



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:50 PM GMT

PDB ID : 4Z7Y  
Title : diphosphomevalonate decarboxylase from the *Sulfolobus solfataricus*, space group P21  
Authors : Hattori, A.; Unno, H.; Hemmi, H.  
Deposited on : 2015-04-08  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

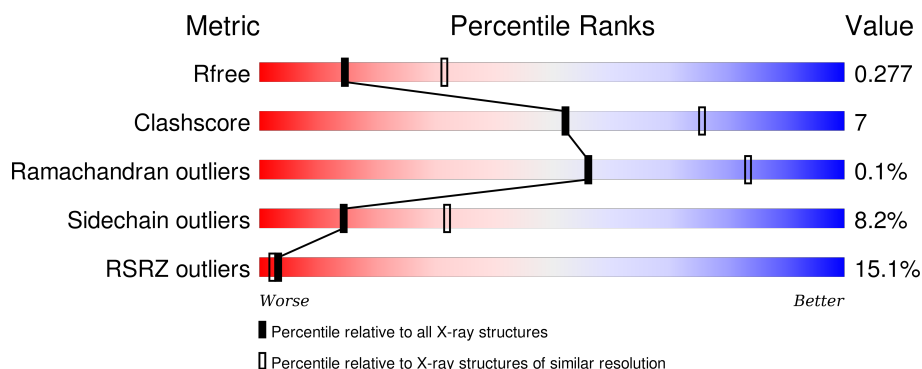
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	324	<div> <div>20%</div> <div>82%</div> <div>16%</div> <div>•</div> </div>
1	B	324	<div> <div>6%</div> <div>82%</div> <div>16%</div> <div>•</div> </div>
1	C	324	<div> <div>9%</div> <div>79%</div> <div>19%</div> <div>•</div> </div>
1	D	324	<div> <div>10%</div> <div>82%</div> <div>16%</div> <div>•</div> </div>
1	E	324	<div> <div>21%</div> <div>84%</div> <div>14%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	324	<div><div></div><div>25%</div><div></div><div>82%</div><div></div><div>15%</div><div></div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 15693 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 Diphosphomevalonate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			
1	B	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			
1	C	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			
1	D	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			
1	E	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			
1	F	324	Total	C	N	O	S	0	0	0
			2597	1654	442	490	11			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

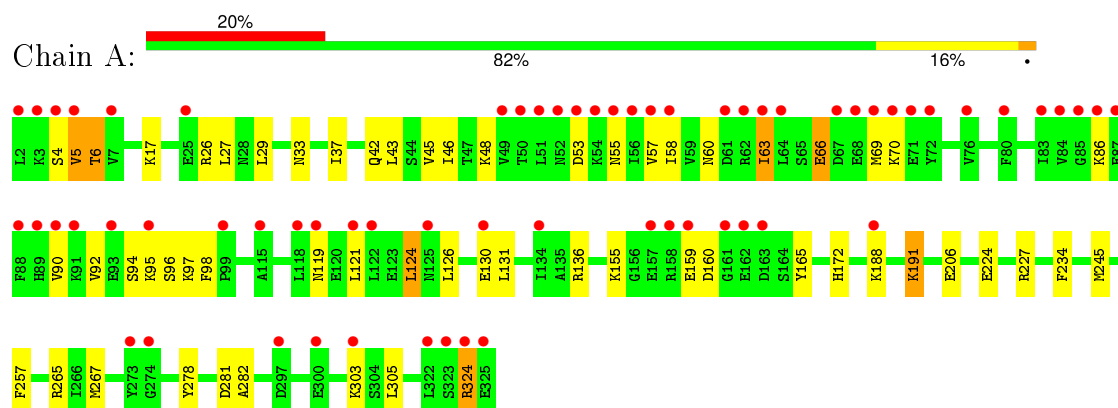
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	11	Total O 11 11	0	0
3	B	22	Total O 22 22	0	0
3	C	21	Total O 21 21	0	0
3	D	14	Total O 14 14	0	0
3	E	3	Total O 3 3	0	0
3	F	10	Total O 10 10	0	0

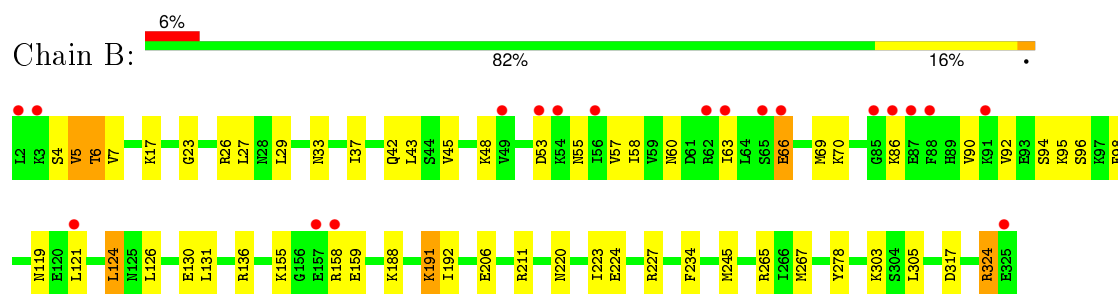
### 3 Residue-property plots [i](#)

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

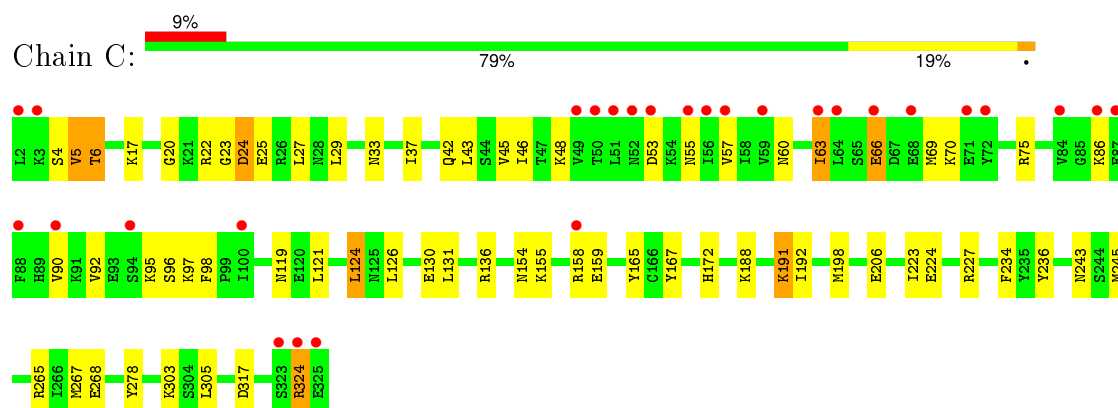
#### • Molecule 1: Diphosphomevalonate decarboxylase



