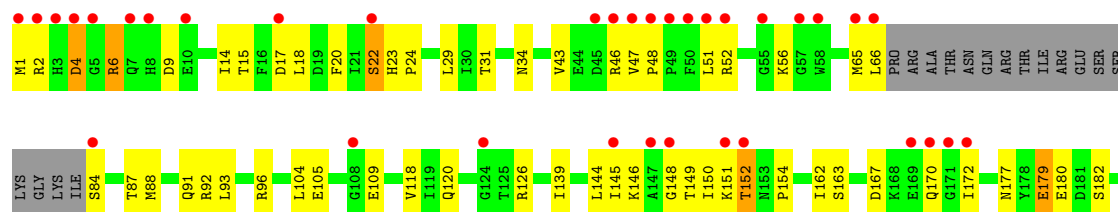
● Molecule 1: Ribonuclease PH



● Molecule 1: Ribonuclease PH



● Molecule 1: Ribonuclease PH



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.31Å 163.56Å 166.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 2.76 29.88 – 2.76	Depositor EDS
% Data completeness (in resolution range)	97.6 (29.88-2.76) 98.6 (29.88-2.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.99 (at 2.76Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.285 , 0.305 0.281 , 0.300	Depositor DCC
R_{free} test set	1841 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 27.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for -h,l,k	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	10368	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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: SO4

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	0.28	0/1738	0.81	2/2343 (0.1%)
1	B	0.28	0/1738	0.81	2/2343 (0.1%)
1	C	0.28	0/1738	0.81	2/2343 (0.1%)
1	D	0.28	0/1738	0.81	2/2343 (0.1%)
1	E	0.27	0/1738	0.80	2/2343 (0.1%)
1	F	0.27	0/1738	0.81	2/2343 (0.1%)
All	All	0.28	0/10428	0.81	12/14058 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	22	SER	N-CA-C	7.83	119.90	111.36
1	E	22	SER	N-CA-C	7.81	119.88	111.36
1	B	22	SER	N-CA-C	7.80	119.87	111.36
1	A	22	SER	N-CA-C	7.79	119.86	111.36
1	C	22	SER	N-CA-C	7.78	119.84	111.36
1	F	22	SER	N-CA-C	7.77	119.83	111.36
1	D	199	VAL	N-CA-C	-7.55	105.79	111.90
1	F	199	VAL	N-CA-C	-7.51	105.81	111.90
1	B	199	VAL	N-CA-C	-7.51	105.82	111.90
1	E	199	VAL	N-CA-C	-7.50	105.83	111.90
1	C	199	VAL	N-CA-C	-7.12	105.84	112.96
1	A	199	VAL	N-CA-C	-7.12	105.84	112.96

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	1718	0	1730	81	0
1	B	1718	0	1730	67	0
1	C	1718	0	1730	61	0
1	D	1718	0	1730	63	0
1	E	1718	0	1730	63	0
1	F	1718	0	1730	65	0
2	A	10	0	0	0	0
2	B	10	0	0	1	0
2	C	10	0	0	0	0
2	D	10	0	0	1	0
2	E	10	0	0	1	0
2	F	10	0	0	1	0
All	All	10368	0	10380	387	0

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 19.

