



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2017 – 12:48 PM EDT

PDB ID : 5LT3  
Title : nucleotide-free kinesin-1 motor domain T87A mutant, P1 crystal form  
Authors : Cao, L.; Gigant, B.  
Deposited on : unknown  
Resolution : 2.59 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.

---

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-20029824  
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-20029824

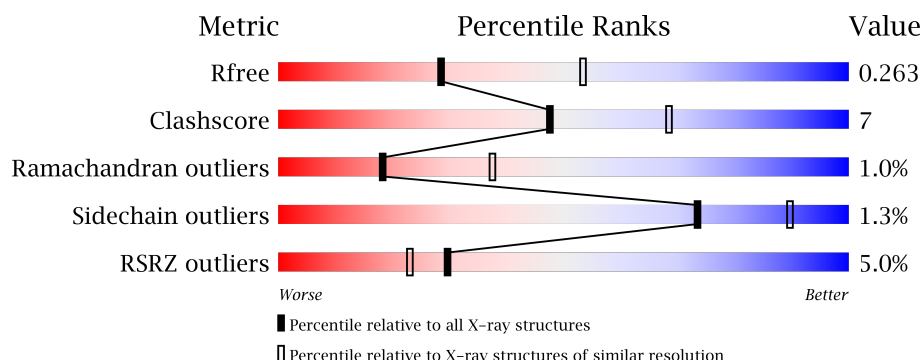
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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	325	<div> <div>2%</div> <div>80% 14% • 6%</div> </div>
1	B	325	<div> <div>9%</div> <div>78% 15% 6%</div> </div>
1	C	325	<div> <div>3%</div> <div>76% 16% 8%</div> </div>
1	D	325	<div> <div>2%</div> <div>80% 15% • •</div> </div>
1	E	325	<div> <div>6%</div> <div>80% 14% 5%</div> </div>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	K	325	

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	D	403	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14006 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 Kinesin-1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	1	0
			2334	1455	402	468	9			
1	B	305	Total	C	N	O	S	0	0	0
			2251	1411	384	447	9			
1	C	300	Total	C	N	O	S	0	0	0
			2280	1427	391	453	9			
1	D	311	Total	C	N	O	S	0	0	0
			2335	1460	405	461	9			
1	E	308	Total	C	N	O	S	0	0	0
			2253	1412	388	444	9			
1	K	312	Total	C	N	O	S	0	0	0
			2313	1452	400	452	9			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	SER	CYS	engineered mutation	UNP P33176
A	65	ALA	CYS	engineered mutation	UNP P33176
A	87	ALA	THR	engineered mutation	UNP P33176
A	168	ALA	CYS	engineered mutation	UNP P33176
A	174	SER	CYS	engineered mutation	UNP P33176
A	294	ALA	CYS	engineered mutation	UNP P33176
B	7	SER	CYS	engineered mutation	UNP P33176
B	65	ALA	CYS	engineered mutation	UNP P33176
B	87	ALA	THR	engineered mutation	UNP P33176
B	168	ALA	CYS	engineered mutation	UNP P33176
B	174	SER	CYS	engineered mutation	UNP P33176
B	294	ALA	CYS	engineered mutation	UNP P33176
C	7	SER	CYS	engineered mutation	UNP P33176
C	65	ALA	CYS	engineered mutation	UNP P33176
C	87	ALA	THR	engineered mutation	UNP P33176
C	168	ALA	CYS	engineered mutation	UNP P33176
C	174	SER	CYS	engineered mutation	UNP P33176

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	294	ALA	CYS	engineered mutation	UNP P33176
D	7	SER	CYS	engineered mutation	UNP P33176
D	65	ALA	CYS	engineered mutation	UNP P33176
D	87	ALA	THR	engineered mutation	UNP P33176
D	168	ALA	CYS	engineered mutation	UNP P33176
D	174	SER	CYS	engineered mutation	UNP P33176
D	294	ALA	CYS	engineered mutation	UNP P33176
E	7	SER	CYS	engineered mutation	UNP P33176
E	65	ALA	CYS	engineered mutation	UNP P33176
E	87	ALA	THR	engineered mutation	UNP P33176
E	168	ALA	CYS	engineered mutation	UNP P33176
E	174	SER	CYS	engineered mutation	UNP P33176
E	294	ALA	CYS	engineered mutation	UNP P33176
K	7	SER	CYS	engineered mutation	UNP P33176
K	65	ALA	CYS	engineered mutation	UNP P33176
K	87	ALA	THR	engineered mutation	UNP P33176
K	168	ALA	CYS	engineered mutation	UNP P33176
K	174	SER	CYS	engineered mutation	UNP P33176
K	294	ALA	CYS	engineered mutation	UNP P33176

- 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

Continued on next page...