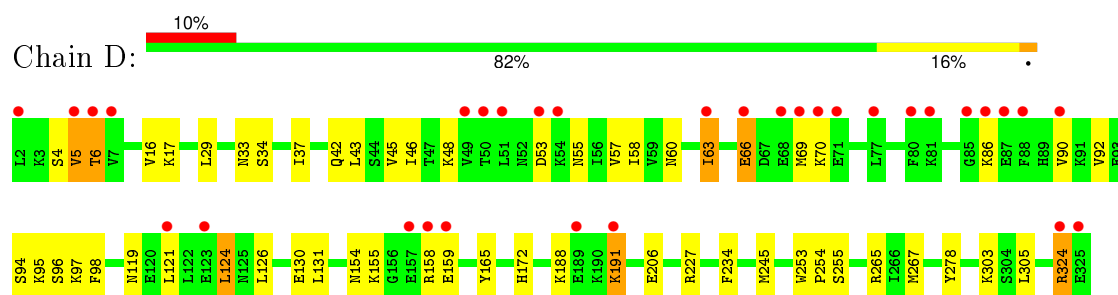
#### • Molecule 1: Diphosphomevalonate decarboxylase



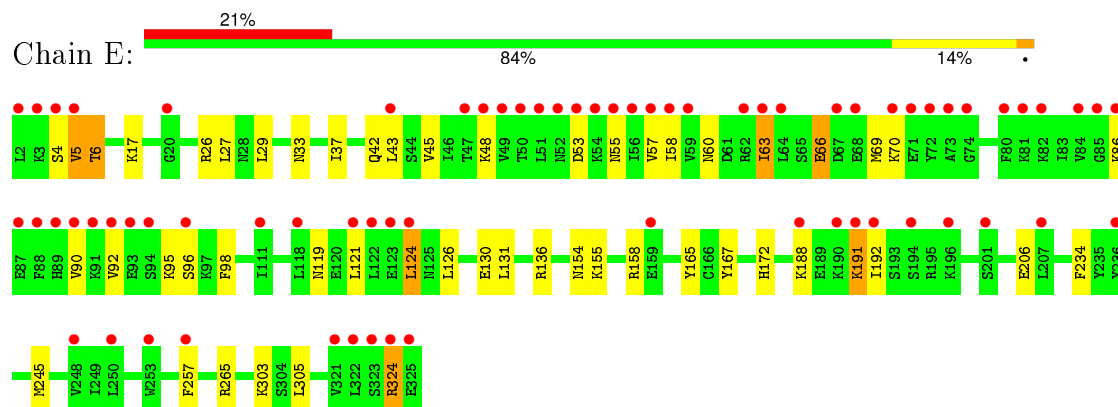
#### • Molecule 1: Diphosphomevalonate decarboxylase



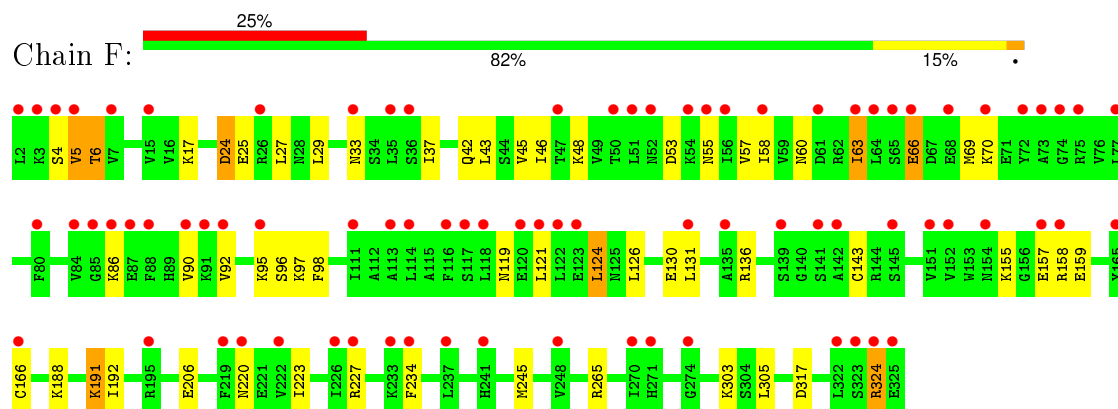
#### • Molecule 1: Diphosphomevalonate decarboxylase



- Molecule 1: Diphosphomevalonate decarboxylase



- Molecule 1: Diphosphomevalonate decarboxylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.90Å 154.39Å 109.97Å 90.00° 114.41° 90.00°	Depositor
Resolution (Å)	47.63 – 2.70 47.63 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.63-2.70) 99.0 (47.63-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.34 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, $R_{free}$	0.254 , 0.277 0.254 , 0.277	Depositor DCC
$R_{free}$ test set	3879 reflections (5.22%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.0	EDS
Estimated twinning fraction	0.001 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 78250 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	15693	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.03 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 3.4226e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.51	0/2645	0.75	0/3558
1	B	0.55	0/2645	0.78	2/3558 (0.1%)
1	C	0.56	0/2645	0.78	1/3558 (0.0%)
1	D	0.52	0/2645	0.76	0/3558
1	E	0.54	0/2645	0.77	0/3558
1	F	0.54	0/2645	0.76	0/3558
All	All	0.54	0/15870	0.77	3/21348 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211	ARG	NE-CZ-NH1	-5.84	117.38	120.30
1	B	317	ASP	CB-CA-C	-5.19	100.01	110.40
1	C	317	ASP	CB-CA-C	-5.07	100.25	110.40

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	2597	0	2622	32	0
1	B	2597	0	2622	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2597	0	2622	74	0
1	D	2597	0	2622	33	0
1	E	2597	0	2622	28	0
1	F	2597	0	2622	46	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	1	0
2	E	5	0	0	1	0
2	F	5	0	0	1	0
3	A	11	0	0	0	0
3	B	22	0	0	1	0
3	C	21	0	0	2	0
3	D	14	0	0	0	0
3	E	3	0	0	0	0
3	F	10	0	0	1	0
All	All	15693	0	15732	209	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 7.