All (387) 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:201:LEU:HD12	1:B:203:GLY:H	1.36	0.88
1:A:47:VAL:HG11	1:A:51:LEU:HB2	1.66	0.76
1:F:47:VAL:HG11	1:F:51:LEU:HB2	1.67	0.76
1:C:47:VAL:HG11	1:C:51:LEU:HB2	1.67	0.76
1:D:1:MET:HG3	1:D:2:ARG:H	1.51	0.76
1:E:47:VAL:HG11	1:E:51:LEU:HB2	1.68	0.76
1:D:47:VAL:HG11	1:D:51:LEU:HB2	1.67	0.74
1:A:56:LYS:HB3	1:A:105:GLU:HG2	1.69	0.74
1:B:47:VAL:HG11	1:B:51:LEU:HB2	1.68	0.74
1:D:56:LYS:HB3	1:D:105:GLU:HG2	1.69	0.74
1:E:190:VAL:HG11	1:E:192:MET:HE2	1.69	0.74
1:E:56:LYS:HB3	1:E:105:GLU:HG2	1.69	0.74
1:E:23:HIS:HB3	1:E:24:PRO:HD3	1.71	0.73
1:F:190:VAL:HG11	1:F:192:MET:HE2	1.69	0.73
1:D:190:VAL:HG11	1:D:192:MET:HE2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:23:HIS:HB3	1:F:24:PRO:HD3	1.70	0.73
1:B:190:VAL:HG11	1:B:192:MET:HE2	1.69	0.73
1:B:23:HIS:HB3	1:B:24:PRO:HD3	1.71	0.73
1:C:56:LYS:HB3	1:C:105:GLU:HG2	1.71	0.73
1:B:56:LYS:HB3	1:B:105:GLU:HG2	1.70	0.72
1:D:23:HIS:HB3	1:D:24:PRO:HD3	1.70	0.72
1:C:190:VAL:HG11	1:C:192:MET:HE2	1.70	0.72
1:F:56:LYS:HB3	1:F:105:GLU:HG2	1.71	0.72
1:A:190:VAL:HG11	1:A:192:MET:HE2	1.70	0.72
1:A:20:PHE:CE1	1:A:29:LEU:HD22	2.24	0.72
1:D:211:SER:OG	1:D:213:GLU:HG2	1.90	0.71
1:A:201:LEU:CD1	1:B:203:GLY:H	2.03	0.71
1:A:23:HIS:HB3	1:A:24:PRO:HD3	1.70	0.71
1:C:211:SER:OG	1:C:213:GLU:HG2	1.90	0.71
1:E:211:SER:OG	1:E:213:GLU:HG2	1.91	0.70
1:B:1:MET:HG3	1:B:2:ARG:H	1.56	0.70
1:C:23:HIS:HB3	1:C:24:PRO:HD3	1.71	0.70
1:F:1:MET:HG3	1:F:2:ARG:H	1.57	0.70
1:F:211:SER:OG	1:F:213:GLU:HG2	1.92	0.70
1:F:34:ASN:O	1:F:120:GLN:HG2	1.93	0.69
1:B:65:MET:HE2	1:B:118:VAL:HG11	1.75	0.69
1:C:1:MET:HG3	1:C:2:ARG:H	1.59	0.68
1:B:211:SER:OG	1:B:213:GLU:HG2	1.92	0.68
1:D:34:ASN:O	1:D:120:GLN:HG2	1.93	0.68
1:E:203:GLY:H	1:F:201:LEU:HD12	1.57	0.68
1:F:144:LEU:O	1:F:149:THR:HG22	1.93	0.68
1:E:46:ARG:HH12	1:E:52:ARG:HD3	1.58	0.68
1:E:65:MET:HE2	1:E:118:VAL:HG11	1.74	0.68
1:E:144:LEU:O	1:E:149:THR:HG22	1.93	0.68
1:D:65:MET:HE2	1:D:118:VAL:HG11	1.74	0.68
1:B:144:LEU:O	1:B:149:THR:HG22	1.94	0.68
1:D:144:LEU:O	1:D:149:THR:HG22	1.93	0.68
1:C:65:MET:HE2	1:C:118:VAL:HG11	1.75	0.67
1:A:34:ASN:O	1:A:120:GLN:HG2	1.94	0.67
1:A:65:MET:HE2	1:A:118:VAL:HG11	1.76	0.67
1:B:167:ASP:HB3	1:B:170:GLN:HB2	1.77	0.67
1:F:167:ASP:HB3	1:F:170:GLN:HB2	1.76	0.67
1:A:1:MET:HG3	1:A:2:ARG:H	1.59	0.67
1:E:167:ASP:HB3	1:E:170:GLN:HB2	1.78	0.66
1:C:167:ASP:HB3	1:C:170:GLN:HB2	1.78	0.66
1:D:46:ARG:HH12	1:D:52:ARG:HD3	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:34:ASN:O	1:E:120:GLN:HG2	1.95	0.66
1:A:144:LEU:O	1:A:149:THR:HG22	1.95	0.66
1:C:145:ILE:HG13	1:C:150:ILE:HD11	1.77	0.66
1:F:145:ILE:HG13	1:F:150:ILE:HD11	1.78	0.66
1:A:211:SER:OG	1:A:213:GLU:HG2	1.96	0.66
1:C:144:LEU:O	1:C:149:THR:HG22	1.95	0.65
1:F:65:MET:HE2	1:F:118:VAL:HG11	1.79	0.65
1:B:145:ILE:HG13	1:B:150:ILE:HD11	1.78	0.65
1:E:1:MET:HG3	1:E:2:ARG:H	1.60	0.65
1:A:167:ASP:HB3	1:A:170:GLN:HB2	1.78	0.65
1:A:2:ARG:NH2	1:A:6:ARG:NH2	2.45	0.65
1:C:34:ASN:O	1:C:120:GLN:HG2	1.97	0.65
1:D:167:ASP:HB3	1:D:170:GLN:HB2	1.80	0.65
1:B:46:ARG:HH12	1:B:52:ARG:HD3	1.62	0.64
1:F:46:ARG:HH12	1:F:52:ARG:HD3	1.63	0.64
1:E:145:ILE:HG13	1:E:150:ILE:HD11	1.78	0.64
1:A:145:ILE:HG13	1:A:150:ILE:HD11	1.80	0.64
1:E:65:MET:HG3	1:E:66:LEU:H	1.63	0.64
1:E:192:MET:HE3	1:E:226:ILE:HD12	1.79	0.64