*Continued from previous page...*

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

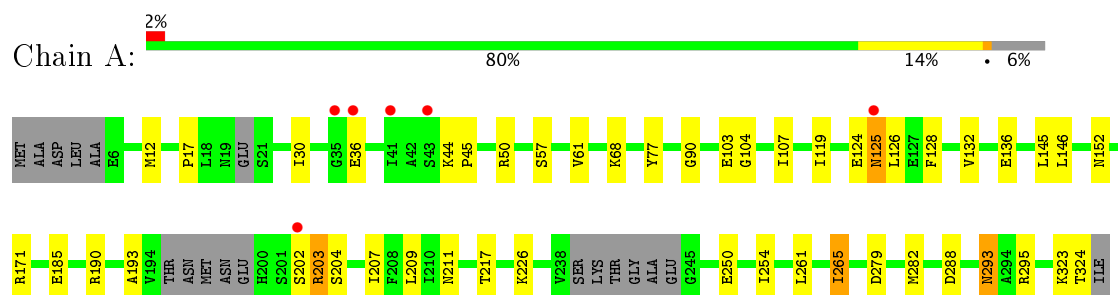
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total	O	0	0
			45	45		
3	B	28	Total	O	0	0
			28	28		
3	C	36	Total	O	0	0
			36	36		
3	D	40	Total	O	0	0
			40	40		
3	E	27	Total	O	0	0
			27	27		
3	K	24	Total	O	0	0
			24	24		

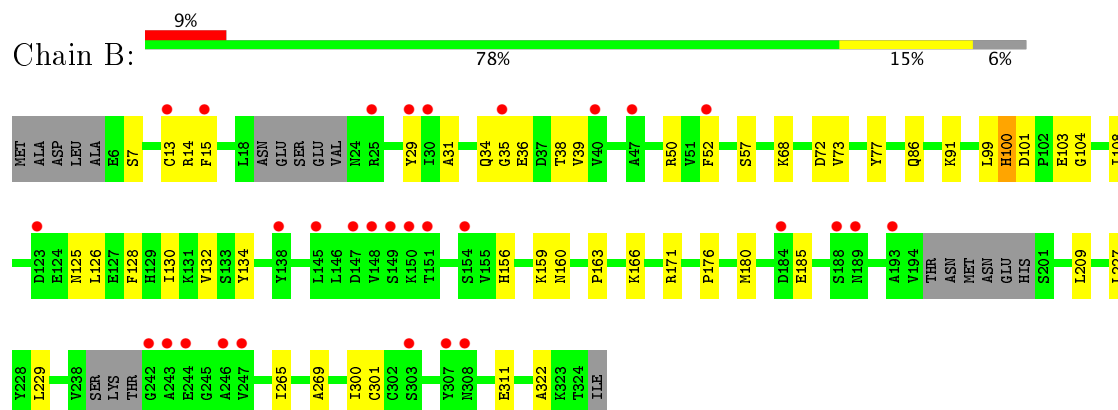
### 3 Residue-property plots [i](#)

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.

