



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:46 PM GMT

PDB ID : 4JFD  
Title : Preservation of peptide specificity during TCR-MHC contact dominated affinity enhancement of a melanoma-specific TCR  
Authors : Rizkallah, P.J.; Cole, D.K.; Madura, F.; Sewell, A.K.  
Deposited on : 2013-02-28  
Resolution : 2.46 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

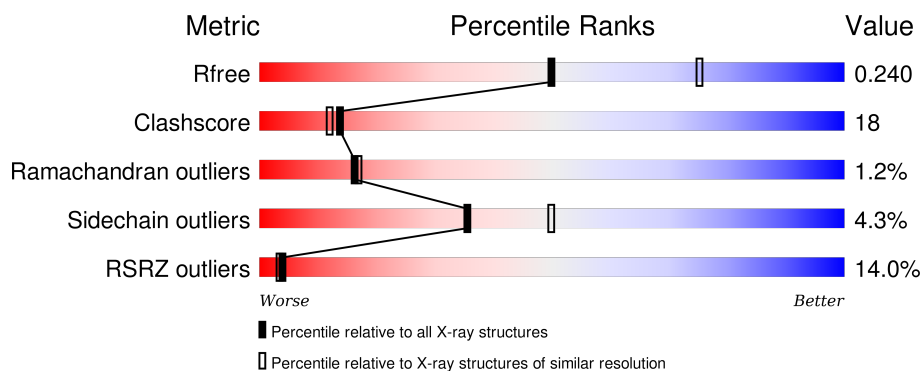
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.46 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	276	<div> <div>28%</div> <div>68%</div> <div>28%</div> <div>•</div> </div>
2	B	100	<div> <div>8%</div> <div>74%</div> <div>24%</div> <div>•</div> </div>
3	C	10	<div> <div>60%</div> <div>40%</div> </div>
4	D	196	<div> <div>12%</div> <div>72%</div> <div>22%</div> <div>5%</div> <div>•</div> </div>
5	E	245	<div> <div>2%</div> <div>71%</div> <div>27%</div> <div>•</div> </div>

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
7	SO4	A	303	-	-	X	-
7	SO4	A	304	-	-	X	-
7	SO4	A	305	-	-	X	-
7	SO4	E	302	-	-	-	X
7	SO4	E	305	-	-	X	-
7	SO4	E	306	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6820 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 HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2253	1408	410	426	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	INITIATING METHIONINE	UNP P61769

- Molecule 3 is a protein called Melanoma peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	10	Total	C	N	O	0	0	0
			70	46	10	14			

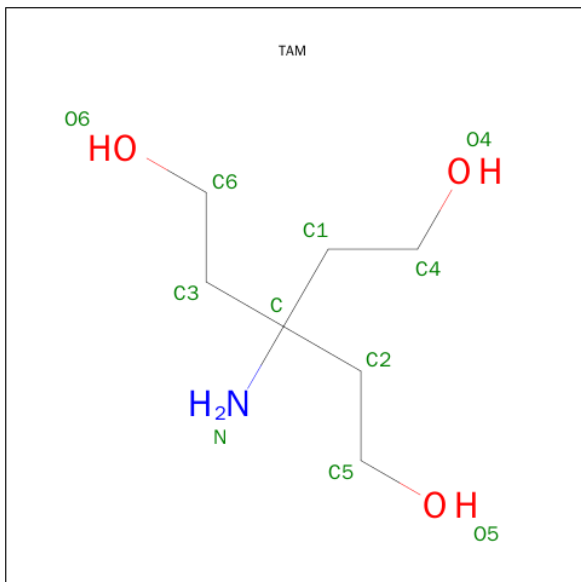
- Molecule 4 is a protein called High Affinity TCR Alpha Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	196	Total	C	N	O	S	0	0	0
			1525	947	255	315	8			

- Molecule 5 is a protein called High Affinity TCR Beta Chain.

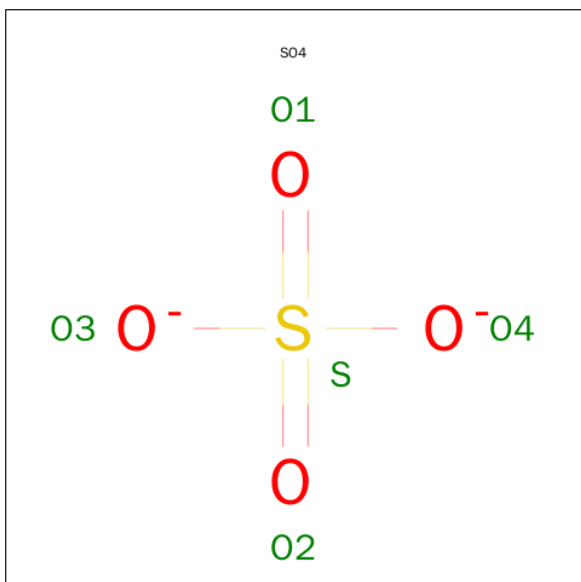
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	245	Total	C	N	O	S	0	0	0
			1944	1235	334	368	7			