1:F:192:MET:HE3	1:F:226:ILE:HD12	1.79	0.64
1:A:46:ARG:HH12	1:A:52:ARG:HD3	1.63	0.63
1:C:46:ARG:HH12	1:C:52:ARG:HD3	1.63	0.63
1:F:177:ASN:CG	1:F:180:GLU:HG3	2.23	0.63
1:C:2:ARG:HB2	1:C:6:ARG:O	1.99	0.63
1:D:145:ILE:HG13	1:D:150:ILE:HD11	1.80	0.63
1:A:2:ARG:HH22	1:A:6:ARG:NH2	1.97	0.63
1:F:177:ASN:OD1	1:F:180:GLU:HG3	1.99	0.63
1:B:2:ARG:HB2	1:B:6:ARG:O	1.99	0.62
1:B:65:MET:HG3	1:B:66:LEU:H	1.65	0.62
1:F:65:MET:HG3	1:F:66:LEU:H	1.64	0.61
1:D:192:MET:HE3	1:D:226:ILE:HD12	1.83	0.61
1:A:2:ARG:HB2	1:A:6:ARG:O	1.99	0.61
1:C:65:MET:HG3	1:C:66:LEU:H	1.65	0.60
1:F:172:ILE:HG22	1:F:221:LEU:HD12	1.84	0.60
1:A:65:MET:HG3	1:A:66:LEU:H	1.65	0.60
1:F:201:LEU:HD12	1:F:201:LEU:O	2.01	0.60
1:D:201:LEU:O	1:D:201:LEU:HD12	2.03	0.59
1:A:17:ASP:HB2	1:A:29:LEU:HB3	1.84	0.59
1:A:201:LEU:HD12	1:A:201:LEU:O	2.02	0.59
1:C:9:ASP:OD1	1:C:224:LYS:HE3	2.02	0.59
1:D:2:ARG:HB2	1:D:6:ARG:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2:ARG:HB2	1:E:6:ARG:O	2.03	0.59
1:E:201:LEU:HD12	1:E:201:LEU:O	2.02	0.59
1:C:201:LEU:HD12	1:C:201:LEU:O	2.02	0.59
1:D:65:MET:HG3	1:D:66:LEU:H	1.66	0.59
1:B:201:LEU:HD12	1:B:201:LEU:O	2.03	0.58
1:C:17:ASP:HB2	1:C:29:LEU:HB3	1.86	0.58
1:A:172:ILE:HG22	1:A:221:LEU:HD12	1.85	0.58
1:B:192:MET:HE3	1:B:226:ILE:HD12	1.86	0.58
1:E:46:ARG:NH1	1:E:52:ARG:HD3	2.19	0.57
1:C:192:MET:HE3	1:C:226:ILE:HD12	1.86	0.57
1:F:17:ASP:HB2	1:F:29:LEU:HB3	1.86	0.57
1:C:51:LEU:CD2	1:C:56:LYS:HG3	2.35	0.57
1:D:51:LEU:CD2	1:D:56:LYS:HG3	2.34	0.57
1:A:192:MET:HE3	1:A:226:ILE:HD12	1.85	0.57
1:C:172:ILE:HG22	1:C:221:LEU:HD12	1.87	0.57
1:D:172:ILE:HG22	1:D:221:LEU:HD12	1.87	0.57
1:A:51:LEU:CD2	1:A:56:LYS:HG3	2.34	0.56
1:F:144:LEU:HG	1:F:149:THR:HG21	1.87	0.56
1:A:2:ARG:NH1	1:A:6:ARG:NH2	2.53	0.56
1:E:17:ASP:HB2	1:E:29:LEU:HB3	1.87	0.56
1:E:144:LEU:HG	1:E:149:THR:HG21	1.87	0.56
1:E:172:ILE:HG22	1:E:221:LEU:HD12	1.87	0.56
1:D:17:ASP:HB2	1:D:29:LEU:HB3	1.87	0.56
1:D:144:LEU:HG	1:D:149:THR:HG21	1.86	0.56
1:B:51:LEU:CD2	1:B:56:LYS:HG3	2.36	0.56
1:B:144:LEU:HG	1:B:149:THR:HG21	1.88	0.56
1:C:144:LEU:HG	1:C:149:THR:HG21	1.88	0.56
1:E:51:LEU:CD2	1:E:56:LYS:HG3	2.36	0.56
1:F:2:ARG:HB2	1:F:6:ARG:O	2.05	0.56
1:B:17:ASP:HB2	1:B:29:LEU:HB3	1.88	0.56
1:B:34:ASN:O	1:B:120:GLN:HG2	2.06	0.56
1:F:51:LEU:CD2	1:F:56:LYS:HG3	2.36	0.56
1:B:172:ILE:HG22	1:B:221:LEU:HD12	1.87	0.55
1:F:18:LEU:HD22	1:F:139:ILE:HD11	1.89	0.55
1:D:20:PHE:CE1	1:D:29:LEU:HD22	2.42	0.55
1:A:46:ARG:NH1	1:A:52:ARG:HD3	2.22	0.55
1:A:144:LEU:HG	1:A:149:THR:HG21	1.88	0.55
1:C:46:ARG:NH1	1:C:52:ARG:HD3	2.22	0.54
1:C:65:MET:CG	1:C:66:LEU:N	2.71	0.54
1:C:201:LEU:HD12	1:D:203:GLY:H	1.73	0.54
1:D:47:VAL:HG13	1:D:48:PRO:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:MET:CG	1:E:66:LEU:N	2.71	0.54
1:B:177:ASN:CG	1:B:180:GLU:HG3	2.33	0.54
1:F:20:PHE:CE1	1:F:29:LEU:HD22	2.43	0.54
1:F:65:MET:CG	1:F:66:LEU:N	2.71	0.54
1:A:65:MET:CG	1:A:66:LEU:N	2.71	0.54
1:C:47:VAL:HG13	1:C:48:PRO:HD2	1.90	0.53
1:D:46:ARG:NH1	1:D:52:ARG:HD3	2.22	0.53
1:B:46:ARG:NH1	1:B:52:ARG:HD3	2.22	0.53
1:B:192:MET:HE1	1:B:223:GLU:HG3	1.90	0.53
1:E:18:LEU:HD22	1:E:139:ILE:HD11	1.90	0.53
1:F:47:VAL:HG13	1:F:48:PRO:HD2	1.90	0.53
1:F:46:ARG:NH1	1:F:52:ARG:HD3	2.24	0.53
1:A:47:VAL:HG13	1:A:48:PRO:HD2	1.89	0.53
1:D:177:ASN:ND2	1:D:180:GLU:HG3	2.24	0.53
1:E:47:VAL:HG13	1:E:48:PRO:HD2	1.91	0.53