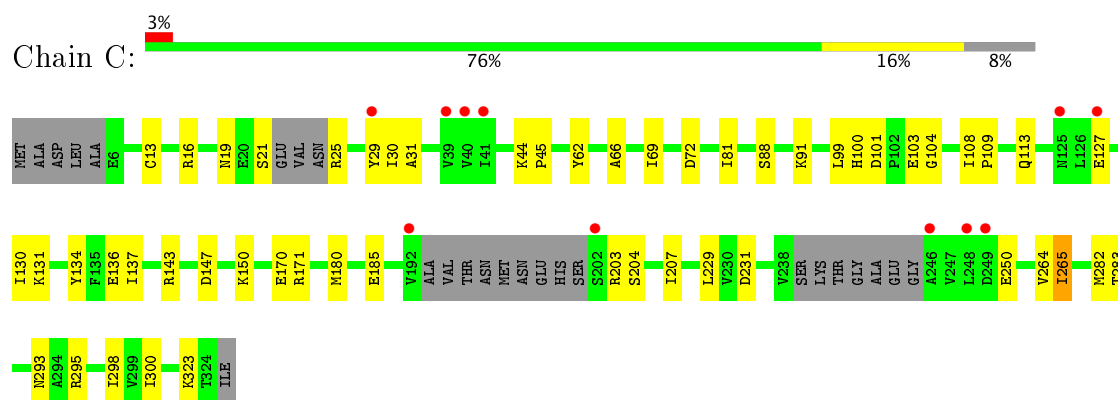
- Molecule 1: Kinesin-1 heavy chain



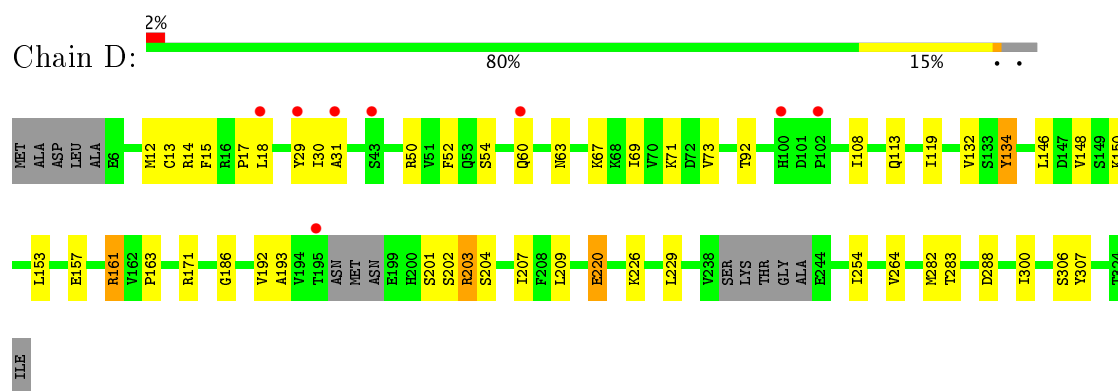
- Molecule 1: Kinesin-1 heavy chain



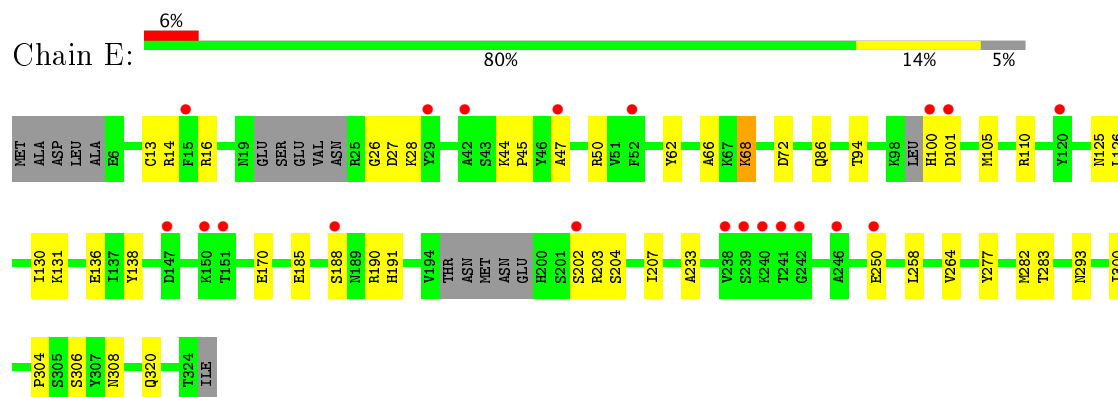
- Molecule 1: Kinesin-1 heavy chain



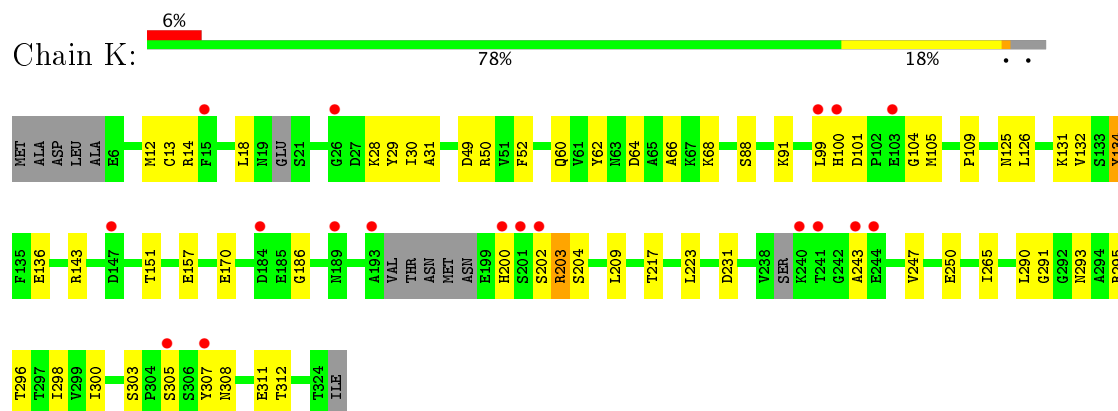
- Molecule 1: Kinesin-1 heavy chain



- Molecule 1: Kinesin-1 heavy chain



- Molecule 1: Kinesin-1 heavy chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.67Å 101.30Å 101.53Å 119.57° 91.91° 91.75°	Depositor
Resolution (Å)	33.18 – 2.59 48.86 – 2.59	Depositor EDS
% Data completeness (in resolution range)	97.2 (33.18-2.59) 77.1 (48.86-2.59)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.25 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.203 , 0.263 0.206 , 0.263	Depositor DCC
$R_{free}$ test set	2762 reflections (4.91%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtriage
Anisotropy	0.556	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 57.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.026 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	14006	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% 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 [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	0/2368	0.69	0/3200
1	B	0.45	0/2286	0.66	0/3098
1	C	0.49	0/2315	0.66	0/3129
1	D	0.48	0/2370	0.66	0/3205
1	E	0.45	0/2287	0.63	0/3103
1	K	0.46	0/2348	0.67	0/3180
All	All	0.47	0/13974	0.66	0/18915