All (209) 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:227:ARG:CZ	1:C:24:ASP:HA	1.42	1.47
1:C:227:ARG:CZ	1:F:24:ASP:HA	1.58	1.30
1:C:227:ARG:NH2	1:F:24:ASP:HA	1.57	1.19
1:B:227:ARG:NH2	1:C:24:ASP:HA	1.63	1.14
1:B:227:ARG:NH2	1:C:24:ASP:CA	2.12	1.11
1:B:227:ARG:CZ	1:C:24:ASP:CA	2.29	1.09
1:C:227:ARG:NH2	1:F:24:ASP:CA	2.17	1.07
1:B:227:ARG:NH1	1:C:24:ASP:HA	1.68	1.07
1:B:227:ARG:NH2	1:C:24:ASP:CB	2.27	0.97
1:A:165:TYR:OH	1:E:158:ARG:NH1	2.05	0.90
1:C:227:ARG:CZ	1:F:24:ASP:CA	2.49	0.87
1:B:159:GLU:HG3	1:F:223:ILE:HD12	1.58	0.86
1:B:227:ARG:NE	1:C:24:ASP:OD1	2.08	0.86
1:C:33:ASN:ND2	1:C:155:LYS:H	1.75	0.85
1:A:33:ASN:ND2	1:A:155:LYS:H	1.76	0.83
1:B:227:ARG:HE	1:C:24:ASP:CG	1.81	0.83
1:F:33:ASN:HD22	1:F:155:LYS:H	1.27	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ASN:HD22	1:C:155:LYS:H	1.25	0.82
1:B:33:ASN:HD22	1:B:155:LYS:H	1.25	0.82
1:B:227:ARG:NE	1:C:24:ASP:CG	2.33	0.82
1:C:75:ARG:NH1	3:C:502:HOH:O	2.07	0.81
1:B:33:ASN:ND2	1:B:155:LYS:H	1.79	0.81
1:A:33:ASN:HD22	1:A:155:LYS:H	1.24	0.81
1:F:33:ASN:ND2	1:F:155:LYS:H	1.78	0.81
1:F:227:ARG:NH2	3:F:501:HOH:O	2.14	0.81
1:E:33:ASN:HD22	1:E:155:LYS:H	1.26	0.81
1:E:33:ASN:ND2	1:E:155:LYS:H	1.80	0.79
1:D:33:ASN:HD22	1:D:155:LYS:H	1.30	0.78
1:C:227:ARG:NH2	1:F:24:ASP:CB	2.47	0.77
1:D:33:ASN:ND2	1:D:155:LYS:H	1.82	0.77
1:D:159:GLU:HB2	1:E:167:TYR:OH	1.86	0.74
1:C:227:ARG:NH1	1:F:24:ASP:HA	2.02	0.73
1:D:158:ARG:HD3	1:E:165:TYR:OH	1.89	0.72
1:B:223:ILE:HG22	1:B:227:ARG:HH22	1.52	0.72
1:A:26:ARG:NH2	1:D:227:ARG:HH21	1.90	0.70
1:B:26:ARG:HH22	1:F:227:ARG:HD3	1.56	0.69
1:B:227:ARG:HH21	1:C:24:ASP:CB	2.05	0.68
1:A:159:GLU:H	1:D:154:ASN:HD21	1.43	0.66
1:D:17:LYS:HG2	1:D:245:MET:SD	2.37	0.65
1:B:227:ARG:NH2	1:C:24:ASP:HB2	2.09	0.64
1:B:223:ILE:HG22	1:B:227:ARG:NH2	2.12	0.64
1:C:154:ASN:ND2	1:F:157:GLU:OE1	2.31	0.64
1:A:17:LYS:HG2	1:A:245:MET:SD	2.38	0.63
1:C:223:ILE:HG22	1:C:227:ARG:HH22	1.62	0.63
1:C:227:ARG:HE	1:F:24:ASP:CG	2.03	0.61
1:B:224:GLU:OE2	1:B:227:ARG:NH1	2.34	0.60
1:B:224:GLU:OE2	1:C:25:GLU:HG3	2.02	0.59
1:B:23:GLY:HA2	1:F:220:ASN:HD22	1.68	0.59
1:C:223:ILE:HG22	1:C:227:ARG:NH2	2.18	0.59
1:C:227:ARG:HH21	1:F:24:ASP:CB	2.14	0.59
1:B:224:GLU:CD	1:C:25:GLU:HG3	2.23	0.59
1:B:227:ARG:CZ	1:C:24:ASP:CG	2.72	0.58
1:E:42:GLN:HA	1:E:98:PHE:CD1	2.39	0.58
1:C:165:TYR:OH	1:F:158:ARG:NE	2.37	0.58
1:C:268:GLU:OE2	1:D:191:LYS:NZ	2.37	0.57
1:D:57:VAL:HG12	1:D:69:MET:HG3	1.87	0.56
1:F:42:GLN:HA	1:F:98:PHE:CD1	2.40	0.55
1:A:165:TYR:CZ	1:E:158:ARG:NH1	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:GLN:HA	1:B:98:PHE:CD1	2.42	0.55
1:B:227:ARG:NH2	1:C:24:ASP:CG	2.60	0.55
1:B:159:GLU:HG3	1:F:223:ILE:CD1	2.33	0.55
1:F:119:ASN:HB2	1:F:131:LEU:HD21	1.89	0.54
1:E:57:VAL:HG12	1:E:69:MET:HG3	1.89	0.54
1:F:143:CYS:HG	1:F:166:CYS:HG	1.54	0.54
1:B:159:GLU:OE1	1:F:220:ASN:CB	2.55	0.54
1:C:227:ARG:NE	1:F:24:ASP:CG	2.61	0.54
1:D:42:GLN:HA	1:D:98:PHE:CD1	2.43	0.54
1:A:6:THR:HG22	1:A:48:LYS:HG3	1.89	0.54
1:B:227:ARG:CB	1:B:227:ARG:CZ	2.86	0.53
1:C:227:ARG:NE	1:F:24:ASP:OD1	2.41	0.53
1:C:158:ARG:NH1	3:C:501:HOH:O	1.97	0.53
1:B:158:ARG:HD3	3:B:501:HOH:O	2.07	0.53