1:B:47:VAL:HG13	1:B:48:PRO:HD2	1.90	0.53
1:B:65:MET:CG	1:B:66:LEU:N	2.71	0.53
1:D:177:ASN:CG	1:D:180:GLU:HG3	2.34	0.53
1:A:151:LYS:O	1:A:152:THR:HB	2.10	0.52
1:C:20:PHE:CE1	1:C:29:LEU:HD22	2.44	0.52
1:A:2:ARG:HH22	1:A:6:ARG:HH21	1.58	0.52
1:B:200:GLU:HG3	1:B:201:LEU:N	2.24	0.52
1:E:213:GLU:CD	1:E:213:GLU:H	2.18	0.52
1:F:43:VAL:HG21	1:F:144:LEU:HD11	1.91	0.52
1:A:18:LEU:HD22	1:A:139:ILE:HD11	1.92	0.52
1:A:197:ARG:NH2	1:B:209:THR:O	2.43	0.52
1:E:152:THR:O	1:E:152:THR:HG23	2.10	0.52
1:A:2:ARG:HH12	1:A:6:ARG:NH2	2.08	0.52
1:D:213:GLU:CD	1:D:213:GLU:H	2.18	0.52
1:C:152:THR:O	1:C:154:PRO:HD3	2.10	0.52
1:D:65:MET:CG	1:D:66:LEU:N	2.72	0.52
1:F:177:ASN:ND2	1:F:180:GLU:HG3	2.25	0.52
1:A:162:ILE:HG13	1:A:163:SER:N	2.25	0.52
1:A:162:ILE:HG13	1:A:163:SER:H	1.75	0.52
1:E:20:PHE:CE1	1:E:29:LEU:HD22	2.44	0.52
1:E:47:VAL:HG21	1:E:109:GLU:HG3	1.92	0.52
1:E:151:LYS:O	1:E:152:THR:HB	2.10	0.52
1:F:152:THR:O	1:F:154:PRO:HD3	2.10	0.52
1:F:192:MET:HE1	1:F:223:GLU:HG3	1.92	0.51
1:A:152:THR:HG23	1:A:152:THR:O	2.10	0.51
1:B:18:LEU:HD22	1:B:139:ILE:HD11	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:VAL:HG21	1:D:144:LEU:HD11	1.93	0.51
1:E:162:ILE:HG13	1:E:163:SER:N	2.26	0.51
1:F:162:ILE:HG13	1:F:163:SER:N	2.25	0.51
1:C:18:LEU:HD22	1:C:139:ILE:HD11	1.91	0.51
1:D:151:LYS:O	1:D:152:THR:HB	2.11	0.51
1:A:2:ARG:CZ	1:A:6:ARG:NH2	2.74	0.51
1:C:152:THR:O	1:C:152:THR:HG23	2.10	0.51
1:A:200:GLU:HG3	1:A:201:LEU:N	2.25	0.51
1:D:152:THR:HG23	1:D:152:THR:O	2.10	0.51
1:E:152:THR:O	1:E:154:PRO:HD3	2.11	0.51
1:A:56:LYS:HE3	1:A:104:LEU:HB2	1.93	0.51
1:B:152:THR:HG23	1:B:152:THR:O	2.10	0.51
1:E:162:ILE:HG13	1:E:163:SER:H	1.76	0.51
1:B:152:THR:O	1:B:154:PRO:HD3	2.11	0.51
1:D:92:ARG:O	1:D:96:ARG:HB2	2.12	0.51
1:D:152:THR:O	1:D:154:PRO:HD3	2.10	0.51
1:A:152:THR:O	1:A:154:PRO:HD3	2.11	0.50
1:B:177:ASN:ND2	1:B:180:GLU:HG3	2.25	0.50
1:E:43:VAL:HG21	1:E:144:LEU:HD11	1.92	0.50
1:F:200:GLU:HG3	1:F:201:LEU:N	2.26	0.50
1:B:56:LYS:HE3	1:B:104:LEU:HB2	1.92	0.50
1:D:18:LEU:HD22	1:D:139:ILE:HD11	1.92	0.50
1:A:43:VAL:HG21	1:A:144:LEU:HD11	1.92	0.50
1:E:56:LYS:HE3	1:E:104:LEU:HB2	1.93	0.50
1:A:2:ARG:NH2	1:A:6:ARG:CZ	2.75	0.50
1:A:192:MET:HE1	1:A:223:GLU:HG3	1.94	0.50
1:C:43:VAL:HG21	1:C:144:LEU:HD11	1.93	0.50
1:B:177:ASN:OD1	1:B:180:GLU:HG3	2.11	0.50
1:C:200:GLU:HG3	1:C:201:LEU:N	2.25	0.50
1:B:151:LYS:O	1:B:152:THR:HB	2.11	0.50
1:C:56:LYS:HE3	1:C:104:LEU:HB2	1.94	0.50
1:F:162:ILE:HG13	1:F:163:SER:H	1.76	0.50
1:B:47:VAL:HG21	1:B:109:GLU:HG3	1.94	0.50
1:F:152:THR:O	1:F:152:THR:HG23	2.10	0.50
1:A:47:VAL:HG21	1:A:109:GLU:HG3	1.94	0.49
1:C:151:LYS:O	1:C:152:THR:HB	2.11	0.49
1:A:14:ILE:HD13	1:A:229:LEU:HD21	1.94	0.49
1:A:213:GLU:CD	1:A:213:GLU:H	2.20	0.49
1:C:213:GLU:CD	1:C:213:GLU:H	2.19	0.49
1:B:43:VAL:HG21	1:B:144:LEU:HD11	1.93	0.49
1:B:92:ARG:O	1:B:96:ARG:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:213:GLU:H	1:B:213:GLU:CD	2.19	0.49
1:C:162:ILE:HG13	1:C:163:SER:N	2.28	0.49
1:E:65:MET:HG3	1:E:66:LEU:N	2.26	0.49
1:D:56:LYS:HE3	1:D:104:LEU:HB2	1.93	0.49
1:F:151:LYS:O	1:F:152:THR:HB	2.11	0.49
1:B:9:ASP:OD1	1:B:224:LYS:HE3	2.13	0.49
1:D:200:GLU:HG3	1:D:201:LEU:N	2.26	0.49
1:B:146:LYS:C	1:B:148:GLY:H	2.21	0.49
1:E:200:GLU:HG3	1:E:201:LEU:N	2.26	0.49
1:E:14:ILE:HD13	1:E:229:LEU:HD21	1.95	0.48
1:A:92:ARG:O	1:A:96:ARG:HB2	2.13	0.48