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PRO	Peptide

### 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	2334	0	2216	35	0
1	B	2251	0	2098	35	0
1	C	2280	0	2165	28	0
1	D	2335	0	2219	32	0
1	E	2253	0	2064	27	0
1	K	2313	0	2170	33	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	15	0	0	0	0
2	E	5	0	0	0	0
2	K	5	0	0	0	0
3	A	45	0	0	3	0
3	B	28	0	0	0	0
3	C	36	0	0	4	0
3	D	40	0	0	6	0
3	E	27	0	0	3	0
3	K	24	0	0	1	0
All	All	14006	0	12932	188	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 (188) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:MET:HG2	1:A:50:ARG:HB2	1.51	0.91
1:C:16:ARG:NH1	1:C:88:SER:O	2.18	0.76
1:A:202:SER:O	1:A:204:SER:N	2.21	0.74
1:D:226:LYS:NZ	1:D:288:ASP:OD2	2.19	0.74
1:C:69:ILE:HG21	3:C:521:HOH:O	1.86	0.73
1:E:202:SER:O	1:E:204:SER:N	2.20	0.73
1:B:86:GLN:HG2	1:B:311:GLU:HB2	1.71	0.73
1:B:29:TYR:CZ	1:B:31:ALA:HB3	2.23	0.73
1:D:12:MET:HG2	1:D:50:ARG:HB2	1.72	0.72
1:D:220:GLU:OE2	3:D:501:HOH:O	2.06	0.72
1:E:190:ARG:O	3:E:501:HOH:O	2.08	0.71
1:C:103:GLU:H	1:C:104:GLY:HA3	1.58	0.69
1:D:157:GLU:OE1	1:D:161:ARG:NH2	2.27	0.67
1:B:156:HIS:CE1	1:B:166:LYS:HD3	2.30	0.67

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:101:ASP:OD2	1:K:104:GLY:N	2.27	0.66
1:D:203:ARG:HA	1:D:254:ILE:HD11	1.78	0.65
1:E:13:CYS:HA	1:E:300:ILE:HG13	1.79	0.65
1:A:103:GLU:N	1:A:104:GLY:HA3	2.12	0.65
1:D:119:ILE:O	3:D:502:HOH:O	2.14	0.64
1:A:226:LYS:NZ	1:A:288:ASP:OD2	2.27	0.64
1:B:34:GLN:OE1	1:B:36:GLU:N	2.31	0.64
1:C:113:GLN:NE2	3:C:502:HOH:O	2.30	0.63
1:K:12:MET:HG2	1:K:50:ARG:HB2	1.81	0.62
1:A:207:ILE:HD11	1:A:282:MET:HE2	1.82	0.62
1:K:13:CYS:HA	1:K:300:ILE:HG13	1.84	0.60
1:A:103:GLU:H	1:A:104:GLY:HA3	1.65	0.59
1:A:132:VAL:HG23	3:A:518:HOH:O	2.02	0.59
1:D:207:ILE:HD11	1:D:282:MET:HE2	1.84	0.59
1:K:68:LYS:NZ	1:K:295:ARG:HH11	2.00	0.59
1:E:293:ASN:ND2	3:E:503:HOH:O	2.35	0.58
1:E:185:GLU:O	1:E:188:SER:OG	2.21	0.58
1:E:131:LYS:HD2	1:E:170:GLU:HB3	1.86	0.57
1:K:60:GLN:NE2	1:K:64:ASP:OD2	2.36	0.57
1:D:17:PRO:HB3	1:D:54:SER:HB3	1.85	0.57
1:C:293:ASN:OD1	3:C:501:HOH:O	2.17	0.56
1:K:202:SER:O	1:K:204:SER:N	2.38	0.56
1:K:243:ALA:HB1	1:K:247:VAL:HG23	1.87	0.56
1:E:14:ARG:NH2	1:E:94:THR:OG1	2.33	0.56
1:D:113:GLN:HG2	3:D:540:HOH:O	2.05	0.55
1:K:99:LEU:HD13	1:K:100:HIS:ND1	2.21	0.55
1:C:108:ILE:HG12	1:C:229:LEU:HD13	1.87	0.55
1:B:156:HIS:HE1	1:B:166:LYS:HD3	1.71	0.55
1:D:60:GLN:NE2	1:D:63:ASN:HD22	2.04	0.55
1:D:17:PRO:HD3	1:D:54:SER:HA	1.90	0.54
1:K:303:SER:O	1:K:312:THR:HG21	2.08	0.53
1:E:190:ARG:CZ	1:E:202:SER:HB2	2.39	0.53
1:K:68:LYS:HZ3	1:K:295:ARG:HH11	1.54	0.53
1:A:211:ASN:HD22	1:A:226:LYS:HG2	1.74	0.53
1:D:14:ARG:HG3	1:D:52:PHE:HB2	1.91	0.52
1:B:73:VAL:HG21	1:B:227:LEU:HB2	1.92	0.52
1:K:91:LYS:HE3	1:K:231:ASP:OD2	2.10	0.52
1:B:108:ILE:HG12	1:B:229:LEU:HD13	1.91	0.52
1:E:68:LYS:NZ	1:E:72:ASP:OD2	2.35	0.52
1:C:207:ILE:HD11	1:C:282:MET:HE2	1.92	0.51
1:C:147:ASP:OD2	1:C:150:LYS:HG3	2.11	0.51