- Molecule 6 is TRIS(HYDROXYETHYL)AMINOMETHANE (three-letter code: TAM) (formula:  $C_7H_{17}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		
7	E	1	Total	O	S	0	0
			5	4	1		

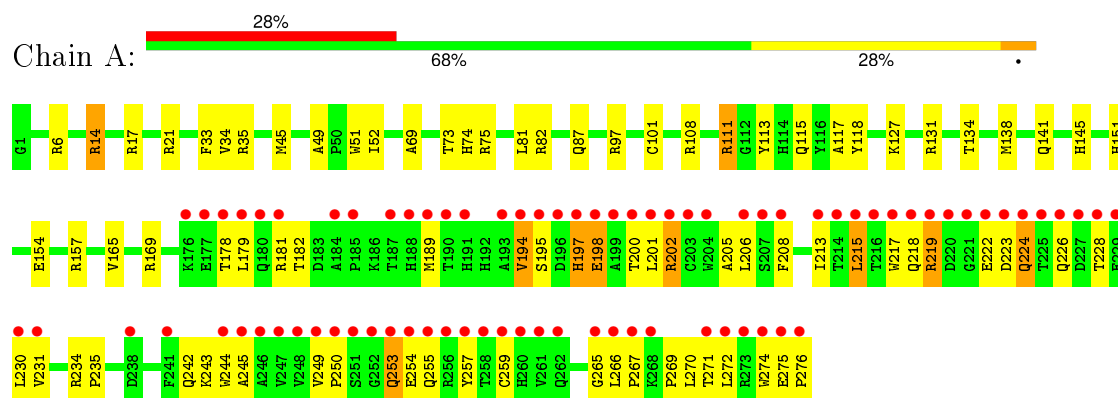
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	31	Total	O	0	0
			31	31		
8	B	13	Total	O	0	0
			13	13		
8	C	1	Total	O	0	0
			1	1		
8	D	32	Total	O	0	0
			32	32		
8	E	48	Total	O	0	0
			48	48		

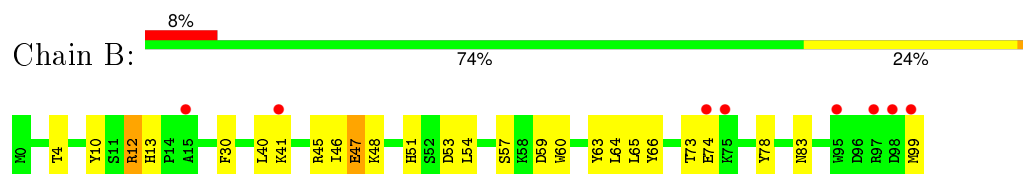
### 3 Residue-property plots [i](#)

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: HLA class I histocompatibility antigen, A-2 alpha chain