1:B:65:MET:HG3	1:B:66:LEU:N	2.28	0.48
1:D:14:ILE:HD13	1:D:229:LEU:HD21	1.94	0.48
1:F:213:GLU:CD	1:F:213:GLU:H	2.21	0.48
1:A:9:ASP:OD1	1:A:224:LYS:HE3	2.13	0.48
1:D:146:LYS:C	1:D:148:GLY:H	2.22	0.48
1:D:162:ILE:HG13	1:D:163:SER:N	2.28	0.48
1:F:56:LYS:HE3	1:F:104:LEU:HB2	1.94	0.48
1:B:4:ASP:HB3	1:B:6:ARG:HG2	1.96	0.48
1:D:188:MET:HG3	1:D:202:GLN:C	2.38	0.48
1:A:2:ARG:CZ	1:A:6:ARG:CZ	2.92	0.47
1:B:162:ILE:HG13	1:B:163:SER:N	2.29	0.47
1:C:47:VAL:HG21	1:C:109:GLU:HG3	1.96	0.47
1:D:177:ASN:OD1	1:D:180:GLU:HG3	2.14	0.47
1:F:65:MET:HG3	1:F:66:LEU:N	2.29	0.47
1:A:146:LYS:C	1:A:148:GLY:H	2.21	0.47
1:D:1:MET:HG3	1:D:2:ARG:N	2.23	0.47
1:D:4:ASP:HB3	1:D:6:ARG:HG2	1.96	0.47
1:D:65:MET:HG3	1:D:66:LEU:N	2.29	0.47
1:D:192:MET:HE1	1:D:223:GLU:HG3	1.96	0.47
1:F:4:ASP:HB3	1:F:6:ARG:HG2	1.96	0.47
1:F:9:ASP:OD1	1:F:224:LYS:HE3	2.15	0.47
1:F:14:ILE:HD13	1:F:229:LEU:HD21	1.95	0.47
1:C:92:ARG:O	1:C:96:ARG:HB2	2.14	0.47
1:C:192:MET:HE1	1:C:223:GLU:HG3	1.96	0.47
1:E:146:LYS:C	1:E:148:GLY:H	2.21	0.47
1:F:47:VAL:HG21	1:F:109:GLU:HG3	1.96	0.47
1:F:188:MET:HG3	1:F:202:GLN:C	2.40	0.47
1:C:162:ILE:HG13	1:C:163:SER:H	1.80	0.47
1:E:92:ARG:O	1:E:96:ARG:HB2	2.13	0.47
1:A:6:ARG:NH2	1:A:175:ASP:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:ARG:HG2	2:B:303:SO4:O4	2.15	0.47
1:A:4:ASP:HB3	1:A:6:ARG:HG2	1.97	0.47
1:B:14:ILE:HD13	1:B:229:LEU:HD21	1.96	0.47
1:A:87:THR:O	1:A:91:GLN:HB2	2.15	0.47
1:D:162:ILE:HG13	1:D:163:SER:H	1.80	0.47
1:E:43:VAL:HG11	1:E:144:LEU:HD21	1.97	0.47
1:F:146:LYS:C	1:F:148:GLY:H	2.22	0.47
1:D:9:ASP:OD1	1:D:224:LYS:HE3	2.15	0.46
1:D:47:VAL:HG21	1:D:109:GLU:HG3	1.97	0.46
1:F:92:ARG:O	1:F:96:ARG:HB2	2.15	0.46
1:C:14:ILE:HD13	1:C:229:LEU:HD21	1.98	0.46
1:C:177:ASN:CG	1:C:180:GLU:HG3	2.40	0.46
1:B:6:ARG:NH2	1:B:175:ASP:O	2.49	0.46
1:C:146:LYS:C	1:C:148:GLY:H	2.23	0.46
1:A:2:ARG:HD2	1:A:180:GLU:OE2	2.16	0.46
1:C:43:VAL:HG11	1:C:144:LEU:HD21	1.98	0.46
1:D:43:VAL:HG11	1:D:144:LEU:HD21	1.97	0.46
1:E:4:ASP:HB3	1:E:6:ARG:HG2	1.97	0.46
1:A:47:VAL:CG1	1:A:51:LEU:HB2	2.43	0.46
1:B:43:VAL:HG11	1:B:144:LEU:HD21	1.97	0.46
1:C:4:ASP:HB3	1:C:6:ARG:HG2	1.97	0.46
1:E:188:MET:HG3	1:E:202:GLN:C	2.41	0.45
1:A:43:VAL:HG11	1:A:144:LEU:HD21	1.99	0.45
1:E:6:ARG:NH2	1:E:175:ASP:O	2.49	0.45
1:A:204:THR:HG21	1:B:96:ARG:CD	2.47	0.45
1:C:177:ASN:OD1	1:C:180:GLU:HG3	2.16	0.45
1:F:87:THR:O	1:F:91:GLN:HB2	2.16	0.45
1:C:51:LEU:HD21	1:C:56:LYS:HG3	1.99	0.45
1:E:215:LEU:HD21	1:F:219:LEU:HD11	1.98	0.45
1:A:20:PHE:HZ	1:F:20:PHE:HZ	1.64	0.45
1:D:15:THR:OG1	1:D:31:THR:HB	2.16	0.45
1:D:87:THR:O	1:D:91:GLN:HB2	2.17	0.45
1:F:47:VAL:CG1	1:F:51:LEU:HB2	2.44	0.45
1:A:177:ASN:ND2	1:A:180:GLU:HG3	2.32	0.45
1:B:190:VAL:HG12	1:B:191:ILE:N	2.32	0.45
1:D:117:ASP:OD1	1:E:117:ASP:OD1	2.35	0.45
1:E:9:ASP:OD1	1:E:224:LYS:HE3	2.16	0.45
1:B:162:ILE:HG13	1:B:163:SER:H	1.81	0.44
1:A:2:ARG:NH1	1:A:180:GLU:OE1	2.50	0.44
1:E:192:MET:HE1	1:E:223:GLU:HG3	2.00	0.44
1:A:2:ARG:HH12	1:A:6:ARG:HH22	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:43:VAL:HG11	1:F:144:LEU:HD21	1.99	0.44
1:A:51:LEU:HD21	1:A:56:LYS:HG3	1.99	0.44
1:C:15:THR:OG1	1:C:31:THR:HB	2.18	0.44
1:E:87:THR:O	1:E:91:GLN:HB2	2.17	0.44
1:A:188:MET:HG3	1:A:202:GLN:C	2.42	0.44
1:C:87:THR:O	1:C:91:GLN:HB2	2.17	0.44
1:F:126:ARG:HG2	2:F:311:SO4:O4	2.18	0.44