1:C:42:GLN:HA	1:C:98:PHE:CD1	2.44	0.53
1:B:60:ASN:HD21	1:B:96:SER:H	1.58	0.52
1:F:57:VAL:HG12	1:F:69:MET:HG3	1.92	0.52
1:D:55:ASN:ND2	1:D:90:VAL:H	2.07	0.52
1:B:227:ARG:HH21	1:C:24:ASP:HB2	1.70	0.52
1:C:57:VAL:HG12	1:C:69:MET:HG3	1.91	0.52
1:D:60:ASN:HD21	1:D:96:SER:H	1.58	0.52
1:D:66:GLU:O	1:D:66:GLU:HG2	2.08	0.51
1:D:6:THR:HG22	1:D:48:LYS:HG3	1.92	0.51
1:F:6:THR:HG22	1:F:48:LYS:HG3	1.90	0.51
1:B:223:ILE:HD11	1:C:159:GLU:HG3	1.92	0.51
1:A:57:VAL:HG12	1:A:69:MET:HG3	1.91	0.51
1:C:66:GLU:HG2	1:C:66:GLU:O	2.11	0.51
1:C:17:LYS:HG2	1:C:245:MET:SD	2.50	0.51
1:E:6:THR:HG22	1:E:48:LYS:HG3	1.91	0.51
1:E:191:LYS:HZ1	1:E:257:PHE:H	1.59	0.51
1:A:165:TYR:CE2	1:E:158:ARG:NH1	2.79	0.51
1:B:66:GLU:O	1:B:66:GLU:HG2	2.11	0.51
1:B:55:ASN:ND2	1:B:90:VAL:H	2.09	0.50
1:B:57:VAL:HG12	1:B:69:MET:HG3	1.92	0.50
1:C:55:ASN:ND2	1:C:90:VAL:H	2.08	0.50
1:B:159:GLU:CG	1:F:223:ILE:HD12	2.38	0.50
1:C:20:GLY:H	1:C:198:MET:HG2	1.77	0.50
1:C:224:GLU:OE2	1:C:227:ARG:NH1	2.44	0.50
1:C:224:GLU:OE2	1:F:25:GLU:HG3	2.10	0.50
1:A:42:GLN:HA	1:A:98:PHE:CD1	2.46	0.50
1:A:55:ASN:ND2	1:A:90:VAL:H	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:ARG:HB2	1:B:227:ARG:CZ	2.40	0.50
1:F:55:ASN:ND2	1:F:90:VAL:H	2.09	0.50
1:C:172:HIS:HB3	2:C:401:SO4:O3	2.12	0.49
1:B:17:LYS:HG2	1:B:245:MET:SD	2.52	0.49
1:F:66:GLU:O	1:F:66:GLU:HG2	2.12	0.49
1:E:37:ILE:HD11	1:E:234:PHE:HZ	1.76	0.49
1:E:66:GLU:O	1:E:66:GLU:HG2	2.11	0.49
1:E:27:LEU:O	1:E:136:ARG:NH1	2.44	0.49
1:E:17:LYS:HG2	1:E:245:MET:SD	2.52	0.49
1:C:243:ASN:ND2	1:D:255:SER:HB2	2.27	0.49
1:A:66:GLU:HG2	1:A:66:GLU:O	2.11	0.49
1:F:60:ASN:HD21	1:F:96:SER:H	1.60	0.49
1:B:224:GLU:HA	1:B:227:ARG:NH1	2.28	0.49
1:E:60:ASN:HD21	1:E:96:SER:H	1.61	0.49
1:E:55:ASN:ND2	1:E:90:VAL:H	2.11	0.48
1:F:37:ILE:HD11	1:F:234:PHE:HZ	1.79	0.48
1:B:159:GLU:OE1	1:F:220:ASN:HB3	2.13	0.48
1:B:191:LYS:HD2	1:B:192:ILE:N	2.29	0.48
1:C:33:ASN:HD22	1:C:155:LYS:N	2.04	0.47
1:D:57:VAL:HG23	1:D:92:VAL:HB	1.96	0.47
1:B:6:THR:HG22	1:B:48:LYS:HG3	1.95	0.47
1:A:5:VAL:HG12	1:A:324:ARG:HB3	1.96	0.47
1:F:124:LEU:HB3	1:F:126:LEU:HG	1.96	0.47
1:C:60:ASN:HD21	1:C:96:SER:H	1.62	0.47
1:A:159:GLU:HG2	1:D:154:ASN:ND2	2.29	0.47
1:A:60:ASN:HD21	1:A:96:SER:H	1.61	0.47
1:C:46:ILE:HD11	1:C:97:LYS:HG3	1.96	0.47
1:A:119:ASN:HB2	1:A:131:LEU:HD21	1.95	0.47
1:F:17:LYS:HG2	1:F:245:MET:SD	2.55	0.47
1:A:172:HIS:ND1	2:A:401:SO4:O2	2.44	0.47
1:E:63:ILE:HG13	1:E:63:ILE:H	1.58	0.47
1:D:172:HIS:HB3	2:D:401:SO4:O1	2.14	0.47
1:B:227:ARG:CZ	1:C:24:ASP:CB	2.82	0.46
1:B:37:ILE:HD11	1:B:234:PHE:HZ	1.79	0.46
1:C:267:MET:HG2	1:C:278:TYR:CE1	2.50	0.46
1:D:37:ILE:HD11	1:D:234:PHE:HZ	1.81	0.46
1:B:223:ILE:CD1	1:C:159:GLU:HG3	2.46	0.46
1:C:227:ARG:CZ	1:C:227:ARG:CB	2.92	0.46
1:C:227:ARG:NH2	1:F:24:ASP:HB2	2.30	0.46
1:B:159:GLU:CD	1:F:220:ASN:HB3	2.34	0.46
1:A:267:MET:HG2	1:A:278:TYR:CE1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:VAL:HG23	1:C:92:VAL:HB	1.97	0.46
1:B:220:ASN:HB2	1:C:23:GLY:H	1.80	0.46
1:A:124:LEU:HB3	1:A:126:LEU:HG	1.98	0.46
1:F:317:ASP:HA	2:F:401:SO4:O4	2.16	0.46
1:B:119:ASN:HB2	1:B:131:LEU:HD21	1.96	0.46
1:A:227:ARG:NH2	1:E:26:ARG:HH22	2.14	0.46