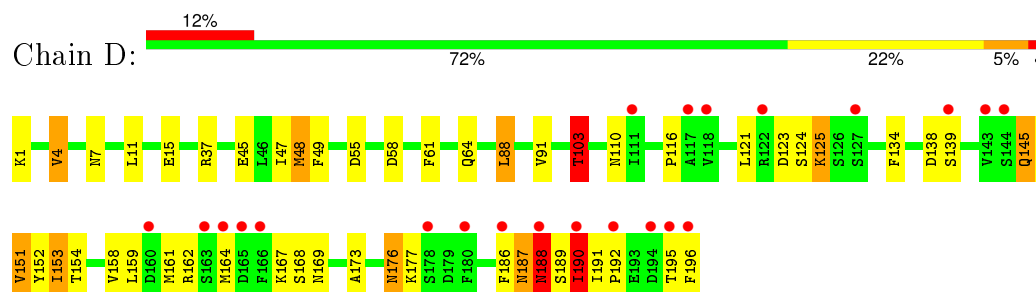
- Molecule 2: Beta-2-microglobulin



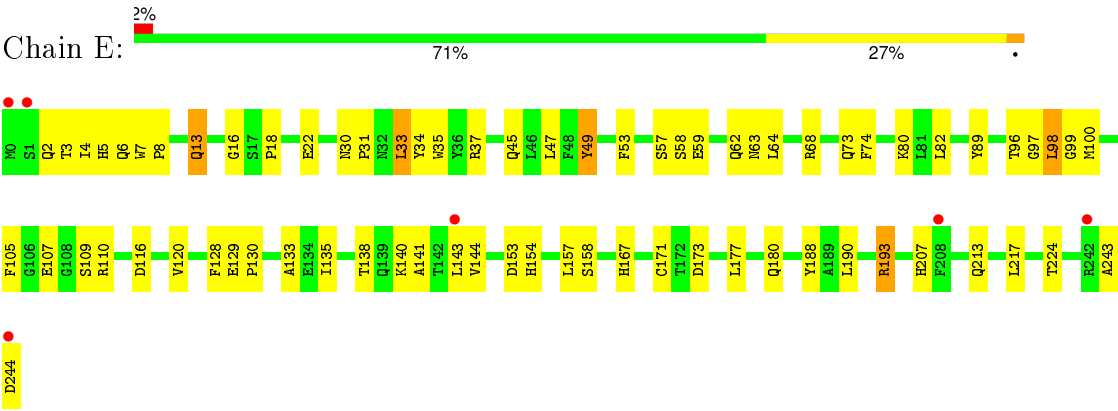
- Molecule 3: Melanoma peptide



- Molecule 4: High Affinity TCR Alpha Chain



- Molecule 5: High Affinity TCR Beta Chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.49 Å 121.49 Å 82.96 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.33 – 2.46 54.33 – 2.46	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.33-2.46) 100.0 (54.33-2.46)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 2.45 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.202 , 0.248 0.195 , 0.240	Depositor DCC
$R_{free}$ test set	2220 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.1	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.5	EDS
Estimated twinning fraction	0.033 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 44161 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6820	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: TAM, 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	0.98	2/2319 (0.1%)	0.54	0/3149
2	B	0.87	0/860	0.57	0/1162
3	C	1.09	0/69	0.60	0/92
4	D	1.04	5/1556 (0.3%)	0.61	0/2107
5	E	1.09	5/2003 (0.2%)	0.60	0/2732
All	All	1.02	12/6807 (0.2%)	0.58	0/9242

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
4	D	0	1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	CYS	CB-SG	-17.85	1.51	1.82
4	D	103	THR	CB-CG2	-7.12	1.28	1.52
4	D	4	VAL	CB-CG1	-6.32	1.39	1.52
5	E	180	GLN	CB-CG	5.82	1.68	1.52
4	D	91	VAL	CB-CG1	-5.60	1.41	1.52
5	E	6	GLN	CB-CG	-5.27	1.38	1.52
5	E	13	GLN	CB-CG	-5.22	1.38	1.52
5	E	116	ASP	CB-CG	5.12	1.62	1.51
4	D	45	GLU	CB-CG	-5.10	1.42	1.52
5	E	105	PHE	CG-CD2	-5.04	1.31	1.38
1	A	154	GLU	CG-CD	5.01	1.59	1.51
4	D	88	LEU	CG-CD1	-5.01	1.33	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	48	MET	Mainchain

## 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	2253	0	2103	99	0
2	B	837	0	803	25	0
3	C	70	0	81	5	0
4	D	1525	0	1439	60	0
5	E	1944	0	1848	74	0
6	A	11	0	17	2	0
7	A	25	0	0	9	0
7	E	30	0	0	5	0
8	A	31	0	0	0	0
8	B	13	0	0	1	0
8	C	1	0	0	0	0
8	D	32	0	0	0	0
8	E	48	0	0	3	0
All	All	6820	0	6291	240	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 18.

