



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 02:32 PM EDT

PDB ID : 1ESJ  
Title : CRYSTAL STRUCTURE OF THIAZOLE KINASE MUTANT (C198S)  
Authors : Campobasso, N.; Mathews, I.I.; Begley, T.P.; Ealick, S.E.  
Deposited on : 2000-04-10  
Resolution : 1.80 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

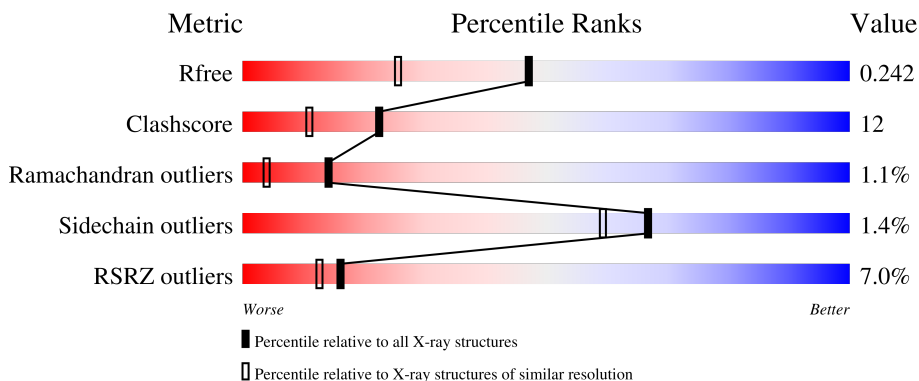
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

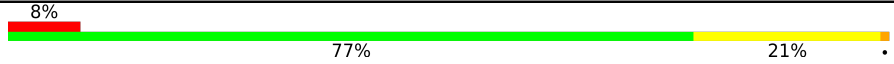
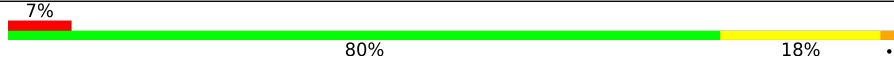

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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  $\geq 3$ , 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	284	
1	B	284	
1	C	284	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6592 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 HYDROXYETHYLTHIAZOLE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	284	2080	1297	374	402	7	45	0	0
1	B	284	2080	1297	374	402	7	62	0	0
1	C	284	2080	1297	374	402	7	38	0	0

There are 39 discrepancies between the modelled and reference sequences:

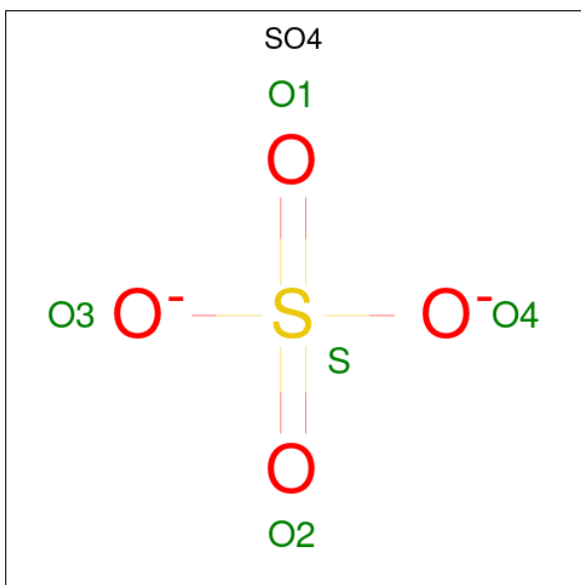
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP P39593
A	-10	ARG	-	expression tag	UNP P39593
A	-9	GLY	-	expression tag	UNP P39593
A	-8	SER	-	expression tag	UNP P39593
A	-7	HIS	-	expression tag	UNP P39593
A	-6	HIS	-	expression tag	UNP P39593
A	-5	HIS	-	expression tag	UNP P39593
A	-4	HIS	-	expression tag	UNP P39593
A	-3	HIS	-	expression tag	UNP P39593
A	-2	HIS	-	expression tag	UNP P39593
A	-1	GLY	-	expression tag	UNP P39593
A	0	SER	-	expression tag	UNP P39593
A	198	SER	CYS	engineered mutation	UNP P39593
B	-11	MET	-	expression tag	UNP P39593
B	-10	ARG	-	expression tag	UNP P39593
B	-9	GLY	-	expression tag	UNP P39593
B	-8	SER	-	expression tag	UNP P39593
B	-7	HIS	-	expression tag	UNP P39593
B	-6	HIS	-	expression tag	UNP P39593
B	-5	HIS	-	expression tag	UNP P39593
B	-4	HIS	-	expression tag	UNP P39593
B	-3	HIS	-	expression tag	UNP P39593
B	-2	HIS	-	expression tag	UNP P39593