1:C:124:LEU:HB3	1:C:126:LEU:HG	1.97	0.46
1:C:119:ASN:HB2	1:C:131:LEU:HD21	1.98	0.46
1:B:224:GLU:HG2	1:C:23:GLY:O	2.16	0.46
1:A:160:ASP:OD2	1:D:165:TYR:OH	2.34	0.46
1:B:227:ARG:HH21	1:C:24:ASP:CG	2.18	0.45
1:F:57:VAL:HG23	1:F:92:VAL:HB	1.97	0.45
1:C:27:LEU:O	1:C:136:ARG:NH1	2.43	0.45
1:D:46:ILE:HD11	1:D:97:LYS:HG3	1.98	0.45
1:C:6:THR:HG22	1:C:48:LYS:HG3	1.98	0.45
1:A:27:LEU:O	1:A:136:ARG:NH1	2.45	0.45
1:F:5:VAL:HG12	1:F:324:ARG:HB3	1.97	0.45
1:F:191:LYS:HD2	1:F:192:ILE:N	2.32	0.45
1:D:119:ASN:HB2	1:D:131:LEU:HD21	1.97	0.45
1:A:159:GLU:H	1:D:154:ASN:ND2	2.10	0.45
1:B:57:VAL:HG23	1:B:92:VAL:HB	1.99	0.45
1:C:227:ARG:HH21	1:F:24:ASP:HB2	1.79	0.45
1:B:159:GLU:OE1	1:F:220:ASN:HB2	2.15	0.45
1:E:5:VAL:HG12	1:E:324:ARG:HB3	1.98	0.45
1:F:63:ILE:H	1:F:63:ILE:HG13	1.58	0.45
1:B:124:LEU:HB3	1:B:126:LEU:HG	1.99	0.45
1:A:191:LYS:HZ1	1:A:257:PHE:H	1.65	0.45
1:C:191:LYS:HD2	1:C:192:ILE:N	2.31	0.44
1:C:5:VAL:HG12	1:C:324:ARG:HB3	1.99	0.44
1:A:57:VAL:HG23	1:A:92:VAL:HB	1.99	0.44
1:A:37:ILE:HD11	1:A:234:PHE:HZ	1.83	0.44
1:E:57:VAL:HG23	1:E:92:VAL:HB	2.00	0.44
1:D:5:VAL:HG12	1:D:324:ARG:HB3	1.99	0.44
1:C:37:ILE:HD11	1:C:234:PHE:HZ	1.83	0.44
1:E:124:LEU:HB3	1:E:126:LEU:HG	1.98	0.44
1:C:167:TYR:OH	1:F:159:GLU:HG2	2.18	0.44
1:E:191:LYS:NZ	1:E:257:PHE:H	2.16	0.44
1:D:63:ILE:H	1:D:63:ILE:HG13	1.58	0.44
1:D:267:MET:HG2	1:D:278:TYR:CE1	2.53	0.44
1:E:119:ASN:HB2	1:E:131:LEU:HD21	2.00	0.43
1:E:172:HIS:HB3	2:E:401:SO4:O2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:TYR:HE1	1:D:253:TRP:CD1	2.36	0.43
1:B:33:ASN:HD22	1:B:155:LYS:N	2.05	0.43
1:B:55:ASN:HD22	1:B:55:ASN:HA	1.67	0.43
1:D:124:LEU:HB3	1:D:126:LEU:HG	2.01	0.43
1:C:63:ILE:H	1:C:63:ILE:HG13	1.59	0.42
1:D:55:ASN:HD22	1:D:55:ASN:HA	1.66	0.42
1:B:5:VAL:HG12	1:B:324:ARG:HB3	2.01	0.42
1:D:159:GLU:HG2	1:E:154:ASN:HD22	1.84	0.42
1:B:227:ARG:NH2	1:C:24:ASP:N	2.65	0.42
1:C:227:ARG:HB2	1:C:227:ARG:CZ	2.48	0.42
1:C:97:LYS:HD3	1:C:98:PHE:CE1	2.55	0.42
1:A:46:ILE:HD11	1:A:97:LYS:HG3	2.02	0.42
1:A:281:ASP:HB3	1:A:282:ALA:H	1.70	0.42
1:D:253:TRP:CD2	1:D:254:PRO:HA	2.54	0.42
1:F:27:LEU:O	1:F:136:ARG:NH1	2.45	0.42
1:A:63:ILE:H	1:A:63:ILE:HG13	1.56	0.42
1:B:267:MET:HG2	1:B:278:TYR:CE1	2.55	0.42
1:E:33:ASN:HD22	1:E:155:LYS:N	2.06	0.42
1:B:191:LYS:HD2	1:B:192:ILE:H	1.85	0.41
1:E:191:LYS:HD2	1:E:192:ILE:N	2.36	0.41
1:F:46:ILE:HD11	1:F:97:LYS:HG3	2.02	0.41
1:B:27:LEU:O	1:B:136:ARG:NH1	2.48	0.41
1:C:267:MET:HG2	1:C:278:TYR:CZ	2.56	0.41
1:A:191:LYS:NZ	1:A:257:PHE:H	2.18	0.41
1:A:224:GLU:OE2	1:A:227:ARG:NH1	2.54	0.41
1:C:22:ARG:NH2	1:C:155:LYS:O	2.53	0.40
1:D:97:LYS:HD3	1:D:98:PHE:CE1	2.56	0.40
1:D:16:VAL:O	1:D:34:SER:HB2	2.22	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	322/324 (99%)	314 (98%)	8 (2%)	0	100	100
1	B	322/324 (99%)	315 (98%)	7 (2%)	0	100	100
1	C	322/324 (99%)	314 (98%)	7 (2%)	1 (0%)	46	75
1	D	322/324 (99%)	315 (98%)	7 (2%)	0	100	100
1	E	322/324 (99%)	314 (98%)	8 (2%)	0	100	100
1	F	322/324 (99%)	314 (98%)	7 (2%)	1 (0%)	46	75
All	All	1932/1944 (99%)	1886 (98%)	44 (2%)	2 (0%)	56	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	24	ASP
1	F	24	ASP

