



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2017 – 06:05 PM EDT

PDB ID : 3IP3  
Title : Structure of putative oxidoreductase (TM\_0425) from *Thermotoga maritima*  
Authors : Ramagopal, U.A.; Morano, C.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)  
Deposited on : unknown  
Resolution : 2.14 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

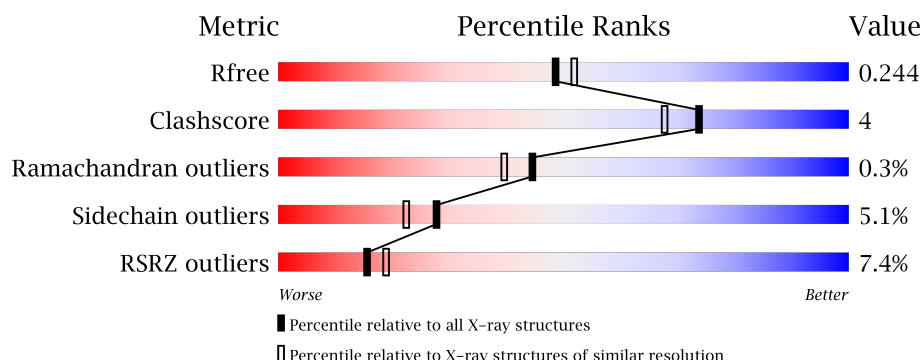
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 Å.

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






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1915 (2.16-2.12)
Clashscore	112137	2047 (2.16-2.12)
Ramachandran outliers	110173	2020 (2.16-2.12)
Sidechain outliers	110143	2019 (2.16-2.12)
RSRZ outliers	101464	1921 (2.16-2.12)

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	337	<div> <div>0.1%</div> <div>86%</div> <div>11%</div> <div>0.2%</div> </div>
1	B	337	<div> <div>0.1%</div> <div>91%</div> <div>7%</div> <div>0.2%</div> </div>
1	C	337	<div> <div>4%</div> <div>86%</div> <div>10%</div> <div>0.2%</div> </div>
1	D	337	<div> <div>0.1%</div> <div>88%</div> <div>9%</div> <div>0.2%</div> </div>
1	E	337	<div> <div>8%</div> <div>84%</div> <div>12%</div> <div>0.2%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	337	
1	G	337	
1	H	337	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	B	338	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21415 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 Oxidoreductase, putative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	Se	0	0	0
			2632	1686	453	484	4	5			
1	B	331	Total	C	N	O	S	Se	0	0	0
			2657	1700	459	489	4	5			
1	C	330	Total	C	N	O	S	Se	0	0	0
			2647	1694	456	488	4	5			
1	D	328	Total	C	N	O	S	Se	0	1	0
			2640	1691	454	486	4	5			
1	E	328	Total	C	N	O	S	Se	0	0	0
			2634	1687	454	484	4	5			
1	F	330	Total	C	N	O	S	Se	0	0	0
			2647	1694	456	488	4	5			
1	G	327	Total	C	N	O	S	Se	0	0	0
			2628	1684	453	482	4	5			
1	H	329	Total	C	N	O	S	Se	0	0	0
			2641	1691	455	486	4	5			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
A	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
A	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
A	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
A	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
A	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
A	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
A	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
A	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
A	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
B	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
B	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
B	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
B	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
C	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
C	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
C	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
C	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
C	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
D	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
D	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
D	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
D	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
D	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
E	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
E	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
E	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
E	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
E	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
F	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
F	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
F	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
F	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
F	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6

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Chain	Residue	Modelled	Actual	Comment	Reference
F	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
F	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
F	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
F	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
F	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
G	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
G	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
G	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
G	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
G	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	0	MSE	-	EXPRESSION TAG	UNP Q9WYQ6
H	1	SER	-	EXPRESSION TAG	UNP Q9WYQ6
H	329	GLU	-	EXPRESSION TAG	UNP Q9WYQ6
H	330	GLY	-	EXPRESSION TAG	UNP Q9WYQ6
H	331	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	332	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	333	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	334	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	335	HIS	-	EXPRESSION TAG	UNP Q9WYQ6
H	336	HIS	-	EXPRESSION TAG	UNP Q9WYQ6

- 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	B	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0
2	F	1	Total O S 5 4 1	0	0

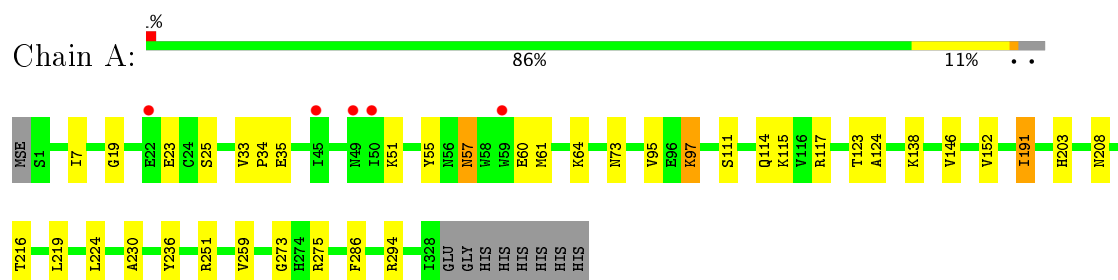
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	59	Total O 59 59	0	0
3	B	67	Total O 67 67	0	0
3	C	18	Total O 18 18	0	0
3	D	30	Total O 30 30	0	0
3	E	19	Total O 19 19	0	0
3	F	59	Total O 59 59	0	0
3	G	8	Total O 8 8	0	0
3	H	4	Total O 4 4	0	0