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P39593
B	0	SER	-	expression tag	UNP P39593
B	198	SER	CYS	engineered mutation	UNP P39593
C	-11	MET	-	expression tag	UNP P39593
C	-10	ARG	-	expression tag	UNP P39593
C	-9	GLY	-	expression tag	UNP P39593
C	-8	SER	-	expression tag	UNP P39593
C	-7	HIS	-	expression tag	UNP P39593
C	-6	HIS	-	expression tag	UNP P39593
C	-5	HIS	-	expression tag	UNP P39593
C	-4	HIS	-	expression tag	UNP P39593
C	-3	HIS	-	expression tag	UNP P39593
C	-2	HIS	-	expression tag	UNP P39593
C	-1	GLY	-	expression tag	UNP P39593
C	0	SER	-	expression tag	UNP P39593
C	198	SER	CYS	engineered mutation	UNP P39593

- 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	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

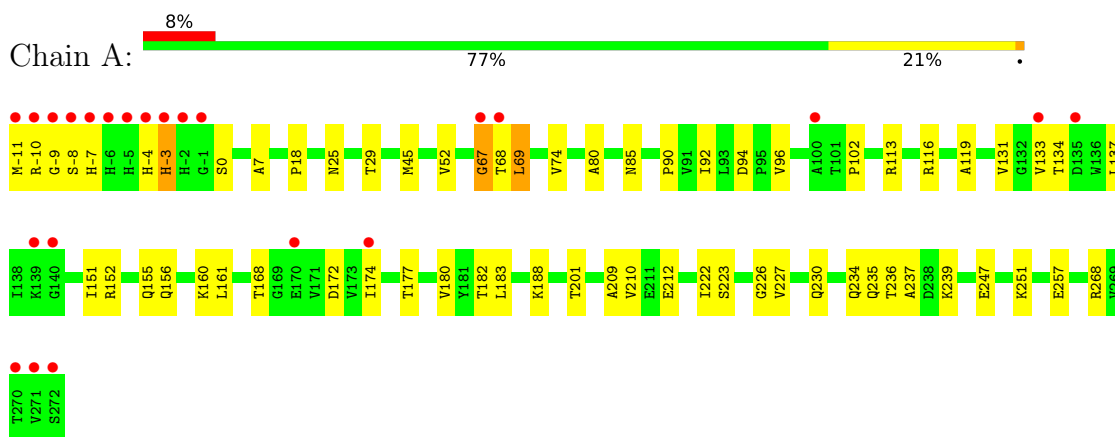
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	99	Total O 99 99	0	0
3	B	100	Total O 100 100	0	0
3	C	143	Total O 143 143	0	0

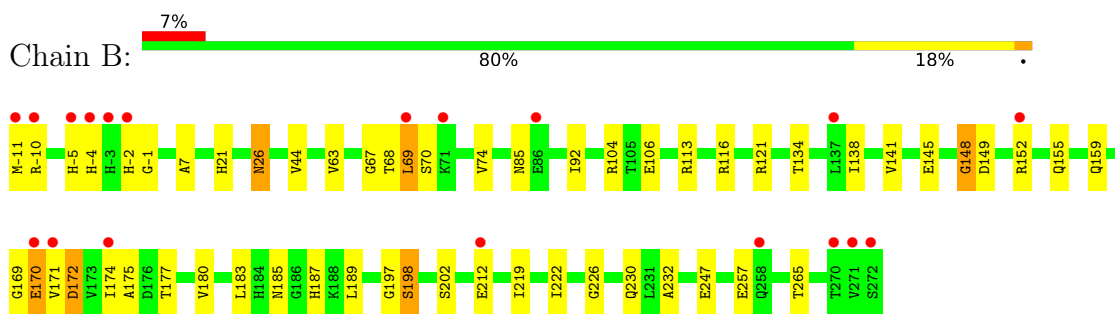
### 3 Residue-property plots [i](#)