### 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	288/288 (100%)	264 (92%)	24 (8%)	14	31
1	B	288/288 (100%)	263 (91%)	25 (9%)	13	29
1	C	288/288 (100%)	266 (92%)	22 (8%)	16	37
1	D	288/288 (100%)	264 (92%)	24 (8%)	14	31
1	E	288/288 (100%)	265 (92%)	23 (8%)	15	33
1	F	288/288 (100%)	265 (92%)	23 (8%)	15	33
All	All	1728/1728 (100%)	1587 (92%)	141 (8%)	14	32

All (141) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	5	VAL
1	A	6	THR

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Mol	Chain	Res	Type
1	A	29	LEU
1	A	43	LEU
1	A	45	VAL
1	A	53	ASP
1	A	58	ILE
1	A	63	ILE
1	A	66	GLU
1	A	70	LYS
1	A	86	LYS
1	A	94	SER
1	A	95	LYS
1	A	121	LEU
1	A	124	LEU
1	A	130	GLU
1	A	188	LYS
1	A	191	LYS
1	A	206	GLU
1	A	265	ARG
1	A	303	LYS
1	A	305	LEU
1	A	324	ARG
1	B	4	SER
1	B	5	VAL
1	B	6	THR
1	B	7	VAL
1	B	29	LEU
1	B	43	LEU
1	B	45	VAL
1	B	53	ASP
1	B	58	ILE
1	B	63	ILE
1	B	66	GLU
1	B	70	LYS
1	B	86	LYS
1	B	94	SER
1	B	95	LYS
1	B	121	LEU
1	B	124	LEU
1	B	130	GLU
1	B	188	LYS
1	B	191	LYS
1	B	206	GLU

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Mol	Chain	Res	Type
1	B	265	ARG
1	B	303	LYS
1	B	305	LEU
1	B	324	ARG
1	C	4	SER
1	C	5	VAL
1	C	6	THR
1	C	29	LEU
1	C	43	LEU
1	C	45	VAL
1	C	53	ASP
1	C	63	ILE
1	C	66	GLU
1	C	70	LYS
1	C	86	LYS
1	C	95	LYS
1	C	121	LEU
1	C	124	LEU
1	C	130	GLU
1	C	188	LYS
1	C	191	LYS
1	C	206	GLU
1	C	265	ARG
1	C	303	LYS
1	C	305	LEU
1	C	324	ARG
1	D	4	SER
1	D	5	VAL
1	D	6	THR
1	D	29	LEU
1	D	43	LEU
1	D	45	VAL
1	D	53	ASP
1	D	58	ILE
1	D	63	ILE
1	D	66	GLU
1	D	70	LYS
1	D	86	LYS
1	D	94	SER
1	D	95	LYS
1	D	121	LEU
1	D	124	LEU

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Mol	Chain	Res	Type
1	D	130	GLU
1	D	188	LYS
1	D	191	LYS
1	D	206	GLU
1	D	265	ARG
1	D	303	LYS
1	D	305	LEU
1	D	324	ARG
1	E	4	SER
1	E	5	VAL
1	E	6	THR
1	E	29	LEU
1	E	43	LEU
1	E	45	VAL
1	E	53	ASP
1	E	58	ILE
1	E	63	ILE
1	E	66	GLU
1	E	70	LYS
1	E	86	LYS
1	E	95	LYS
1	E	121	LEU
1	E	124	LEU
1	E	130	GLU
1	E	188	LYS
1	E	191	LYS
1	E	206	GLU
1	E	265	ARG
1	E	303	LYS
1	E	305	LEU
1	E	324	ARG
1	F	4	SER
1	F	5	VAL
1	F	6	THR
1	F	29	LEU
1	F	43	LEU
1	F	45	VAL
1	F	53	ASP
1	F	58	ILE
1	F	63	ILE
1	F	66	GLU
1	F	70	LYS

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Mol	Chain	Res	Type
1	F	86	LYS
1	F	95	LYS
1	F	121	LEU
1	F	124	LEU
1	F	130	GLU
1	F	188	LYS
1	F	191	LYS
1	F	206	GLU
1	F	265	ARG
1	F	303	LYS
1	F	305	LEU
1	F	324	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	33	ASN
1	A	55	ASN
1	A	60	ASN
1	A	246	HIS
1	B	28	ASN
1	B	33	ASN
1	B	55	ASN
1	B	60	ASN
1	C	28	ASN
1	C	33	ASN
1	C	55	ASN
1	C	60	ASN
1	C	246	HIS
1	D	28	ASN
1	D	33	ASN
1	D	55	ASN
1	D	60	ASN
1	D	154	ASN
1	E	28	ASN
1	E	33	ASN
1	E	55	ASN
1	E	60	ASN
1	E	154	ASN
1	F	28	ASN
1	F	33	ASN

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Mol	Chain	Res	Type
1	F	55	ASN
1	F	60	ASN
1	F	220	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