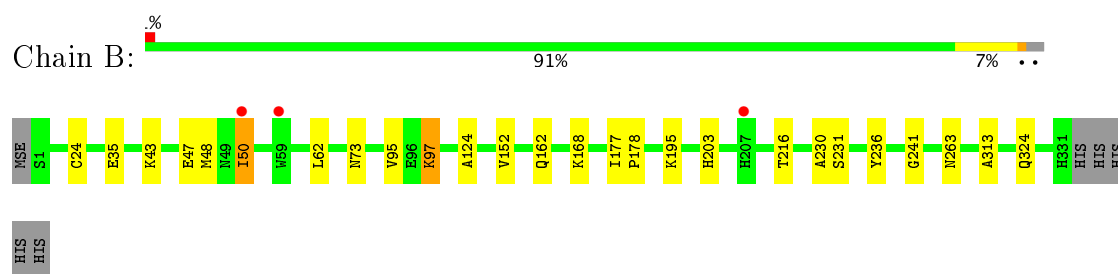
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

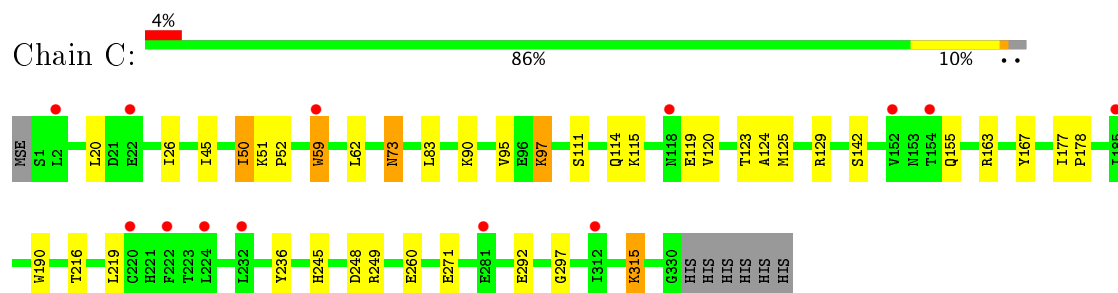
- Molecule 1: Oxidoreductase, putative



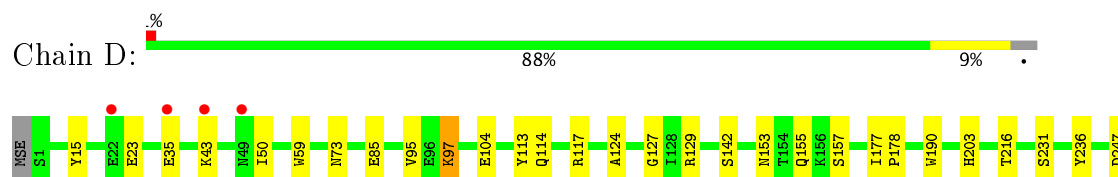
- Molecule 1: Oxidoreductase, putative



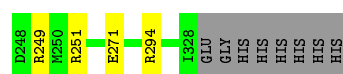
- Molecule 1: Oxidoreductase, putative



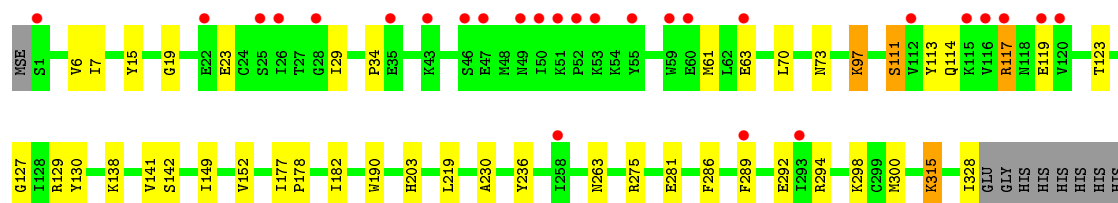
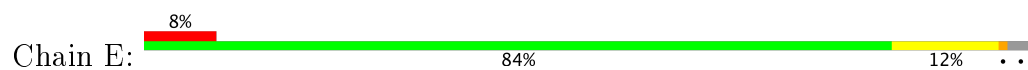
- Molecule 1: Oxidoreductase, putative



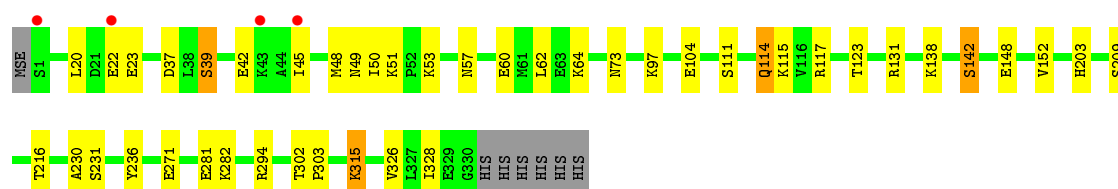
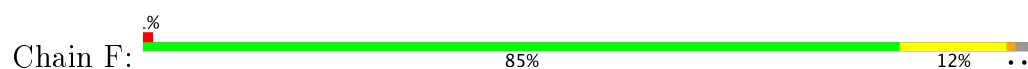