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.

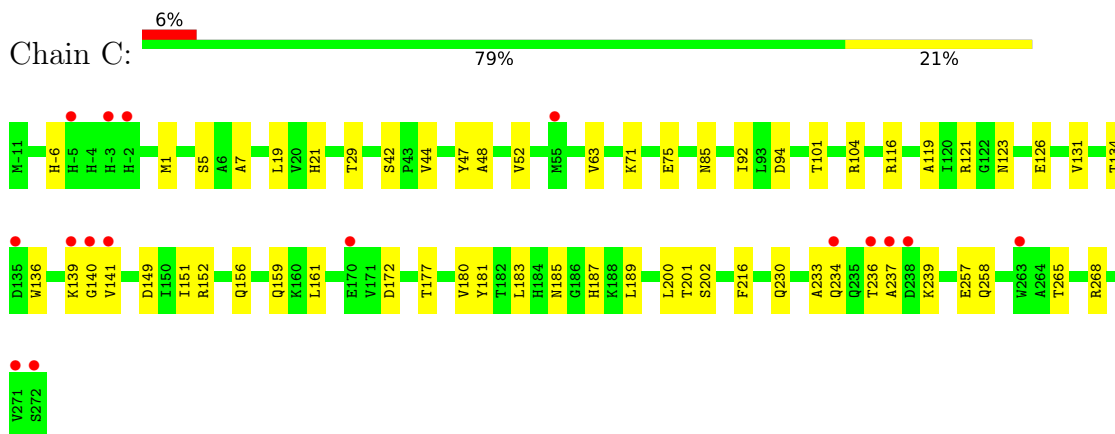
#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE



#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE



#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.06Å 100.89Å 73.07Å 90.00° 96.02° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 19.96 – 1.70	Depositor EDS
% Data completeness (in resolution range)	89.8 (20.00-1.80) 98.7 (19.96-1.70)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.95 (at 1.70Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.229 , 0.253 0.242 , 0.242	Depositor DCC
$R_{free}$ test set	4175 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.1	Xtrriage
Anisotropy	0.255	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6592	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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	0.30	0/2111	0.57	0/2870
1	B	0.30	0/2111	0.56	0/2870
1	C	0.31	0/2111	0.59	0/2870
All	All	0.30	0/6333	0.58	0/8610

There are no bond length outliers.

There are no bond angle outliers.

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	2080	0	2100	50	0
1	B	2080	0	2100	47	0
1	C	2080	0	2100	48	0
2	A	5	0	0	0	0
2	C	5	0	0	0	0
3	A	99	0	0	3	0
3	B	100	0	0	3	0
3	C	143	0	0	0	0
All	All	6592	0	6300	143	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 12.