6 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	401	-	4,4,4	0.53	0	6,6,6	0.53	0
2	SO4	B	401	-	4,4,4	0.59	0	6,6,6	0.21	0
2	SO4	C	401	-	4,4,4	0.41	0	6,6,6	0.12	0
2	SO4	D	401	-	4,4,4	0.43	0	6,6,6	0.63	0
2	SO4	E	401	-	4,4,4	0.52	0	6,6,6	0.19	0
2	SO4	F	401	-	4,4,4	0.52	0	6,6,6	0.22	0

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
2	SO4	A	401	-	-	0/0/0/0	0/0/0/0
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
2	SO4	C	401	-	-	0/0/0/0	0/0/0/0
2	SO4	D	401	-	-	0/0/0/0	0/0/0/0
2	SO4	E	401	-	-	0/0/0/0	0/0/0/0
2	SO4	F	401	-	-	0/0/0/0	0/0/0/0

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.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	SO4	1	0
2	C	401	SO4	1	0
2	D	401	SO4	1	0
2	E	401	SO4	1	0
2	F	401	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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	324/324 (100%)	0.88	64 (19%) 1 1	20, 59, 134, 162	0
1	B	324/324 (100%)	0.35	19 (5%) 26 24	21, 44, 98, 151	0
1	C	324/324 (100%)	0.51	28 (8%) 13 10	20, 46, 102, 148	0
1	D	324/324 (100%)	0.51	32 (9%) 9 7	22, 50, 109, 137	0
1	E	324/324 (100%)	1.19	69 (21%) 1 1	33, 61, 133, 167	0
1	F	324/324 (100%)	1.37	81 (25%) 1 1	29, 64, 124, 177	0
All	All	1944/1944 (100%)	0.80	293 (15%) 3 2	20, 54, 120, 177	0