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:26:GLY:O	1:E:28:LYS:N	2.33	0.51
1:D:264:VAL:HG21	1:D:283:THR:HG21	1.93	0.51
1:B:29:TYR:CE2	1:B:31:ALA:HB3	2.46	0.51
1:D:202:SER:O	1:D:204:SER:N	2.44	0.50
1:B:34:GLN:OE1	1:B:35:GLY:N	2.44	0.50
1:A:57:SER:HB3	1:B:57:SER:HB3	1.94	0.50
1:B:265:ILE:HG23	1:B:322:ALA:HB2	1.93	0.50
1:A:203:ARG:HD3	1:A:250:GLU:OE1	2.11	0.49
1:D:67:LYS:HG2	1:D:71:LYS:HE2	1.93	0.49
1:A:68:LYS:NZ	1:A:295:ARG:HH11	2.10	0.49
1:D:69:ILE:O	1:D:73:VAL:HG23	2.13	0.49
1:E:264:VAL:HG21	1:E:283:THR:HG21	1.95	0.48
1:K:307:TYR:CG	1:K:308:ASN:N	2.81	0.48
1:A:125:ASN:HA	1:A:217:THR:HB	1.96	0.48
1:C:130:ILE:HD12	1:C:130:ILE:N	2.29	0.48
1:C:131:LYS:HD2	1:C:170:GLU:HB3	1.94	0.48
1:E:16:ARG:O	1:E:304:PRO:HG3	2.13	0.48
1:B:34:GLN:CB	1:B:38:THR:HB	2.43	0.48
1:B:7:SER:HB3	1:B:269:ALA:HA	1.95	0.48
1:A:36:GLU:HB3	1:A:50:ARG:HH21	1.77	0.48
1:B:13:CYS:HA	1:B:300:ILE:HG13	1.95	0.48
1:C:72:ASP:OD2	1:C:295:ARG:HG3	2.13	0.48
1:K:307:TYR:CD1	1:K:308:ASN:N	2.81	0.48
1:B:99:LEU:O	1:B:100:HIS:ND1	2.46	0.47
1:A:77:TYR:HE1	1:A:293:ASN:HD22	1.60	0.47
1:K:62:TYR:CD1	1:K:66:ALA:HB3	2.50	0.47
1:A:125:ASN:O	1:A:126:LEU:HD12	2.15	0.47
1:C:264:VAL:HG21	1:C:283:THR:HG21	1.97	0.47
1:B:159:LYS:HE2	1:B:160:ASN:OD1	2.14	0.47
1:K:132:VAL:HA	1:K:209:LEU:O	2.15	0.47
1:C:21:SER:HA	1:C:25:ARG:N	2.30	0.46
1:B:126:LEU:HB3	1:B:128:PHE:CE1	2.51	0.46
1:A:132:VAL:HA	1:A:209:LEU:O	2.15	0.46
1:A:211:ASN:ND2	1:A:226:LYS:CG	2.79	0.46
1:E:105:MET:O	1:E:110:ARG:NH1	2.44	0.46
1:K:88:SER:O	1:K:88:SER:OG	2.27	0.46
1:C:29:TYR:O	1:C:31:ALA:N	2.49	0.46
1:D:134:TYR:CD2	1:D:186:GLY:HA3	2.51	0.45
1:K:105:MET:HB2	1:K:109:PRO:HG2	1.98	0.45
1:E:130:ILE:N	1:E:130:ILE:HD12	2.32	0.45
1:B:91:LYS:HA	1:B:301:CYS:SG	2.56	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:ILE:HG13	3:C:521:HOH:O	2.16	0.45
1:A:211:ASN:HD22	1:A:226:LYS:CG	2.29	0.45
1:A:261:LEU:HG	1:A:265:ILE:HD12	1.99	0.45
1:B:103:GLU:H	1:B:104:GLY:HA3	1.81	0.45
1:B:29:TYR:HD1	1:B:29:TYR:HA	1.63	0.45
1:E:47:ALA:O	1:E:320:GLN:NE2	2.45	0.45
1:B:99:LEU:O	1:B:100:HIS:CB	2.64	0.45
1:K:134:TYR:CD2	1:K:186:GLY:HA3	2.52	0.45
1:A:152:ASN:OD1	1:D:171:ARG:NH2	2.44	0.45
1:B:99:LEU:O	1:B:100:HIS:HB3	2.16	0.45
1:B:130:ILE:HD12	1:B:130:ILE:N	2.32	0.45
1:E:207:ILE:HD11	1:E:282:MET:HE2	1.99	0.45
1:K:131:LYS:HD2	1:K:170:GLU:HB3	1.99	0.45
1:C:136:GLU:OE2	1:C:143:ARG:NH1	2.50	0.45
1:A:279:ASP:HB2	3:A:522:HOH:O	2.17	0.44
1:K:14:ARG:HG3	1:K:52:PHE:HB2	2.00	0.44
1:A:171:ARG:NH1	1:A:185:GLU:OE1	2.40	0.44
1:B:99:LEU:HD12	1:B:99:LEU:O	2.18	0.44
1:D:163:PRO:HD2	1:D:288:ASP:HB3	2.00	0.44
1:E:264:VAL:HG23	3:E:505:HOH:O	2.17	0.43
1:E:62:TYR:CD1	1:E:66:ALA:HB3	2.53	0.43
1:A:324:THR:HG23	3:A:515:HOH:O	2.18	0.43
1:K:308:ASN:HB3	1:K:311:GLU:CB	2.48	0.43
1:D:92:THR:HA	3:D:537:HOH:O	2.17	0.43
1:E:306:SER:C	1:E:308:ASN:H	2.20	0.43
1:A:190:ARG:CZ	1:A:202:SER:HB3	2.48	0.43
1:C:109:PRO:HA	1:C:180:MET:CE	2.49	0.43
1:D:148:VAL:HG22	3:D:526:HOH:O	2.19	0.43
1:E:138:TYR:CE1	1:E:250:GLU:HG2	2.54	0.43
1:K:203:ARG:HD3	1:K:250:GLU:OE1	2.18	0.43
1:K:290:LEU:HD13	1:K:296:THR:HG21	2.00	0.43