All (143) 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:C:7:ALA:HB1	1:C:257:GLU:HG3	1.30	1.12
1:B:185:ASN:HD21	1:B:265:THR:H	1.10	0.99
1:B:85:ASN:HD21	1:B:116:ARG:H	1.14	0.92
1:B:7:ALA:HB1	1:B:257:GLU:HG2	1.57	0.86
1:C:185:ASN:HD21	1:C:265:THR:H	1.22	0.85
1:C:159:GLN:HG2	1:C:177:THR:HG23	1.57	0.85
1:C:85:ASN:HD21	1:C:116:ARG:H	1.23	0.84
1:C:1:MET:HE3	1:C:216:PHE:CD2	2.15	0.81
1:B:187:HIS:HD2	1:B:189:LEU:H	1.27	0.80
3:A:670:HOH:O	1:C:71:LYS:HE2	1.83	0.78
1:A:133:VAL:HG23	1:A:134:THR:HG23	1.64	0.78
1:C:-6:HIS:HB3	1:C:1:MET:HE1	1.68	0.75
1:C:71:LYS:O	1:C:75:GLU:HG3	1.87	0.74
1:B:85:ASN:ND2	1:B:116:ARG:H	1.89	0.71
1:C:121:ARG:NH2	1:C:200:LEU:HD23	2.06	0.71
1:B:159:GLN:HG2	1:B:177:THR:HG23	1.72	0.71
1:B:69:LEU:HD22	1:B:104:ARG:NE	2.06	0.71
1:C:1:MET:HE3	1:C:216:PHE:CG	2.27	0.70
1:A:183:LEU:HD22	1:A:183:LEU:N	2.06	0.70
1:A:92:ILE:HD12	1:A:119:ALA:HB3	1.77	0.67
1:B:170:GLU:H	1:B:170:GLU:CD	2.00	0.65
1:A:85:ASN:HD21	1:A:116:ARG:H	1.41	0.65
1:C:21:HIS:HA	1:C:44:VAL:HG23	1.77	0.65
1:C:187:HIS:HD2	1:C:189:LEU:H	1.45	0.64
1:B:174:ILE:HD11	1:B:222:ILE:HD12	1.80	0.63
1:A:174:ILE:HD11	1:A:222:ILE:HD12	1.80	0.62
1:B:69:LEU:HD22	1:B:104:ARG:HE	1.62	0.62
1:B:185:ASN:ND2	1:B:265:THR:H	1.92	0.62
1:B:187:HIS:CD2	1:B:189:LEU:H	2.15	0.61
1:C:131:VAL:HG12	1:C:161:LEU:HD11	1.82	0.61
1:A:96:VAL:HG22	3:A:502:HOH:O	2.00	0.61
1:C:121:ARG:HH21	1:C:200:LEU:HD23	1.67	0.60
1:A:25:ASN:O	1:A:29:THR:HG23	2.02	0.59
1:A:-8:SER:HB2	1:A:212:GLU:CD	2.23	0.59
1:B:198:SER:HB3	3:B:454:HOH:O	2.03	0.59
1:C:187:HIS:CD2	1:C:189:LEU:H	2.21	0.58
1:C:85:ASN:ND2	1:C:116:ARG:H	1.99	0.58
1:C:7:ALA:CB	1:C:257:GLU:HG3	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:GLY:O	1:A:230:GLN:HG3	2.05	0.57
1:C:92:ILE:HD12	1:C:119:ALA:HB3	1.86	0.56
1:A:69:LEU:CD2	1:A:69:LEU:H	2.19	0.56
1:B:148:GLY:O	1:B:152:ARG:HG3	2.05	0.56
1:A:-10:ARG:HD2	1:A:90:PRO:HD3	1.88	0.56
1:A:247:GLU:O	1:A:251:LYS:HG2	2.06	0.55
1:C:230:GLN:O	1:C:234:GLN:HG2	2.06	0.54
1:B:85:ASN:HD21	1:B:116:ARG:N	1.93	0.54
1:A:52:VAL:HB	1:A:80:ALA:HB2	1.89	0.53
1:B:121:ARG:HH12	1:B:197:GLY:CA	2.21	0.53
1:A:160:LYS:O	1:A:160:LYS:HD3	2.09	0.53