All (293) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	122	LEU	7.6
1	F	3	LYS	7.2
1	E	90	VAL	7.0
1	E	2	LEU	7.0
1	A	71	GLU	6.5
1	E	84	VAL	6.3
1	A	300	GLU	6.3
1	F	73	ALA	6.3
1	E	57	VAL	5.8
1	F	84	VAL	5.8
1	F	4	SER	5.8
1	F	135	ALA	5.8
1	F	2	LEU	5.7
1	E	4	SER	5.6
1	E	80	PHE	5.4
1	D	51	LEU	5.4
1	F	63	ILE	5.4
1	F	66	GLU	5.3
1	D	121	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
1	D	2	LEU	5.2
1	E	54	LYS	5.2
1	E	72	TYR	5.1
1	E	56	ILE	5.1
1	F	72	TYR	5.1
1	D	88	PHE	5.1
1	A	51	LEU	5.0
1	F	56	ILE	5.0
1	A	54	LYS	5.0
1	F	51	LEU	5.0
1	B	63	ILE	4.9
1	C	324	ARG	4.8
1	E	50	THR	4.7
1	F	325	GLU	4.5
1	E	64	LEU	4.5
1	E	3	LYS	4.5
1	E	325	GLU	4.5
1	A	86	LYS	4.5
1	F	80	PHE	4.5
1	F	118	LEU	4.5
1	A	56	ILE	4.4
1	E	51	LEU	4.4
1	F	74	GLY	4.4
1	A	88	PHE	4.4
1	E	74	GLY	4.4
1	F	114	LEU	4.3
1	F	77	LEU	4.2
1	F	222	VAL	4.1
1	F	88	PHE	4.1
1	A	87	GLU	4.1
1	F	50	THR	4.1
1	E	323	SER	4.0
1	A	85	GLY	4.0
1	C	57	VAL	4.0
1	E	89	HIS	3.9
1	E	71	GLU	3.9
1	F	47	THR	3.9
1	F	139	SER	3.9
1	E	85	GLY	3.9
1	F	85	GLY	3.9
1	E	92	VAL	3.9
1	B	121	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	F	121	LEU	3.8
1	A	3	LYS	3.8
1	F	52	ASN	3.8
1	E	62	ARG	3.7
1	D	68	GLU	3.7
1	F	220	ASN	3.7
1	F	227	ARG	3.7
1	E	324	ARG	3.7
1	E	5	VAL	3.6
1	C	86	LYS	3.6
1	E	190	LYS	3.6
1	F	91	LYS	3.5
1	A	89	HIS	3.5
1	E	49	VAL	3.5
1	C	51	LEU	3.5
1	A	303	LYS	3.5
1	E	63	ILE	3.5
1	E	88	PHE	3.5
1	A	72	TYR	3.4
1	E	68	GLU	3.4
1	C	2	LEU	3.4
1	F	70	LYS	3.4
1	F	87	GLU	3.4
1	E	191	LYS	3.4
1	E	58	ILE	3.3
1	F	157	GLU	3.3
1	D	53	ASP	3.3
1	B	88	PHE	3.3
1	A	2	LEU	3.3
1	D	324	ARG	3.3
1	D	63	ILE	3.3
1	E	55	ASN	3.2
1	F	65	SER	3.2
1	B	66	GLU	3.2
1	C	55	ASN	3.2
1	F	141	SER	3.2
1	A	50	THR	3.2
1	F	123	GLU	3.2
1	B	87	GLU	3.2
1	D	71	GLU	3.2
1	A	61	ASP	3.2
1	B	3	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	90	VAL	3.2
1	F	86	LYS	3.2
1	A	5	VAL	3.2
1	C	71	GLU	3.2
1	A	64	LEU	3.2
1	E	121	LEU	3.2
1	A	157	GLU	3.1
1	E	47	THR	3.1
1	A	323	SER	3.1
1	A	55	ASN	3.1
1	C	64	LEU	3.1
1	F	58	ILE	3.1
1	E	321	VAL	3.1
1	A	69	MET	3.1
1	E	207	LEU	3.1
1	E	159	GLU	3.1
1	C	84	VAL	3.1
1	F	92	VAL	3.0
1	C	87	GLU	3.0
1	E	70	LYS	3.0
1	D	50	THR	3.0
1	C	53	ASP	3.0
1	E	201	SER	3.0
1	D	86	LYS	3.0
1	B	2	LEU	3.0
1	A	63	ILE	3.0
1	F	95	LYS	3.0
1	A	53	ASP	2.9
1	B	54	LYS	2.9
1	A	324	ARG	2.9
1	C	59	VAL	2.9
1	D	81	LYS	2.9
1	F	68	GLU	2.9
1	A	80	PHE	2.9
1	C	325	GLU	2.9
1	B	53	ASP	2.9
1	F	113	ALA	2.8
1	A	68	GLU	2.8
1	A	188	LYS	2.8
1	E	82	LYS	2.8
1	A	122	LEU	2.8
1	D	77	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	163	ASP	2.8
1	D	70	LYS	2.8
1	E	67	ASP	2.8
1	F	142	ALA	2.8
1	D	66	GLU	2.8
1	C	90	VAL	2.8
1	E	59	VAL	2.8
1	F	36	SER	2.8
1	C	68	GLU	2.8
1	F	55	ASN	2.8
1	E	87	GLU	2.8
1	F	324	ARG	2.8
1	A	325	GLU	2.7
1	C	158	ARG	2.7
1	C	50	THR	2.7
1	A	57	VAL	2.7
1	D	157	GLU	2.7
1	B	325	GLU	2.7
1	E	123	GLU	2.7
1	F	274	GLY	2.7
1	A	297	ASP	2.7
1	F	151	VAL	2.7
1	D	87	GLU	2.7
1	C	88	PHE	2.7
1	A	162	GLU	2.6
1	A	62	ARG	2.6
1	F	271	HIS	2.6
1	E	48	LYS	2.6
1	E	194	SER	2.6
1	F	226	ILE	2.6
1	A	84	VAL	2.6
1	E	81	LYS	2.6
1	E	91	LYS	2.6
1	E	111	ILE	2.6
1	F	54	LYS	2.6
1	A	52	ASN	2.6
1	D	158	ARG	2.6
1	A	70	LYS	2.6
1	D	7	VAL	2.6
1	E	94	SER	2.6
1	A	95	LYS	2.5
1	F	237	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	117	SER	2.5
1	A	7	VAL	2.5
1	A	121	LEU	2.5
1	E	250	LEU	2.5
1	F	195	ARG	2.5
1	A	76	VAL	2.5
1	E	124	LEU	2.5
1	F	241	HIS	2.5
1	A	49	VAL	2.5
1	D	54	LYS	2.5
1	F	233	LYS	2.5
1	E	52	ASN	2.5
1	E	118	LEU	2.5
1	A	99	PRO	2.4
1	D	5	VAL	2.4
1	F	61	ASP	2.4
1	A	93	GLU	2.4
1	C	3	LYS	2.4
1	A	115	ALA	2.4
1	F	248	VAL	2.4
1	F	64	LEU	2.4
1	D	90	VAL	2.4
1	A	125	ASN	2.4
1	E	73	ALA	2.4
1	C	323	SER	2.4
1	D	6	THR	2.4
1	D	159	GLU	2.4
1	A	161	GLY	2.4
1	D	189	GLU	2.4
1	D	85	GLY	2.4
1	A	273	TYR	2.4
1	A	4	SER	2.4
1	E	122	LEU	2.4
1	E	20	GLY	2.4
1	F	33	ASN	2.4
1	F	5	VAL	2.4
1	A	83	ILE	2.3
1	C	63	ILE	2.3
1	B	91	LYS	2.3
1	E	53	ASP	2.3
1	E	86	LYS	2.3
1	D	49	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	91	LYS	2.3
1	F	35	LEU	2.3
1	F	158	ARG	2.3
1	F	323	SER	2.3
1	D	80	PHE	2.3
1	F	152	VAL	2.3
1	E	43	LEU	2.3
1	E	96	SER	2.3
1	E	192	ILE	2.3
1	E	196	LYS	2.3
1	C	94	SER	2.2
1	A	58	ILE	2.2
1	A	134	ILE	2.2
1	A	274	GLY	2.2
1	F	15	VAL	2.2
1	F	75	ARG	2.2
1	F	270	ILE	2.2
1	F	234	PHE	2.2
1	F	322	LEU	2.2
1	E	248	VAL	2.2
1	F	7	VAL	2.2
1	F	90	VAL	2.2
1	E	253	TRP	2.2
1	B	85	GLY	2.2
1	A	119	ASN	2.2
1	A	118	LEU	2.2
1	B	157	GLU	2.2
1	E	322	LEU	2.2
1	E	188	LYS	2.1
1	B	49	VAL	2.1
1	F	111	ILE	2.1
1	F	120	GLU	2.1
1	A	158	ARG	2.1
1	B	86	LYS	2.1
1	F	165	TYR	2.1
1	D	191	LYS	2.1
1	F	26	ARG	2.1
1	D	123	GLU	2.1
1	A	322	LEU	2.1
1	B	158	ARG	2.1
1	C	56	ILE	2.1
1	E	236	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	131	LEU	2.1
1	C	66	GLU	2.1
1	B	65	SER	2.1
1	C	100	ILE	2.1
1	A	25	GLU	2.1
1	F	154	ASN	2.1
1	A	67	ASP	2.1
1	C	72	TYR	2.0
1	A	130	GLU	2.0
1	A	159	GLU	2.0
1	E	257	PHE	2.0
1	F	219	PHE	2.0
1	C	49	VAL	2.0
1	B	56	ILE	2.0
1	D	325	GLU	2.0
1	C	52	ASN	2.0
1	F	145	SER	2.0
1	D	69	MET	2.0
1	F	116	PHE	2.0
1	B	62	ARG	2.0
1	F	166	CYS	2.0
1	E	93	GLU	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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	A	401	5/5	0.91	0.18	-0.73	50,51,64,66	0
2	SO4	C	401	5/5	0.95	0.17	-0.88	65,66,70,79	0
2	SO4	F	401	5/5	0.93	0.17	-1.33	54,65,67,69	0
2	SO4	D	401	5/5	0.97	0.11	-1.49	59,60,63,66	0
2	SO4	E	401	5/5	0.94	0.12	-1.92	67,67,72,77	0
2	SO4	B	401	5/5	0.96	0.10	-2.12	59,60,64,68	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.