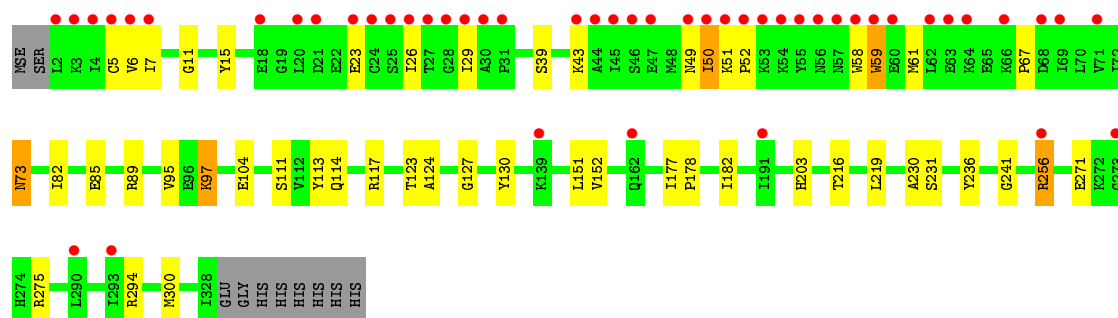
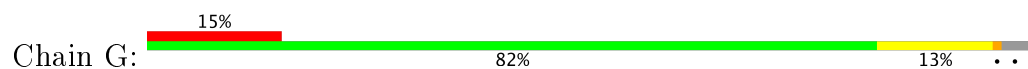
- Molecule 1: Oxidoreductase, putative



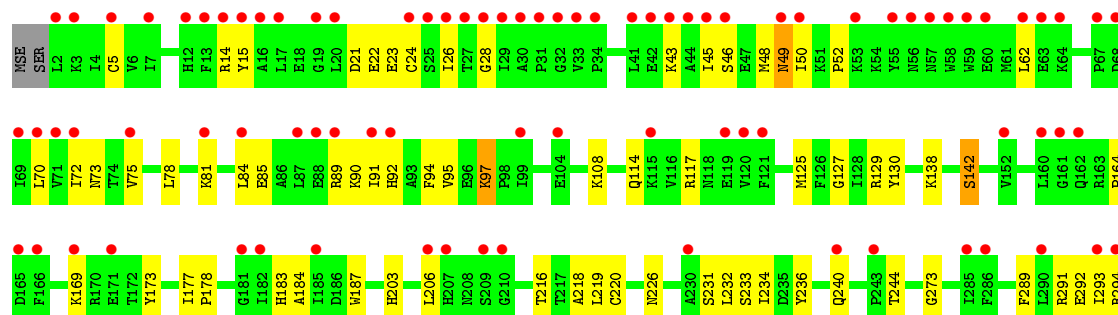
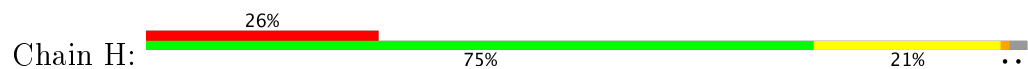
- Molecule 1: Oxidoreductase, putative



- Molecule 1: Oxidoreductase, putative



- Molecule 1: Oxidoreductase, putative





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.01Å 94.18Å 142.85Å 90.00° 91.91° 90.00°	Depositor
Resolution (Å)	50.00 – 2.14 44.65 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-2.14) 99.4 (44.65-2.14)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 2.14Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.204 , 0.242 0.208 , 0.244	Depositor DCC
$R_{free}$ test set	8541 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 37.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	21415	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

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	0.66	0/2683	0.69	2/3615 (0.1%)
1	B	0.76	1/2709 (0.0%)	0.69	0/3649
1	C	0.58	0/2698	0.65	2/3634 (0.1%)
1	D	0.60	0/2694	0.65	0/3629
1	E	0.53	0/2685	0.63	0/3617
1	F	0.65	0/2698	0.67	0/3634
1	G	0.48	0/2679	0.57	0/3609
1	H	0.47	0/2692	0.59	0/3626
All	All	0.60	1/21538 (0.0%)	0.64	4/29013 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	24	CYS	CB-SG	-6.75	1.70	1.82

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	C	59	TRP	CA-CB-CG	5.61	124.35	113.70
1	A	251	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	C	248	ASP	CB-CG-OD1	5.11	122.90	118.30

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	2632	0	2659	18	0
1	B	2657	0	2682	11	0
1	C	2647	0	2675	19	0
1	D	2640	0	2672	16	0
1	E	2634	0	2666	22	0
1	F	2647	0	2675	18	0
1	G	2628	0	2658	26	0
1	H	2641	0	2667	40	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
2	F	10	0	0	0	0
3	A	59	0	0	0	0
3	B	67	0	0	1	0
3	C	18	0	0	0	0
3	D	30	0	0	0	0
3	E	19	0	0	0	0
3	F	59	0	0	1	0
3	G	8	0	0	1	0
3	H	4	0	0	0	0
All	All	21415	0	21354	161	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 4.