1:K:28:LYS:O	1:K:305:SER:HA	2.18	0.43
1:K:29:TYR:O	1:K:31:ALA:N	2.51	0.43
1:D:150:LYS:HB3	1:D:153:LEU:HD21	2.00	0.43
1:A:44:LYS:HA	1:A:45:PRO:HD3	1.91	0.43
1:C:62:TYR:CD1	1:C:66:ALA:HB3	2.54	0.43
1:D:13:CYS:HA	1:D:300:ILE:HG13	2.01	0.43
1:C:171:ARG:HH12	1:C:185:GLU:CD	2.22	0.42
1:D:17:PRO:HA	1:D:18:LEU:HA	1.80	0.42
1:E:125:ASN:O	1:E:126:LEU:HD12	2.19	0.42
1:K:136:GLU:OE2	1:K:143:ARG:NH1	2.52	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ASN:O	1:B:126:LEU:HD12	2.19	0.42
1:E:136:GLU:OE2	1:E:191:HIS:ND1	2.40	0.42
1:K:265:ILE:HD13	1:K:298:ILE:HD11	2.01	0.42
1:A:211:ASN:ND2	1:A:226:LYS:HG3	2.34	0.42
1:B:159:LYS:HE2	1:B:159:LYS:HB3	1.65	0.42
1:D:193:ALA:HB3	1:D:203:ARG:HD2	2.01	0.42
1:B:156:HIS:O	1:B:163:PRO:HA	2.19	0.42
1:E:233:ALA:O	1:E:258:LEU:HD11	2.19	0.42
1:K:125:ASN:HA	1:K:217:THR:HB	2.01	0.42
1:B:72:ASP:HB3	1:B:77:TYR:HB2	2.02	0.42
1:C:203:ARG:HD3	1:C:250:GLU:OE1	2.20	0.42
1:C:91:LYS:HE3	1:C:231:ASP:OD1	2.20	0.42
1:D:226:LYS:NZ	3:D:504:HOH:O	2.46	0.42
1:K:125:ASN:O	1:K:126:LEU:HD12	2.19	0.42
1:B:132:VAL:HA	1:B:209:LEU:O	2.20	0.42
1:C:103:GLU:N	1:C:104:GLY:HA3	2.26	0.42
1:D:108:ILE:HG12	1:D:229:LEU:HD13	2.01	0.42
1:D:29:TYR:O	1:D:31:ALA:N	2.53	0.41
1:E:50:ARG:HH11	1:E:50:ARG:HG3	1.85	0.41
1:K:49:ASP:O	1:K:50:ARG:HG2	2.20	0.41
1:A:61:VAL:HG12	1:A:107:ILE:HD11	2.01	0.41
1:A:323:LYS:HA	1:A:323:LYS:HD2	1.86	0.41
1:E:44:LYS:HA	1:E:45:PRO:HD3	1.97	0.41
1:B:265:ILE:CG2	1:B:322:ALA:HB2	2.50	0.41
1:C:44:LYS:HA	1:C:45:PRO:HD3	1.93	0.41
1:A:136:GLU:HG2	1:A:145:LEU:HD21	2.00	0.41
1:K:291:GLY:N	3:K:501:HOH:O	2.34	0.41
1:B:101:ASP:C	1:B:103:GLU:H	2.22	0.41
1:C:99:LEU:C	1:C:101:ASP:H	2.23	0.41
1:D:132:VAL:HA	1:D:209:LEU:O	2.21	0.41
1:D:192:VAL:HG13	1:D:201:SER:O	2.21	0.41
1:E:100:HIS:ND1	1:E:100:HIS:O	2.53	0.41
1:E:277:TYR:O	1:E:283:THR:OG1	2.28	0.41
1:A:202:SER:C	1:A:204:SER:H	2.20	0.41
1:B:176:PRO:O	1:B:180:MET:HG2	2.21	0.41
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.88	0.41
1:B:171:ARG:HH12	1:B:185:GLU:CD	2.23	0.41
1:C:137:ILE:O	1:C:204:SER:HB2	2.20	0.41
1:C:265:ILE:HD13	1:C:298:ILE:HD11	2.03	0.41
1:B:15:PHE:CE2	1:B:39:VAL:HG21	2.56	0.41
1:A:90:GLY:N	2:A:401:SO4:O4	2.36	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:223:LEU:HA	1:K:223:LEU:HD23	1.73	0.40
1:K:68:LYS:HZ3	1:K:295:ARG:HG3	1.84	0.40
1:C:13:CYS:HA	1:C:300:ILE:HG13	2.02	0.40
1:D:13:CYS:HG	1:D:15:PHE:HE1	1.67	0.40
1:D:146:LEU:HD23	1:D:146:LEU:HA	1.91	0.40
1:A:193:ALA:HB3	1:A:203:ARG:HD2	2.02	0.40
1:B:14:ARG:HG3	1:B:52:PHE:HB2	2.03	0.40
1:C:171:ARG:NH1	1:C:185:GLU:OE1	2.49	0.40
1:A:119:ILE:HG12	1:A:128:PHE:CD1	2.57	0.40
1:A:203:ARG:HA	1:A:254:ILE:HD11	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	300/325 (92%)	290 (97%)	6 (2%)	4 (1%)	14	29
1	B	297/325 (91%)	282 (95%)	14 (5%)	1 (0%)	44	70
1	C	292/325 (90%)	280 (96%)	9 (3%)	3 (1%)	18	37
1	D	305/325 (94%)	292 (96%)	10 (3%)	3 (1%)	18	37
1	E	300/325 (92%)	284 (95%)	13 (4%)	3 (1%)	18	37
1	K	304/325 (94%)	292 (96%)	8 (3%)	4 (1%)	14	29
All	All	1798/1950 (92%)	1720 (96%)	60 (3%)	18 (1%)	18	37