1:B:185:ASN:HD21	1:B:265:THR:N	1.94	0.53
1:A:223:SER:O	1:A:227:VAL:HG23	2.08	0.53
1:B:171:VAL:O	1:B:183:LEU:O	2.27	0.52
1:B:26:ASN:HD21	1:C:29:THR:HG21	1.75	0.52
1:A:174:ILE:CD1	1:A:222:ILE:HD12	2.39	0.52
1:A:183:LEU:HB3	3:A:517:HOH:O	2.09	0.52
1:B:-4:HIS:C	1:B:-2:HIS:N	2.62	0.52
1:C:134:THR:HG21	1:C:136:TRP:NE1	2.25	0.52
1:A:-11:MET:HG3	1:A:209:ALA:O	2.10	0.52
1:A:151:ILE:HG23	1:A:180:VAL:HG11	1.91	0.52
1:B:21:HIS:HA	1:B:44:VAL:CG1	2.40	0.52
1:C:63:VAL:HG21	1:C:202:SER:HA	1.91	0.52
1:B:63:VAL:HG21	1:B:202:SER:HA	1.93	0.51
1:B:21:HIS:HA	1:B:44:VAL:HG13	1.92	0.51
1:B:149:ASP:HA	1:B:152:ARG:HH11	1.76	0.51
1:A:235:GLN:HB3	1:A:247:GLU:HG2	1.92	0.51
1:C:-6:HIS:HD2	1:C:5:SER:OG	1.93	0.51
1:A:69:LEU:HD12	1:A:74:VAL:CG2	2.41	0.51
1:A:151:ILE:O	1:A:155:GLN:HG3	2.11	0.50
1:C:185:ASN:ND2	1:C:265:THR:H	2.00	0.50
1:C:19:LEU:HD23	1:C:42:SER:HB2	1.93	0.50
1:B:155:GLN:O	1:B:159:GLN:HG3	2.12	0.49
1:A:69:LEU:H	1:A:69:LEU:HD23	1.78	0.49
1:C:94:ASP:HB2	1:C:201:THR:HG21	1.93	0.49
1:B:92:ILE:HD12	1:B:92:ILE:N	2.26	0.49
1:C:233:ALA:O	1:C:237:ALA:HB2	2.13	0.49
1:B:172:ASP:HB2	1:B:183:LEU:HB2	1.95	0.49
1:B:121:ARG:HH12	1:B:197:GLY:HA2	1.78	0.48
1:A:-7:HIS:HE1	1:A:210:VAL:O	1.95	0.48
1:C:101:THR:OG1	1:C:104:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:LEU:HD23	1:A:69:LEU:N	2.29	0.48
1:B:67:GLY:O	1:B:68:THR:C	2.51	0.48
1:A:230:GLN:O	1:A:234:GLN:HG3	2.13	0.48
1:A:94:ASP:HB2	1:A:201:THR:HG21	1.96	0.47
1:B:169:GLY:C	1:B:171:VAL:H	2.17	0.47
1:B:171:VAL:O	1:B:172:ASP:O	2.32	0.47
1:B:-10:ARG:HH11	1:B:-10:ARG:HG2	1.80	0.47
1:B:174:ILE:CD1	1:B:183:LEU:HD11	2.44	0.47
1:A:183:LEU:N	1:A:183:LEU:CD2	2.77	0.47
1:C:1:MET:CE	1:C:216:PHE:CG	2.96	0.47
1:C:151:ILE:HG23	1:C:180:VAL:HG11	1.97	0.47
1:A:131:VAL:HG22	1:A:161:LEU:HD11	1.96	0.47
1:A:25:ASN:HB2	1:A:68:THR:OG1	2.15	0.46
1:B:226:GLY:O	1:B:230:GLN:HG3	2.14	0.46
1:A:-4:HIS:O	1:A:-3:HIS:HB2	2.15	0.46
1:A:-9:GLY:O	1:A:212:GLU:N	2.41	0.46
1:B:68:THR:HB	1:C:47:TYR:CE2	2.51	0.46
1:B:69:LEU:CD2	1:B:104:ARG:HE	2.27	0.46
1:C:185:ASN:HD21	1:C:265:THR:N	2.03	0.46
1:A:152:ARG:O	1:A:156:GLN:HG3	2.16	0.45