All (161) 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:G:256:ARG:HG3	1:G:256:ARG:HH11	1.28	0.98
1:H:129:ARG:HD2	1:H:300:MSE:HE3	1.68	0.73
1:F:131:ARG:HD3	3:F:365:HOH:O	1.89	0.72
1:G:256:ARG:HG3	1:G:256:ARG:NH1	2.03	0.71
1:H:291:ARG:HG2	1:H:296:GLN:HB2	1.74	0.70
1:C:111:SER:O	1:C:114:GLN:HG2	1.94	0.68
1:C:45:ILE:HB	1:C:50:ILE:CD1	2.24	0.67
1:E:130:TYR:CZ	1:E:300:MSE:HE2	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:GLU:HB2	1:E:294:ARG:NH2	2.11	0.66
1:A:57:ASN:ND2	1:A:60:GLU:H	1.95	0.65
1:E:113:TYR:O	1:E:117:ARG:HB3	1.97	0.64
1:F:138:LYS:O	1:F:142:SER:HB2	1.98	0.64
1:D:59:TRP:CH2	1:D:85[A]:GLU:HG2	2.34	0.63
1:H:177:ILE:HB	1:H:178:PRO:HD3	1.80	0.63
1:C:45:ILE:HB	1:C:50:ILE:HD13	1.82	0.62
1:H:220:CYS:HB2	1:H:232:LEU:HB3	1.81	0.61
1:G:113:TYR:O	1:G:117:ARG:HB3	2.01	0.61
1:E:130:TYR:CE2	1:E:300:MSE:HE2	2.37	0.60
1:E:7:ILE:HG12	1:E:61:MSE:HE1	1.84	0.59
1:G:241:GLY:O	1:H:273:GLY:HA2	2.04	0.58
1:B:195:LYS:HE2	3:G:338:HOH:O	2.03	0.58
1:A:55:TYR:HE2	1:A:64:LYS:HD2	1.66	0.58
1:H:294:ARG:HB3	1:H:296:GLN:HE22	1.70	0.57
1:E:292:GLU:OE2	1:E:298:LYS:HA	2.05	0.57
1:H:97:LYS:HE3	1:H:97:LYS:O	2.05	0.56
1:E:97:LYS:HD2	1:E:182:ILE:CG2	2.35	0.56
1:C:260:GLU:OE2	1:D:249:ARG:NH1	2.29	0.56
1:H:15:TYR:CE1	1:H:127:GLY:HA3	2.41	0.56
1:D:23:GLU:HB2	1:D:294:ARG:NH2	2.22	0.55
1:E:315:LYS:HG2	1:E:328:ILE:HG12	1.88	0.55
1:F:315:LYS:HG3	1:F:326:VAL:HG11	1.90	0.54
1:G:23:GLU:HB2	1:G:294:ARG:NH2	2.23	0.54
1:D:15:TYR:CZ	1:D:127:GLY:HA3	2.44	0.53
1:G:5:CYS:HB2	1:G:67:PRO:HG3	1.90	0.53
1:H:89:ARG:O	1:H:91:ILE:HG13	2.08	0.53
1:H:240:GLN:HE21	1:H:240:GLN:HA	1.74	0.52
1:H:72:ILE:HB	1:H:95:VAL:HG23	1.92	0.52
1:E:6:VAL:HB	1:E:29:ILE:HG22	1.92	0.52
1:E:129:ARG:HD2	1:E:300:MSE:HE3	1.92	0.52
1:H:92:HIS:CD2	1:H:293:ILE:HD12	2.45	0.52
1:H:43:LYS:HD2	1:H:43:LYS:N	2.25	0.51
1:D:104:GLU:H	1:D:104:GLU:CD	2.12	0.51
1:H:22:GLU:C	1:H:24:CYS:H	2.14	0.51
1:G:39:SER:O	1:G:43:LYS:HD3	2.10	0.51
1:G:15:TYR:CE1	1:G:127:GLY:HA3	2.46	0.51
1:D:153:ASN:HD21	1:D:251:ARG:HH11	1.58	0.50
1:F:114:GLN:NE2	1:F:115:LYS:HE3	2.26	0.50
1:H:84:LEU:HD13	1:H:108:LYS:HB3	1.94	0.50
1:G:130:TYR:CZ	1:G:300:MSE:HE2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:LEU:HD11	1:D:231:SER:HB3	1.94	0.50
1:A:152:VAL:O	1:A:230:ALA:HA	2.12	0.49
1:F:302:THR:HB	1:F:303:PRO:HD2	1.94	0.49
1:H:97:LYS:HD3	1:H:183:HIS:CE1	2.47	0.49
1:B:35:GLU:H	1:B:35:GLU:CD	2.16	0.49
1:B:152:VAL:O	1:B:230:ALA:HA	2.12	0.49
1:E:7:ILE:HG13	1:E:70:LEU:HD11	1.93	0.49
1:F:114:GLN:HE21	1:F:115:LYS:HG3	1.77	0.49
1:F:152:VAL:O	1:F:230:ALA:HA	2.13	0.49
1:A:57:ASN:HD22	1:A:57:ASN:C	2.17	0.49
1:D:155:GLN:HB3	1:D:249:ARG:HB2	1.95	0.49
1:G:6:VAL:HB	1:G:29:ILE:HG22	1.95	0.49
1:H:26:ILE:HG22	1:H:28:GLY:H	1.78	0.48
1:H:85:GLU:OE1	1:H:89:ARG:HD2	2.12	0.48
1:H:169:LYS:O	1:H:173:TYR:HB3	2.13	0.48
1:G:152:VAL:O	1:G:230:ALA:HA	2.13	0.48
1:G:7:ILE:HG12	1:G:61:MSE:HE1	1.95	0.48
1:A:57:ASN:HD21	1:A:60:GLU:H	1.62	0.48
1:C:155:GLN:HB3	1:C:249:ARG:HB2	1.96	0.48
1:F:37:ASP:OD1	1:F:39:SER:OG	2.32	0.48
1:E:19:GLY:HA3	1:E:286:PHE:HB3	1.95	0.48
1:F:23:GLU:HB2	1:F:294:ARG:NH2	2.29	0.47
1:A:138:LYS:HA	1:A:191:ILE:CD1	2.45	0.47
1:F:315:LYS:HG2	1:F:328:ILE:HG12	1.96	0.47
1:E:292:GLU:OE1	1:E:298:LYS:NZ	2.46	0.47
1:G:50:ILE:HG23	1:G:52:PRO:HD3	1.97	0.47
1:A:111:SER:O	1:A:114:GLN:HG2	2.15	0.47
1:G:97:LYS:HD2	1:G:182:ILE:CG2	2.45	0.46
1:A:19:GLY:HA3	1:A:286:PHE:HB3	1.97	0.46
1:B:48:MSE:HB2	1:B:50:ILE:HD13	1.96	0.46
1:D:113:TYR:O	1:D:117:ARG:HB3	2.16	0.46
1:G:58:TRP:HH2	1:G:85:GLU:HG3	1.81	0.46
1:G:151:LEU:HD21	1:H:233:SER:OG	2.14	0.46
1:B:168:LYS:HE3	3:B:370:HOH:O	2.16	0.45
1:C:95:VAL:O	1:C:124:ALA:HA	2.16	0.45
1:G:59:TRP:CZ3	1:G:89:ARG:NH2	2.84	0.45