1:B:1:MET:HG3	1:B:2:ARG:N	2.28	0.43
1:B:87:THR:O	1:B:91:GLN:HB2	2.17	0.43
1:C:194:GLY:HA2	1:C:230:ILE:HD13	2.00	0.43
1:D:84:SER:HA	1:D:87:THR:HB	2.00	0.43
1:F:1:MET:HG3	1:F:2:ARG:N	2.28	0.43
1:A:204:THR:CG2	1:B:96:ARG:HD2	2.48	0.43
1:F:15:THR:OG1	1:F:31:THR:HB	2.18	0.43
1:E:15:THR:OG1	1:E:31:THR:HB	2.18	0.43
1:F:179:GLU:HG3	1:F:180:GLU:N	2.33	0.43
1:B:188:MET:HG3	1:B:202:GLN:C	2.42	0.43
1:C:6:ARG:NH2	1:C:175:ASP:O	2.50	0.43
1:A:204:THR:HG23	1:B:200:GLU:OE2	2.17	0.43
1:C:177:ASN:ND2	1:C:180:GLU:HG3	2.33	0.43
1:C:190:VAL:HG12	1:C:191:ILE:N	2.34	0.43
1:D:190:VAL:HG12	1:D:191:ILE:N	2.33	0.43
1:A:2:ARG:CD	1:A:180:GLU:OE2	2.67	0.43
1:B:47:VAL:CG1	1:B:51:LEU:HB2	2.44	0.43
1:B:185:GLU:HB2	1:B:208:ALA:HB3	2.01	0.43
1:D:185:GLU:HB2	1:D:208:ALA:HB3	2.01	0.43
1:E:56:LYS:CE	1:E:104:LEU:HD12	2.49	0.43
1:F:194:GLY:HA2	1:F:230:ILE:HD13	2.01	0.43
1:A:149:THR:HG23	1:A:150:ILE:HG23	2.01	0.42
1:A:190:VAL:HG12	1:A:191:ILE:N	2.34	0.42
1:C:84:SER:HA	1:C:87:THR:HB	2.01	0.42
1:E:190:VAL:HG12	1:E:191:ILE:N	2.33	0.42
1:A:177:ASN:CG	1:A:180:GLU:HG3	2.44	0.42
1:A:15:THR:OG1	1:A:31:THR:HB	2.19	0.42
1:B:134:PHE:CZ	1:B:158:PHE:HA	2.55	0.42
1:D:126:ARG:HG2	2:D:307:SO4:O4	2.19	0.42
1:A:1:MET:HG3	1:A:2:ARG:N	2.31	0.42
1:A:84:SER:HA	1:A:87:THR:HB	2.01	0.42
1:A:194:GLY:HA2	1:A:230:ILE:HD13	2.01	0.42
1:C:179:GLU:HG3	1:C:180:GLU:N	2.35	0.42
1:D:6:ARG:NH2	1:D:175:ASP:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:233:GLN:O	1:D:237:LEU:HB2	2.20	0.42
1:F:51:LEU:HD21	1:F:56:LYS:HG3	2.01	0.42
1:B:15:THR:OG1	1:B:31:THR:HB	2.20	0.42
1:D:51:LEU:HD21	1:D:56:LYS:HG3	2.00	0.42
1:B:84:SER:HA	1:B:87:THR:HB	2.02	0.42
1:D:153:ASN:HA	1:D:154:PRO:HD3	1.88	0.42
1:E:51:LEU:HD21	1:E:56:LYS:HG3	2.01	0.42
1:E:126:ARG:HG2	2:E:309:SO4:O4	2.19	0.42
1:E:194:GLY:HA2	1:E:230:ILE:HD13	2.01	0.42
1:B:51:LEU:HD21	1:B:56:LYS:HG3	2.01	0.41
1:B:194:GLY:HA2	1:B:230:ILE:HD13	2.01	0.41
1:C:185:GLU:HB2	1:C:208:ALA:HB3	2.02	0.41
1:F:172:ILE:HG22	1:F:221:LEU:CD1	2.48	0.41
1:F:233:GLN:O	1:F:237:LEU:HB2	2.21	0.41
1:A:51:LEU:HD22	1:A:56:LYS:O	2.20	0.41
1:B:233:GLN:O	1:B:237:LEU:HB2	2.21	0.41
1:E:84:SER:HA	1:E:87:THR:HB	2.03	0.41
1:E:185:GLU:HB2	1:E:208:ALA:HB3	2.02	0.41
1:E:149:THR:HG23	1:E:150:ILE:HG23	2.02	0.41
1:E:192:MET:HG2	1:E:198:PHE:HA	2.02	0.41
1:A:233:GLN:O	1:A:237:LEU:HB2	2.21	0.41
1:C:188:MET:HG3	1:C:202:GLN:C	2.46	0.41
1:C:149:THR:HG23	1:C:150:ILE:HG23	2.02	0.41
1:C:233:GLN:O	1:C:237:LEU:HB2	2.21	0.41
1:E:47:VAL:CG1	1:E:51:LEU:HB2	2.45	0.41
1:A:134:PHE:CZ	1:A:158:PHE:HA	2.55	0.41
1:A:177:ASN:OD1	1:A:180:GLU:HG3	2.21	0.41
1:A:192:MET:HG2	1:A:198:PHE:HA	2.02	0.41
1:D:56:LYS:CE	1:D:104:LEU:HD12	2.51	0.41
1:D:194:GLY:HA2	1:D:230:ILE:HD13	2.01	0.41
1:E:198:PHE:O	1:F:209:THR:HB	2.21	0.41
1:F:51:LEU:HD22	1:F:56:LYS:O	2.21	0.41
1:F:56:LYS:CE	1:F:104:LEU:HD12	2.50	0.41
1:B:34:ASN:HB2	1:B:122:ASP:OD2	2.21	0.41
1:E:233:GLN:O	1:E:237:LEU:HB2	2.22	0.40
1:A:179:GLU:HG3	1:A:180:GLU:N	2.36	0.40
1:E:177:ASN:ND2	1:E:180:GLU:HG3	2.36	0.40
1:C:47:VAL:CG1	1:C:51:LEU:HB2	2.44	0.40
1:C:134:PHE:CZ	1:C:158:PHE:HA	2.56	0.40
1:A:212:ARG:HB2	1:B:198:PHE:HE1	1.85	0.40
1:F:14:ILE:HA	1:F:31:THR:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:LEU:HD23	1:C:221:LEU:HA	1.88	0.40
1:D:134:PHE:CZ	1:D:158:PHE:HA	2.57	0.40
1:F:84:SER:HA	1:F:87:THR:HB	2.03	0.40