1:C:236:THR:HG22	1:C:239:LYS:HD2	1.98	0.45
1:A:85:ASN:ND2	1:A:116:ARG:H	2.10	0.45
1:A:113:ARG:HH11	1:A:113:ARG:HG3	1.81	0.45
1:C:48:ALA:O	1:C:52:VAL:HG13	2.17	0.45
1:A:0:SER:HB3	1:A:268:ARG:HH11	1.82	0.45
1:B:175:ALA:CB	1:B:180:VAL:HG22	2.47	0.44
1:C:181:TYR:CZ	1:C:268:ARG:HD3	2.53	0.44
1:C:-6:HIS:CB	1:C:1:MET:HE1	2.41	0.44
1:C:139:LYS:O	1:C:141:VAL:N	2.47	0.44
1:A:-10:ARG:CB	1:A:-10:ARG:NH1	2.81	0.43
1:A:-10:ARG:HH11	1:A:-10:ARG:HB2	1.83	0.43
1:A:25:ASN:ND2	1:A:67:GLY:HA3	2.32	0.43
1:C:258:GLN:N	1:C:258:GLN:CD	2.72	0.43
1:A:168:THR:HA	1:A:172:ASP:OD1	2.19	0.43
1:B:70:SER:O	1:B:74:VAL:HG23	2.18	0.43
1:C:152:ARG:HH11	1:C:152:ARG:HG3	1.83	0.43
1:B:-5:HIS:O	1:B:-2:HIS:HB2	2.19	0.43
1:C:-6:HIS:ND1	1:C:1:MET:HE2	2.33	0.43
1:B:121:ARG:NH1	1:B:197:GLY:O	2.52	0.43
1:A:236:THR:O	1:A:237:ALA:HB3	2.19	0.42
1:A:102:PRO:HG2	3:B:455:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-2:HIS:N	1:B:-2:HIS:CD2	2.86	0.42
1:C:172:ASP:HB2	1:C:183:LEU:HB2	2.00	0.42
1:B:-10:ARG:NH2	1:B:212:GLU:HA	2.34	0.42
1:A:-11:MET:SD	1:A:18:PRO:HB3	2.60	0.42
1:B:-4:HIS:C	1:B:-2:HIS:H	2.23	0.41
1:B:134:THR:HG22	3:B:662:HOH:O	2.20	0.41
1:A:94:ASP:OD1	1:A:96:VAL:CG2	2.68	0.41
1:A:177:THR:O	1:A:177:THR:HG22	2.19	0.41
1:C:152:ARG:HG3	1:C:152:ARG:NH1	2.35	0.41
1:A:7:ALA:HB1	1:A:257:GLU:HG2	2.00	0.41
1:A:182:THR:C	1:A:183:LEU:HD22	2.40	0.41
1:A:236:THR:O	1:A:239:LYS:HG3	2.20	0.41
1:C:19:LEU:HD23	1:C:42:SER:CB	2.51	0.41
1:A:25:ASN:CB	1:A:68:THR:OG1	2.69	0.41
1:B:106:GLU:OE2	1:B:113:ARG:NH2	2.53	0.41
1:B:232:ALA:HB1	1:B:247:GLU:HB3	2.03	0.41
1:C:139:LYS:C	1:C:141:VAL:H	2.21	0.41
1:C:152:ARG:O	1:C:156:GLN:HG3	2.21	0.41
1:B:174:ILE:HD12	1:B:219:ILE:HG12	2.03	0.40
1:A:94:ASP:OD1	1:A:96:VAL:HG23	2.20	0.40
1:C:123:ASN:OD1	1:C:126:GLU:HG3	2.20	0.40
1:C:149:ASP:OD1	1:C:149:ASP:N	2.55	0.40
1:C:-6:HIS:CD2	1:C:5:SER:OG	2.74	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	282/284 (99%)	267 (95%)	13 (5%)	2 (1%)	22 10
1	B	282/284 (99%)	261 (93%)	15 (5%)	6 (2%)	7 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	282/284 (99%)	266 (94%)	15 (5%)	1 (0%)	34	21
All	All	846/852 (99%)	794 (94%)	43 (5%)	9 (1%)	14	4