1:E:138:LYS:HG2	1:E:190:TRP:CZ2	2.51	0.45
1:G:256:ARG:CG	1:G:256:ARG:NH1	2.75	0.45
1:D:97:LYS:HG3	1:D:97:LYS:H	1.56	0.45
1:G:95:VAL:O	1:G:124:ALA:HA	2.16	0.45
1:D:177:ILE:HB	1:D:178:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LYS:HG3	1:A:97:LYS:H	1.57	0.45
1:D:95:VAL:O	1:D:124:ALA:HA	2.16	0.45
1:E:15:TYR:CZ	1:E:127:GLY:HA3	2.51	0.45
1:H:45:ILE:HG13	1:H:46:SER:N	2.31	0.45
1:A:273:GLY:HA2	1:B:241:GLY:O	2.17	0.44
1:D:153:ASN:ND2	1:D:251:ARG:HH11	2.14	0.44
1:H:138:LYS:O	1:H:142:SER:HB3	2.17	0.44
1:A:138:LYS:HA	1:A:191:ILE:HD11	1.99	0.44
1:C:163:ARG:HD2	1:C:167:TYR:CE2	2.53	0.44
1:F:114:GLN:HA	1:F:117:ARG:NH1	2.33	0.44
1:F:114:GLN:HE21	1:F:115:LYS:HE3	1.83	0.44
1:H:240:GLN:NE2	1:H:240:GLN:HA	2.32	0.44
1:F:281:GLU:HG3	1:F:282:LYS:N	2.31	0.44
1:C:177:ILE:HB	1:C:178:PRO:HD3	2.00	0.43
1:E:97:LYS:H	1:E:97:LYS:HG3	1.67	0.43
1:F:315:LYS:HG3	1:F:326:VAL:CG1	2.47	0.43
1:G:219:LEU:HD11	1:H:231:SER:HB3	2.00	0.43
1:A:35:GLU:N	1:A:35:GLU:OE2	2.35	0.43
1:B:97:LYS:H	1:B:97:LYS:HG3	1.59	0.43
1:B:178:PRO:HA	1:B:313:ALA:HB1	2.00	0.43
1:E:289:PHE:O	1:E:292:GLU:HB3	2.18	0.43
1:H:218:ALA:HB3	1:H:234:ILE:HB	2.00	0.43
1:C:83:LEU:HD22	1:C:95:VAL:HG11	2.01	0.43
1:A:7:ILE:HG12	1:A:61:MSE:HE1	2.01	0.43
1:E:177:ILE:HB	1:E:178:PRO:HD3	2.01	0.43
1:F:42:GLU:HA	1:F:45:ILE:HG12	2.00	0.43
1:H:94:PHE:CE2	1:H:125:MSE:HG2	2.54	0.43
1:H:130:TYR:CZ	1:H:300:MSE:HE2	2.53	0.43
1:A:219:LEU:HD11	1:B:231:SER:HB3	2.01	0.43
1:B:95:VAL:O	1:B:124:ALA:HA	2.18	0.43
1:A:208:ASN:HA	1:A:216:THR:HG21	2.00	0.43
1:H:21:ASP:H	1:H:24:CYS:HB2	1.84	0.43
1:C:111:SER:O	1:C:114:GLN:CG	2.64	0.43
1:C:97:LYS:H	1:C:97:LYS:HG3	1.48	0.43
1:H:48:MSE:O	1:H:49:ASN:HB2	2.19	0.42
1:H:78:LEU:HA	1:H:81:LYS:HD3	2.00	0.42
1:C:315:LYS:HD2	1:C:315:LYS:HA	1.81	0.42
1:G:7:ILE:HD12	1:G:82:ILE:HG21	2.01	0.42
1:A:23:GLU:HB2	1:A:294:ARG:NH2	2.34	0.42
1:E:141:VAL:HG11	1:E:149:ILE:HD11	2.02	0.42
1:E:219:LEU:HD11	1:F:231:SER:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:5:CYS:O	1:H:70:LEU:HD12	2.19	0.42
1:E:111:SER:O	1:E:114:GLN:HG2	2.20	0.42
1:G:11:GLY:HA3	1:G:73:ASN:HB2	2.02	0.42
1:G:26:ILE:O	1:G:52:PRO:HB3	2.20	0.42
1:C:114:GLN:HE21	1:C:115:LYS:NZ	2.17	0.42
1:H:329:GLU:HA	1:H:329:GLU:OE2	2.20	0.41
1:C:129:ARG:HD3	1:C:190:TRP:CD2	2.55	0.41
1:C:292:GLU:HA	1:C:297:GLY:O	2.20	0.41
1:H:23:GLU:HB2	1:H:294:ARG:NH2	2.35	0.41
1:C:45:ILE:HD12	1:C:52:PRO:HG2	2.03	0.41
1:F:57:ASN:HD22	1:F:60:GLU:CD	2.23	0.41
1:H:184:ALA:HA	1:H:187:TRP:CD2	2.55	0.41
1:H:84:LEU:HD22	1:H:108:LYS:HD3	2.02	0.41
1:G:231:SER:HB3	1:H:219:LEU:HD21	2.02	0.41
1:H:289:PHE:O	1:H:293:ILE:HG12	2.20	0.41
1:D:157:SER:HB3	1:D:247:ASP:HB3	2.03	0.41
1:C:20:LEU:HD11	1:C:26:ILE:HD11	2.02	0.41
1:D:129:ARG:HD3	1:D:190:TRP:CD2	2.55	0.41
1:D:35:GLU:HG2	1:D:35:GLU:O	2.20	0.41
1:E:152:VAL:O	1:E:230:ALA:HA	2.21	0.41
1:C:73:ASN:HB3	1:C:125:MSE:HE1	2.04	0.40
1:F:20:LEU:HD12	1:F:48:MSE:HE1	2.03	0.40
1:H:178:PRO:HG2	1:H:317:ARG:HD3	2.03	0.40
1:H:184:ALA:HA	1:H:187:TRP:CE3	2.56	0.40
1:A:95:VAL:O	1:A:124:ALA:HA	2.22	0.40
1:H:292:GLU:OE2	1:H:298:LYS:HA	2.22	0.40
1:A:146:VAL:CG1	1:A:259:VAL:HG23	2.52	0.40
1:G:50:ILE:HD13	1:G:51:LYS:N	2.36	0.40
1:B:177:ILE:HB	1:B:178:PRO:HD3	2.02	0.40
1:G:177:ILE:HB	1:G:178:PRO:HD3	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	326/337 (97%)	313 (96%)	12 (4%)	1 (0%)	44	39
1	B	329/337 (98%)	318 (97%)	11 (3%)	0	100	100
1	C	328/337 (97%)	315 (96%)	13 (4%)	0	100	100
1	D	327/337 (97%)	316 (97%)	11 (3%)	0	100	100
1	E	326/337 (97%)	309 (95%)	16 (5%)	1 (0%)	44	39
1	F	328/337 (97%)	319 (97%)	9 (3%)	0	100	100
1	G	325/337 (96%)	304 (94%)	20 (6%)	1 (0%)	44	39
1	H	327/337 (97%)	297 (91%)	25 (8%)	5 (2%)	12	5
All	All	2616/2696 (97%)	2491 (95%)	117 (4%)	8 (0%)	44	39