There are no symmetry-related clashes.

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	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	24	43
1	B	222/245 (91%)	200 (90%)	21 (10%)	1 (0%)	24	43
1	C	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	24	43
1	D	222/245 (91%)	200 (90%)	21 (10%)	1 (0%)	24	43
1	E	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	24	43
1	F	222/245 (91%)	199 (90%)	22 (10%)	1 (0%)	24	43
All	All	1332/1470 (91%)	1196 (90%)	130 (10%)	6 (0%)	24	43

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	THR
1	B	152	THR
1	C	152	THR
1	D	152	THR
1	E	152	THR
1	F	152	THR

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	184/201 (92%)	176 (96%)	8 (4%)	26	47
1	B	184/201 (92%)	176 (96%)	8 (4%)	26	47
1	C	184/201 (92%)	176 (96%)	8 (4%)	26	47
1	D	184/201 (92%)	176 (96%)	8 (4%)	26	47
1	E	184/201 (92%)	176 (96%)	8 (4%)	26	47
1	F	184/201 (92%)	176 (96%)	8 (4%)	26	47
All	All	1104/1206 (92%)	1056 (96%)	48 (4%)	26	47

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	6	ARG
1	A	22	SER
1	A	88	MET
1	A	93	LEU
1	A	179	GLU
1	A	182	SER
1	A	213	GLU
1	B	4	ASP
1	B	6	ARG
1	B	22	SER
1	B	88	MET
1	B	93	LEU
1	B	179	GLU
1	B	182	SER
1	B	213	GLU
1	C	4	ASP
1	C	6	ARG
1	C	22	SER
1	C	88	MET
1	C	93	LEU
1	C	179	GLU

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Mol	Chain	Res	Type
1	C	182	SER
1	C	213	GLU
1	D	4	ASP
1	D	6	ARG
1	D	22	SER
1	D	88	MET
1	D	93	LEU
1	D	179	GLU
1	D	182	SER
1	D	213	GLU
1	E	4	ASP
1	E	6	ARG
1	E	22	SER
1	E	88	MET
1	E	93	LEU
1	E	179	GLU
1	E	182	SER
1	E	213	GLU
1	F	4	ASP
1	F	6	ARG
1	F	22	SER
1	F	88	MET
1	F	93	LEU
1	F	179	GLU
1	F	182	SER
1	F	213	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	170	GLN
1	B	7	GLN
1	B	170	GLN
1	C	7	GLN
1	C	40	ASN
1	C	170	GLN
1	D	7	GLN
1	D	153	ASN
1	D	170	GLN
1	E	7	GLN
1	E	40	ASN

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Mol	Chain	Res	Type
1	E	170	GLN
1	F	153	ASN
1	F	170	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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	$\# Z > 2$
2	SO4	A	302	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	D	308	-	4,4,4	0.36	0	6,6,6	0.08	0
2	SO4	C	306	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	E	309	-	4,4,4	0.36	0	6,6,6	0.07	0
2	SO4	E	310	-	4,4,4	0.36	0	6,6,6	0.08	0
2	SO4	D	307	-	4,4,4	0.36	0	6,6,6	0.07	0
2	SO4	F	312	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	B	304	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	F	311	-	4,4,4	0.36	0	6,6,6	0.07	0
2	SO4	A	301	-	4,4,4	0.37	0	6,6,6	0.07	0
2	SO4	B	303	-	4,4,4	0.36	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	C	305	-	4,4,4	0.37	0	6,6,6	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	309	SO4	1	0
2	D	307	SO4	1	0
2	F	311	SO4	1	0
2	B	303	SO4	1	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	226/245 (92%)	1.00	33 (14%) 6 5	13, 31, 55, 68	0
1	B	226/245 (92%)	1.20	49 (21%) 2 2	14, 32, 55, 67	0
1	C	226/245 (92%)	1.14	44 (19%) 3 2	14, 31, 56, 68	0
1	D	226/245 (92%)	0.97	33 (14%) 6 5	14, 31, 56, 67	0
1	E	226/245 (92%)	1.06	40 (17%) 4 3	14, 31, 57, 68	0
1	F	226/245 (92%)	1.05	42 (18%) 3 2	13, 31, 55, 68	0
All	All	1356/1470 (92%)	1.07	241 (17%) 4 3	13, 31, 57, 68	0