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	ILE
1	A	124	GLU

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	A	203	ARG
1	D	30	ILE
1	D	203	ARG
1	E	203	ARG
1	K	203	ARG
1	A	125	ASN
1	B	100	HIS
1	D	307	TYR
1	E	27	ASP
1	K	18	LEU
1	C	30	ILE
1	C	100	HIS
1	K	30	ILE
1	C	19	ASN
1	E	101	ASP
1	K	200	HIS

### 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	248/285 (87%)	246 (99%)	2 (1%)	85	94
1	B	230/285 (81%)	227 (99%)	3 (1%)	73	90
1	C	241/285 (85%)	237 (98%)	4 (2%)	66	86
1	D	244/285 (86%)	240 (98%)	4 (2%)	68	87
1	E	221/285 (78%)	219 (99%)	2 (1%)	82	93
1	K	234/285 (82%)	230 (98%)	4 (2%)	66	86
All	All	1418/1710 (83%)	1399 (99%)	19 (1%)	73	90

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	265	ILE
1	A	293	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	50	ARG
1	B	68	LYS
1	B	134	TYR
1	C	127	GLU
1	C	134	TYR
1	C	265	ILE
1	C	323	LYS
1	D	134	TYR
1	D	161	ARG
1	D	220	GLU
1	D	306	SER
1	E	68	LYS
1	E	86	GLN
1	K	134	TYR
1	K	151	THR
1	K	157	GLU
1	K	293	ASN

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

Mol	Chain	Res	Type
1	A	211	ASN
1	A	293	ASN
1	B	156	HIS
1	C	113	GLN
1	C	293	ASN
1	D	60	GLN
1	E	293	ASN
1	K	113	GLN
1	K	308	ASN