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-3	HIS
1	B	172	ASP
1	B	-1	GLY
1	B	138	ILE
1	B	170	GLU
1	B	148	GLY
1	A	67	GLY
1	B	141	VAL
1	C	140	GLY

### 5.3.2 Protein sidechains [i](#)

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	216/216 (100%)	212 (98%)	4 (2%)	57	46
1	B	216/216 (100%)	211 (98%)	5 (2%)	50	37
1	C	216/216 (100%)	216 (100%)	0	100	100
All	All	648/648 (100%)	639 (99%)	9 (1%)	67	59

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	MET
1	A	69	LEU
1	A	137	LEU
1	A	188	LYS
1	B	-11	MET
1	B	26	ASN

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Mol	Chain	Res	Type
1	B	69	LEU
1	B	145	GLU
1	B	198	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-6	HIS
1	A	85	ASN
1	A	235	GLN
1	A	258	GLN
1	A	261	GLN
1	B	-6	HIS
1	B	-4	HIS
1	B	-2	HIS
1	B	26	ASN
1	B	85	ASN
1	B	156	GLN
1	B	159	GLN
1	B	185	ASN
1	B	187	HIS
1	B	234	GLN
1	B	261	GLN
1	C	-6	HIS
1	C	85	ASN
1	C	159	GLN
1	C	185	ASN
1	C	187	HIS
1	C	235	GLN
1	C	261	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 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	C	325	-	4,4,4	0.26	0	6,6,6	0.09	0
2	SO4	A	315	-	4,4,4	0.30	0	6,6,6	0.10	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 [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	276/284 (97%)	0.70	23 (8%) 11 8	10, 19, 40, 57	0
1	B	274/284 (96%)	0.50	19 (6%) 16 13	9, 18, 37, 54	0
1	C	277/284 (97%)	0.30	16 (5%) 23 18	8, 15, 29, 43	0
All	All	827/852 (97%)	0.50	58 (7%) 16 13	8, 17, 35, 57	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	GLY	14.1
1	C	272	SER	10.4
1	A	-11	MET	9.4
1	A	-7	HIS	9.0
1	B	-11	MET	8.7
1	B	271	VAL	8.5
1	B	272	SER	8.5
1	A	-2	HIS	8.4
1	A	-5	HIS	8.4
1	A	-3	HIS	8.2
1	A	272	SER	8.2
1	B	-2	HIS	7.7
1	A	-4	HIS	7.6
1	A	-8	SER	7.1
1	A	-10	ARG	6.8
1	B	-10	ARG	5.9
1	C	141	VAL	5.8
1	B	171	VAL	5.7
1	A	-6	HIS	5.6
1	A	271	VAL	5.4
1	C	237	ALA	5.4
1	A	-9	GLY	5.3
1	A	-1	GLY	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	-3	HIS	5.0
1	B	137	LEU	4.9
1	B	-5	HIS	4.7
1	C	236	THR	4.1
1	C	135	ASP	4.1
1	B	170	GLU	3.9
1	C	139	LYS	3.8
1	A	139	LYS	3.8
1	C	-3	HIS	3.7
1	A	133	VAL	3.7
1	C	238	ASP	3.6
1	A	270	THR	3.3
1	C	-5	HIS	3.1
1	C	140	GLY	3.0
1	C	-2	HIS	2.9
1	A	135	ASP	2.9
1	A	67	GLY	2.8
1	C	263	TRP	2.8
1	B	270	THR	2.7
1	B	152	ARG	2.6
1	C	234	GLN	2.6
1	B	174	ILE	2.5
1	C	271	VAL	2.5
1	B	69	LEU	2.4
1	C	170	GLU	2.4
1	B	-4	HIS	2.4
1	C	55	MET	2.3
1	A	100	ALA	2.3
1	B	86	GLU	2.3
1	B	212	GLU	2.2
1	B	258	GLN	2.2
1	A	174	ILE	2.2
1	A	170	GLU	2.2
1	A	68	THR	2.1
1	B	71	LYS	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	C	325	5/5	0.95	0.10	27,27,28,28	0
2	SO4	A	315	5/5	0.96	0.10	30,30,31,31	0

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

There are no such residues in this entry.