All (241) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	50	PHE	5.4
1	E	50	PHE	5.0
1	C	50	PHE	4.9
1	D	49	PRO	4.9
1	C	239	ASP	4.7
1	C	4	ASP	4.7
1	A	50	PHE	4.7
1	D	50	PHE	4.6
1	B	4	ASP	4.6
1	C	1	MET	4.6
1	E	66	LEU	4.5
1	F	50	PHE	4.5
1	C	151	LYS	4.5
1	B	48	PRO	4.5
1	E	243	GLU	4.5
1	F	171	GLY	4.5
1	E	3	HIS	4.4
1	C	170	GLN	4.4
1	A	243	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	22	SER	4.3
1	A	4	ASP	4.2
1	A	5	GLY	4.2
1	C	8	HIS	4.2
1	B	49	PRO	4.2
1	C	179	GLU	4.1
1	C	5	GLY	4.1
1	D	171	GLY	4.0
1	D	4	ASP	4.0
1	F	243	GLU	4.0
1	B	54	GLY	4.0
1	C	3	HIS	4.0
1	E	54	GLY	4.0
1	E	51	LEU	3.9
1	F	4	ASP	3.9
1	D	170	GLN	3.9
1	B	8	HIS	3.8
1	F	151	LYS	3.8
1	A	66	LEU	3.8
1	A	195	SER	3.8
1	A	239	ASP	3.7
1	D	151	LYS	3.7
1	B	105	GLU	3.7
1	F	207	GLU	3.7
1	E	65	MET	3.7
1	C	53	GLY	3.7
1	B	242	PRO	3.7
1	E	49	PRO	3.7
1	B	203	GLY	3.7
1	F	152	THR	3.6
1	C	146	LYS	3.6
1	E	48	PRO	3.6
1	C	171	GLY	3.6
1	A	213	GLU	3.6
1	A	109	GLU	3.6
1	B	51	LEU	3.6
1	A	151	LYS	3.5
1	B	151	LYS	3.5
1	E	4	ASP	3.5
1	E	169	GLU	3.4
1	D	1	MET	3.4
1	A	169	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	8	HIS	3.4
1	C	2	ARG	3.3
1	D	7	GLN	3.3
1	E	179	GLU	3.3
1	C	17	ASP	3.3
1	D	242	PRO	3.2
1	E	5	GLY	3.2
1	E	170	GLN	3.2
1	B	111	THR	3.2
1	F	1	MET	3.1
1	C	66	LEU	3.1
1	A	165	GLY	3.1
1	D	86	ARG	3.1
1	F	51	LEU	3.1
1	A	49	PRO	3.1
1	A	2	ARG	3.1
1	F	65	MET	3.1
1	C	7	GLN	3.1
1	B	53	GLY	3.1
1	F	5	GLY	3.1
1	B	66	LEU	3.0
1	D	179	GLU	3.0
1	C	169	GLU	3.0
1	F	48	PRO	3.0
1	F	49	PRO	3.0
1	D	3	HIS	3.0
1	F	8	HIS	3.0
1	B	5	GLY	3.0
1	A	167	ASP	3.0
1	B	204	THR	3.0
1	D	152	THR	3.0
1	C	51	LEU	2.9
1	E	182	SER	2.9
1	A	152	THR	2.9
1	E	56	LYS	2.9
1	D	5	GLY	2.9
1	C	243	GLU	2.9
1	E	207	GLU	2.9
1	D	150	ILE	2.9
1	E	53	GLY	2.9
1	A	51	LEU	2.9
1	B	179	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	200	GLU	2.9
1	F	169	GLU	2.9
1	C	52	ARG	2.9
1	B	46	ARG	2.8
1	B	238	GLY	2.8
1	C	167	ASP	2.8
1	F	66	LEU	2.8
1	C	45	ASP	2.8
1	A	52	ARG	2.8
1	E	52	ARG	2.8
1	F	84	SER	2.8
1	B	1	MET	2.8
1	C	206	GLU	2.8
1	E	1	MET	2.8
1	B	150	ILE	2.8
1	F	145	ILE	2.8
1	F	172	ILE	2.8
1	E	55	GLY	2.8
1	A	222	ALA	2.8
1	B	171	GLY	2.7
1	B	148	GLY	2.7
1	A	45	ASP	2.7
1	F	238	GLY	2.7
1	E	151	LYS	2.7
1	D	110	ARG	2.7
1	C	84	SER	2.7
1	B	55	GLY	2.6
1	D	48	PRO	2.6
1	A	205	GLY	2.6
1	D	53	GLY	2.6
1	F	57	GLY	2.6
1	E	242	PRO	2.6
1	E	152	THR	2.6
1	A	3	HIS	2.5
1	C	207	GLU	2.5
1	F	148	GLY	2.5
1	F	186	VAL	2.5
1	D	240	SER	2.5
1	D	51	LEU	2.5
1	B	3	HIS	2.5
1	C	238	GLY	2.5
1	D	231	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	235	GLU	2.5
1	C	240	SER	2.4
1	A	204	THR	2.4
1	C	172	ILE	2.4
1	A	235	GLU	2.4
1	C	9	ASP	2.4
1	D	169	GLU	2.4
1	F	10	GLU	2.4
1	D	55	GLY	2.4
1	E	84	SER	2.4
1	E	239	ASP	2.4
1	B	88	MET	2.4
1	A	6	ARG	2.4
1	F	147	ALA	2.4
1	B	216	ASN	2.3
1	D	105	GLU	2.3
1	E	109	GLU	2.3
1	B	207	GLU	2.3
1	C	64	SER	2.3
1	A	46	ARG	2.3
1	B	7	GLN	2.3
1	B	96	ARG	2.3
1	F	170	GLN	2.3
1	D	172	ILE	2.3
1	B	45	ASP	2.3
1	B	239	ASP	2.3
1	C	211	SER	2.3
1	B	209	THR	2.3
1	E	206	GLU	2.3
1	F	45	ASP	2.3
1	B	85	GLY	2.3
1	F	58	TRP	2.3
1	E	208	ALA	2.2
1	B	149	THR	2.2
1	F	185	GLU	2.2
1	F	242	PRO	2.2
1	F	47	VAL	2.2
1	B	56	LYS	2.2
1	B	152	THR	2.2
1	B	213	GLU	2.2
1	D	206	GLU	2.2
1	F	22	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	3	HIS	2.2
1	D	87	THR	2.2
1	D	109	GLU	2.2
1	F	204	THR	2.2
1	F	2	ARG	2.2
1	F	46	ARG	2.2
1	F	7	GLN	2.2
1	C	183	SER	2.2
1	A	65	MET	2.2
1	E	47	VAL	2.2
1	A	206	GLU	2.2
1	B	185	GLU	2.2
1	B	223	GLU	2.2
1	C	212	ARG	2.2
1	E	177	ASN	2.2
1	C	187	ASP	2.2
1	E	8	HIS	2.2
1	B	243	GLU	2.1
1	C	173	LEU	2.1
1	F	124	GLY	2.1
1	C	145	ILE	2.1
1	C	44	GLU	2.1
1	E	105	GLU	2.1
1	D	148	GLY	2.1
1	B	195	SER	2.1
1	B	212	ARG	2.1
1	D	6	ARG	2.1
1	E	13	PRO	2.1
1	A	148	GLY	2.1
1	C	23	HIS	2.1
1	F	108	GLY	2.1
1	A	59	ILE	2.1
1	A	200	GLU	2.1
1	B	146	LYS	2.1
1	A	48	PRO	2.1
1	E	88	MET	2.1
1	E	148	GLY	2.1
1	D	239	ASP	2.0
1	E	115	ASP	2.0
1	F	17	ASP	2.0
1	E	10	GLU	2.0
1	E	44	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	52	ARG	2.0
1	C	149	THR	2.0
1	B	52	ARG	2.0
1	C	110	ARG	2.0
1	B	84	SER	2.0
1	C	242	PRO	2.0
1	D	149	THR	2.0
1	E	7	GLN	2.0
1	C	150	ILE	2.0
1	F	55	GLY	2.0
1	A	212	ARG	2.0
1	C	86	ARG	2.0

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 oligosaccharides 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(Å ²)	Q<0.9
2	SO4	E	310	5/5	0.53	0.20	85,85,86,87	0
2	SO4	F	312	5/5	0.62	0.21	85,86,86,86	0
2	SO4	B	304	5/5	0.66	0.27	85,85,86,86	0
2	SO4	C	306	5/5	0.72	0.14	81,81,81,82	0
2	SO4	A	302	5/5	0.75	0.20	83,84,84,84	0
2	SO4	D	308	5/5	0.78	0.17	82,82,83,84	0
2	SO4	B	303	5/5	0.81	0.18	43,45,45,47	0
2	SO4	E	309	5/5	0.85	0.13	44,45,45,46	0
2	SO4	F	311	5/5	0.91	0.12	42,43,44,45	0
2	SO4	A	301	5/5	0.93	0.10	40,40,42,43	0
2	SO4	C	305	5/5	0.93	0.12	40,41,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	D	307	5/5	0.95	0.09	45,45,45,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.