### 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

8 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	0.21	0	6,6,6	0.17	0
2	SO4	B	401	-	4,4,4	0.18	0	6,6,6	0.18	0
2	SO4	C	401	-	4,4,4	0.23	0	6,6,6	0.25	0
2	SO4	D	401	-	4,4,4	0.16	0	6,6,6	0.23	0
2	SO4	D	402	-	4,4,4	0.23	0	6,6,6	0.25	0
2	SO4	D	403	-	4,4,4	0.37	0	6,6,6	0.13	0
2	SO4	E	401	-	4,4,4	0.20	0	6,6,6	0.16	0
2	SO4	K	401	-	4,4,4	0.20	0	6,6,6	0.38	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	D	402	-	-	0/0/0/0	0/0/0/0
2	SO4	D	403	-	-	0/0/0/0	0/0/0/0
2	SO4	E	401	-	-	0/0/0/0	0/0/0/0
2	SO4	K	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	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	307/325 (94%)	0.23	6 (1%) 65 59	20, 36, 71, 95	0
1	B	305/325 (93%)	0.68	30 (9%) 8 5	28, 54, 90, 117	0
1	C	300/325 (92%)	0.40	11 (3%) 42 34	19, 40, 71, 90	0
1	D	311/325 (95%)	0.24	8 (2%) 56 49	22, 41, 72, 100	0
1	E	308/325 (94%)	0.54	20 (6%) 20 14	24, 51, 88, 117	0
1	K	312/325 (96%)	0.46	18 (5%) 24 18	23, 48, 88, 108	0
All	All	1843/1950 (94%)	0.43	93 (5%) 30 23	19, 45, 84, 117	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	243	ALA	7.8
1	B	35	GLY	7.5
1	E	239	SER	7.0
1	B	29	TYR	5.8
1	K	99	LEU	5.1
1	E	240	LYS	4.9
1	E	241	THR	4.7
1	K	307	TYR	4.5
1	E	29	TYR	4.4
1	E	242	GLY	4.4
1	B	15	PHE	4.3
1	K	243	ALA	4.3
1	E	100	HIS	4.2
1	B	244	GLU	4.2
1	C	40	VAL	4.1
1	K	241	THR	3.9
1	C	249	ASP	3.8
1	B	13	CYS	3.7
1	B	149	SER	3.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	246	ALA	3.6
1	C	41	ILE	3.6
1	B	148	VAL	3.5
1	K	103	GLU	3.5
1	B	30	ILE	3.4
1	K	202	SER	3.3
1	K	193	ALA	3.3
1	E	238	VAL	3.3
1	B	154	SER	3.2
1	E	150	LYS	3.1
1	B	25	ARG	3.1
1	E	15	PHE	3.1
1	K	15	PHE	3.1
1	C	192	VAL	3.0
1	K	147	ASP	3.0
1	B	151	THR	3.0
1	K	244	GLU	3.0
1	B	40	VAL	3.0
1	C	29	TYR	2.9
1	E	246	ALA	2.9
1	E	202	SER	2.9
1	B	247	VAL	2.8
1	E	151	THR	2.8
1	D	18	LEU	2.8
1	K	201	SER	2.7
1	E	52	PHE	2.7
1	C	248	LEU	2.7
1	A	36	GLU	2.7
1	C	246	ALA	2.7
1	E	188	SER	2.6
1	B	47	ALA	2.6
1	B	242	GLY	2.6
1	D	43	SER	2.6
1	A	43	SER	2.6
1	B	303	SER	2.6
1	A	41	ILE	2.6
1	K	305	SER	2.6
1	D	195	THR	2.5
1	A	202	SER	2.5
1	B	193	ALA	2.5
1	B	147	ASP	2.5
1	B	184	ASP	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	E	42	ALA	2.5
1	E	147	ASP	2.4
1	B	307	TYR	2.4
1	E	101	ASP	2.4
1	B	189	ASN	2.4
1	E	47	ALA	2.3
1	C	125	ASN	2.3
1	B	150	LYS	2.3
1	B	52	PHE	2.3
1	D	102	PRO	2.3
1	A	35	GLY	2.3
1	K	189	ASN	2.3
1	B	188	SER	2.3
1	B	123	ASP	2.3
1	D	100	HIS	2.3
1	B	308	ASN	2.2
1	D	60	GLN	2.2
1	B	145	LEU	2.2
1	C	127	GLU	2.2
1	C	202	SER	2.2
1	D	29	TYR	2.2
1	K	240	LYS	2.2
1	K	100	HIS	2.1
1	K	200	HIS	2.1
1	E	120	TYR	2.1
1	E	250	GLU	2.1
1	D	31	ALA	2.1
1	C	39	VAL	2.0
1	K	26	GLY	2.0
1	K	184	ASP	2.0
1	A	125	ASN	2.0
1	B	138	TYR	2.0

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

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

## 6.3 Carbohydrates ⓘ

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	D	403	5/5	0.82	0.33	4.49	60,63,64,64	0
2	SO4	D	401	5/5	0.94	0.15	-0.62	44,47,53,56	0
2	SO4	D	402	5/5	0.93	0.16	-0.76	63,63,66,71	0
2	SO4	E	401	5/5	0.92	0.12	-1.05	68,69,77,78	0
2	SO4	K	401	5/5	0.89	0.12	-1.66	61,65,68,68	0
2	SO4	C	401	5/5	0.95	0.12	-1.78	38,58,62,70	0
2	SO4	B	401	5/5	0.96	0.10	-1.89	68,68,71,78	0
2	SO4	A	401	5/5	0.95	0.11	-2.34	49,54,56,58	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.