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	49	ASN
1	E	34	PRO
1	G	49	ASN
1	H	90	LYS
1	H	164	PRO
1	H	52	PRO
1	A	34	PRO
1	H	75	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	286/289 (99%)	272 (95%)	14 (5%)	29	24
1	B	289/289 (100%)	277 (96%)	12 (4%)	34	31
1	C	288/289 (100%)	272 (94%)	16 (6%)	25	19
1	D	288/289 (100%)	278 (96%)	10 (4%)	41	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	287/289 (99%)	273 (95%)	14 (5%)	29	24
1	F	288/289 (100%)	266 (92%)	22 (8%)	15	9
1	G	286/289 (99%)	272 (95%)	14 (5%)	29	24
1	H	287/289 (99%)	271 (94%)	16 (6%)	25	19
All	All	2299/2312 (99%)	2181 (95%)	118 (5%)	28	22

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	SER
1	A	33	VAL
1	A	51	LYS
1	A	57	ASN
1	A	73	ASN
1	A	97	LYS
1	A	115	LYS
1	A	117	ARG
1	A	123	THR
1	A	191	ILE
1	A	203	HIS
1	A	224	LEU
1	A	236	TYR
1	A	275	ARG
1	B	43	LYS
1	B	47	GLU
1	B	50	ILE
1	B	62	LEU
1	B	73	ASN
1	B	97	LYS
1	B	162	GLN
1	B	203	HIS
1	B	216	THR
1	B	236	TYR
1	B	263	ASN
1	B	324	GLN
1	C	50	ILE
1	C	51	LYS
1	C	59	TRP
1	C	62	LEU
1	C	73	ASN
1	C	90	LYS

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Mol	Chain	Res	Type
1	C	97	LYS
1	C	119	GLU
1	C	120	VAL
1	C	123	THR
1	C	142	SER
1	C	216	THR
1	C	236	TYR
1	C	245	HIS
1	C	271	GLU
1	C	315	LYS
1	D	43	LYS
1	D	50	ILE
1	D	73	ASN
1	D	97	LYS
1	D	114	GLN
1	D	142	SER
1	D	203	HIS
1	D	216	THR
1	D	236	TYR
1	D	271	GLU
1	E	63	GLU
1	E	73	ASN
1	E	97	LYS
1	E	111	SER
1	E	117	ARG
1	E	119	GLU
1	E	123	THR
1	E	142	SER
1	E	203	HIS
1	E	236	TYR
1	E	263	ASN
1	E	275	ARG
1	E	281	GLU
1	E	315	LYS
1	F	22	GLU
1	F	39	SER
1	F	49	ASN
1	F	50	ILE
1	F	51	LYS
1	F	53	LYS
1	F	62	LEU
1	F	64	LYS

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Mol	Chain	Res	Type
1	F	73	ASN
1	F	97	LYS
1	F	104	GLU
1	F	111	SER
1	F	114	GLN
1	F	123	THR
1	F	142	SER
1	F	148	GLU
1	F	203	HIS
1	F	209	SER
1	F	216	THR
1	F	236	TYR
1	F	271	GLU
1	F	315	LYS
1	G	50	ILE
1	G	59	TRP
1	G	73	ASN
1	G	97	LYS
1	G	104	GLU
1	G	111	SER
1	G	114	GLN
1	G	123	THR
1	G	203	HIS
1	G	216	THR
1	G	236	TYR
1	G	256	ARG
1	G	271	GLU
1	G	275	ARG
1	H	14	ARG
1	H	50	ILE
1	H	62	LEU
1	H	73	ASN
1	H	97	LYS
1	H	114	GLN
1	H	117	ARG
1	H	142	SER
1	H	203	HIS
1	H	206	LEU
1	H	216	THR
1	H	226	ASN
1	H	236	TYR
1	H	244	THR

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Mol	Chain	Res	Type
1	H	315	LYS
1	H	329	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	114	GLN
1	A	118	ASN
1	A	240	GLN
1	A	245	HIS
1	B	114	GLN
1	B	118	ASN
1	C	114	GLN
1	C	203	HIS
1	D	153	ASN
1	D	207	HIS
1	F	57	ASN
1	F	114	GLN
1	F	240	GLN
1	F	274	HIS
1	G	240	GLN
1	H	114	GLN
1	H	226	ASN
1	H	240	GLN
1	H	296	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

5 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	337	-	4,4,4	0.18	0	6,6,6	0.07	0
2	SO4	B	337	-	4,4,4	0.16	0	6,6,6	0.16	0
2	SO4	B	338	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	F	337	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	F	338	-	4,4,4	0.15	0	6,6,6	0.11	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	337	-	-	0/0/0/0	0/0/0/0
2	SO4	B	337	-	-	0/0/0/0	0/0/0/0
2	SO4	B	338	-	-	0/0/0/0	0/0/0/0
2	SO4	F	337	-	-	0/0/0/0	0/0/0/0
2	SO4	F	338	-	-	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.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	323/337 (95%)	-0.00	5 (1%) 74 78	27, 41, 68, 80	0
1	B	326/337 (96%)	-0.08	3 (0%) 84 87	26, 35, 54, 70	0
1	C	325/337 (96%)	0.36	13 (4%) 39 45	35, 50, 65, 74	0
1	D	323/337 (95%)	-0.12	4 (1%) 79 83	30, 45, 59, 70	0
1	E	323/337 (95%)	0.60	27 (8%) 12 15	32, 53, 89, 96	0
1	F	325/337 (96%)	-0.12	4 (1%) 79 83	28, 38, 53, 65	0
1	G	322/337 (95%)	0.88	49 (15%) 2 3	33, 65, 104, 109	0
1	H	324/337 (96%)	1.48	87 (26%) 1 1	36, 77, 120, 122	0
All	All	2591/2696 (96%)	0.37	192 (7%) 15 19	26, 47, 94, 122	0

All (192) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	34	PRO	10.9
1	G	6	VAL	7.5
1	H	5	CYS	7.4
1	G	50	ILE	7.3
1	H	33	VAL	7.2
1	H	59	TRP	7.1
1	H	50	ILE	7.0
1	G	26	ILE	6.9
1	H	26	ILE	6.9
1	G	59	TRP	6.6
1	G	5	CYS	6.3
1	H	45	ILE	6.3
1	H	13	PHE	6.2
1	G	49	ASN	6.2
1	H	20	LEU	6.2
1	G	45	ILE	5.9

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Mol	Chain	Res	Type	RSRZ
1	G	62	LEU	5.7
1	H	68	ASP	5.7
1	H	69	ILE	5.7
1	H	62	LEU	5.6
1	E	26	ILE	5.6
1	G	55	TYR	5.3
1	G	64	LYS	5.3
1	G	24	CYS	5.2
1	H	166	PHE	5.1
1	H	290	LEU	5.1
1	G	60	GLU	5.0
1	H	84	LEU	4.9
1	H	28	GLY	4.9
1	G	4	ILE	4.7
1	E	59	TRP	4.7
1	H	293	ILE	4.7
1	H	162	GLN	4.7
1	G	46	SER	4.6
1	H	49	ASN	4.6
1	H	297	GLY	4.5
1	G	28	GLY	4.3
1	H	2	LEU	4.3
1	H	53	LYS	4.3
1	H	286	PHE	4.2
1	H	27	THR	4.2
1	E	51	LYS	4.1
1	H	24	CYS	4.1
1	H	31	PRO	4.0
1	G	20	LEU	3.9
1	G	68	ASP	3.9
1	H	19	GLY	3.9
1	G	63	GLU	3.9
1	H	55	TYR	3.9
1	G	23	GLU	3.9
1	C	59	TRP	3.9
1	H	7	ILE	3.9
1	E	46	SER	3.8
1	G	56	ASN	3.7
1	H	115	LYS	3.7
1	E	52	PRO	3.7
1	H	67	PRO	3.7
1	H	295	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	G	2	LEU	3.7
1	G	3	LYS	3.7
1	H	58	TRP	3.7
1	E	293	ILE	3.6
1	E	22	GLU	3.5
1	G	54	LYS	3.5
1	G	29	ILE	3.5
1	H	120	VAL	3.5
1	H	60	GLU	3.5
1	H	63	GLU	3.5
1	G	30	ALA	3.5
1	E	43	LYS	3.5
1	E	49	ASN	3.5
1	H	75	VAL	3.5
1	E	50	ILE	3.4
1	G	293	ILE	3.4
1	G	53	LYS	3.4
1	H	70	LEU	3.3
1	H	87	LEU	3.3
1	E	60	GLU	3.3
1	E	117	ARG	3.2
1	E	119	GLU	3.1
1	H	43	LYS	3.1
1	G	25	SER	3.1
1	G	44	ALA	3.1
1	H	56	ASN	3.0
1	H	64	LYS	3.0
1	G	69	ILE	3.0
1	H	160	LEU	3.0
1	A	49	ASN	3.0
1	G	256	ARG	3.0
1	H	207	HIS	2.9
1	G	7	ILE	2.9
1	G	66	LYS	2.9
1	G	71	VAL	2.9
1	H	240	GLN	2.9
1	C	118	ASN	2.9
1	H	119	GLU	2.9
1	H	30	ALA	2.9
1	H	17	LEU	2.9
1	G	31	PRO	2.9
1	G	51	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	169	LYS	2.8
1	B	207	HIS	2.8
1	E	115	LYS	2.8
1	G	27	THR	2.8
1	E	120	VAL	2.8
1	C	220	CYS	2.8
1	G	43	LYS	2.8
1	H	230	ALA	2.7
1	H	41	LEU	2.7
1	C	185	ILE	2.7
1	H	3	LYS	2.7
1	B	59	TRP	2.6
1	H	12	HIS	2.6
1	F	1	SER	2.6
1	A	45	ILE	2.6
1	H	161	GLY	2.6
1	E	55	TYR	2.6
1	E	53	LYS	2.6
1	E	258	ILE	2.6
1	E	47	GLU	2.6
1	H	121	PHE	2.6
1	C	152	VAL	2.6
1	H	25	SER	2.6
1	H	285	ILE	2.6
1	H	32	GLY	2.6
1	D	22	GLU	2.5
1	E	25	SER	2.5
1	H	171	GLU	2.5
1	H	312	ILE	2.5
1	E	1	SER	2.5
1	H	165	ASP	2.5
1	E	116	VAL	2.5
1	G	273	GLY	2.4
1	C	224	LEU	2.4
1	C	22	GLU	2.4
1	E	63	GLU	2.4
1	G	58	TRP	2.4
1	H	182	ILE	2.4
1	H	92	HIS	2.4
1	H	72	ILE	2.4
1	H	209	SER	2.4
1	G	52	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	312	ILE	2.3
1	G	47	GLU	2.3
1	H	185	ILE	2.3
1	G	21	ASP	2.3
1	H	152	VAL	2.3
1	G	162	GLN	2.3
1	D	49	ASN	2.3
1	H	42	GLU	2.3
1	C	232	LEU	2.2
1	A	59	TRP	2.2
1	B	50	ILE	2.2
1	H	44	ALA	2.2
1	E	35	GLU	2.2
1	G	18	GLU	2.2
1	H	14	ARG	2.2
1	H	81	LYS	2.2
1	H	210	GLY	2.2
1	H	104	GLU	2.2
1	E	28	GLY	2.2
1	G	290	LEU	2.2
1	H	46	SER	2.2
1	H	88	GLU	2.2
1	D	43	LYS	2.2
1	A	22	GLU	2.2
1	H	294	ARG	2.2
1	C	154	THR	2.2
1	F	45	ILE	2.1
1	D	35	GLU	2.1
1	E	289	PHE	2.1
1	H	71	VAL	2.1
1	H	57	ASN	2.1
1	H	15	TYR	2.1
1	H	16	ALA	2.1
1	H	243	PRO	2.1
1	C	281	GLU	2.1
1	H	29	ILE	2.1
1	H	91	ILE	2.1
1	F	22	GLU	2.1
1	G	57	ASN	2.1
1	G	191	ILE	2.0
1	H	99	ILE	2.0
1	H	206	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	43	LYS	2.0
1	G	139	LYS	2.0
1	C	222	PHE	2.0
1	H	89	ARG	2.0
1	C	2	LEU	2.0
1	E	112	VAL	2.0
1	A	50	ILE	2.0
1	H	181	GLY	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(Å <sup>2</sup> )	Q<0.9
2	SO4	B	338	5/5	0.80	0.20	5.29	108,108,108,109	0
2	SO4	F	337	5/5	0.91	0.14	0.15	102,102,102,102	0
2	SO4	F	338	5/5	0.93	0.09	-1.09	96,96,96,96	0
2	SO4	B	337	5/5	0.94	0.11	-1.76	88,88,89,89	0
2	SO4	A	337	5/5	0.95	0.11	-2.44	105,105,106,106	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.