All (240) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:HD12	1:A:217:TRP:CZ2	1.66	1.30
5:E:63:ASN:ND2	5:E:82:LEU:HD13	1.65	1.11
1:A:131:ARG:NH2	7:A:303:SO4:O3	1.87	1.08
1:A:201:LEU:CD1	1:A:217:TRP:CZ2	2.46	0.99
1:A:215:LEU:HD11	1:A:245:ALA:HB2	1.45	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:63:ASN:HD21	5:E:82:LEU:HD13	1.19	0.97
1:A:201:LEU:HD13	1:A:202:ARG:N	1.82	0.94
4:D:147:LYS:O	4:D:149:SER:N	2.02	0.93
5:E:135:ILE:HD11	5:E:141:ALA:HB2	1.50	0.92
5:E:63:ASN:HD21	5:E:82:LEU:CD1	1.82	0.91
5:E:58:SER:N	7:E:305:SO4:O1	2.03	0.91
1:A:215:LEU:HD12	1:A:215:LEU:O	1.73	0.88
1:A:182:THR:HG21	1:A:265:GLY:HA3	1.54	0.88
1:A:194:VAL:HG13	1:A:195:SER:H	1.38	0.87
1:A:111:ARG:HD2	1:A:113:TYR:CZ	2.09	0.87
5:E:130:PRO:HD3	5:E:143:LEU:HD23	1.58	0.85
2:B:47:GLU:OE2	2:B:48:LYS:N	2.12	0.83
1:A:217:TRP:O	1:A:218:GLN:HG3	1.77	0.82
1:A:270:LEU:HD23	1:A:271:THR:N	1.96	0.80
1:A:201:LEU:HD12	1:A:217:TRP:HZ2	1.36	0.79
1:A:111:ARG:HD2	1:A:113:TYR:CE2	2.17	0.79
4:D:7:ASN:O	4:D:103:THR:HB	1.81	0.79
1:A:69:ALA:O	1:A:73:THR:HG23	1.84	0.78
1:A:266:LEU:HD12	1:A:267:PRO:HD2	1.64	0.77
1:A:201:LEU:CD1	1:A:217:TRP:HZ2	1.92	0.77
4:D:48:MET:HE1	4:D:61:PHE:O	1.85	0.77
5:E:3:THR:HG21	5:E:5:HIS:CE1	2.21	0.76
1:A:73:THR:HG21	5:E:97:GLY:HA2	1.67	0.76
4:D:190:ILE:N	4:D:190:ILE:HD12	2.02	0.75
1:A:21:ARG:NH1	7:A:302:SO4:O4	2.20	0.75
1:A:49:ALA:O	1:A:52:ILE:HG22	1.87	0.75
2:B:30:PHE:HZ	2:B:64:LEU:HD13	1.51	0.74
1:A:157:ARG:NH1	7:A:303:SO4:O2	2.20	0.74
1:A:201:LEU:HD12	1:A:217:TRP:CH2	2.23	0.74
2:B:63:TYR:C	2:B:64:LEU:HD12	2.08	0.73
4:D:195:THR:HG21	5:E:133:ALA:HB1	1.71	0.73
2:B:63:TYR:O	2:B:64:LEU:HD12	1.89	0.73
4:D:47:ILE:HG22	4:D:48:MET:HG3	1.71	0.72
1:A:157:ARG:NH1	7:A:303:SO4:O3	2.24	0.71
1:A:73:THR:CG2	5:E:97:GLY:HA2	2.20	0.71
5:E:243:ALA:O	5:E:244:ASP:OD1	2.08	0.71
4:D:190:ILE:HG22	4:D:191:ILE:H	1.55	0.70
1:A:215:LEU:CD1	1:A:245:ALA:HB2	2.20	0.69
1:A:217:TRP:O	1:A:218:GLN:CG	2.40	0.69
5:E:37:ARG:HD2	8:E:448:HOH:O	1.93	0.69
5:E:3:THR:CG2	5:E:5:HIS:CE1	2.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:130:PRO:HD3	5:E:143:LEU:CD2	2.23	0.68
4:D:48:MET:HE3	4:D:58:ASP:HB3	1.75	0.68
5:E:129:GLU:HA	5:E:143:LEU:HD23	1.75	0.67
1:A:228:THR:O	1:A:228:THR:HG22	1.94	0.67
4:D:146:SER:HB3	4:D:153:ILE:HG22	1.78	0.66
1:A:127:LYS:NZ	1:A:134:THR:OG1	2.26	0.66
4:D:37:ARG:HB2	4:D:47:ILE:HD11	1.77	0.66
4:D:159:LEU:HB3	5:E:171:CYS:HB2	1.77	0.65
1:A:215:LEU:HD12	1:A:215:LEU:C	2.16	0.65
1:A:33:PHE:CD2	1:A:34:VAL:HG13	2.31	0.65
5:E:110:ARG:HD3	5:E:154:HIS:CD2	2.31	0.65
1:A:201:LEU:HD13	1:A:201:LEU:C	2.17	0.65
1:A:74:HIS:HE1	1:A:97:ARG:HH21	1.45	0.63
4:D:164:MET:SD	5:E:140:LYS:HD3	2.38	0.63
4:D:189:SER:C	4:D:190:ILE:HD12	2.19	0.63
4:D:161:MET:HE1	5:E:140:LYS:HD2	1.81	0.63
3:C:9:THR:HG21	5:E:96:THR:HG21	1.81	0.63
2:B:30:PHE:CZ	2:B:64:LEU:HD13	2.33	0.62
5:E:63:ASN:O	5:E:64:LEU:HD12	1.99	0.62
1:A:51:TRP:CZ2	1:A:179:LEU:HD11	2.35	0.62
1:A:157:ARG:NH1	7:A:303:SO4:S	2.71	0.62
5:E:37:ARG:HB2	5:E:47:LEU:HD21	1.80	0.62
4:D:176:ASN:HD22	4:D:176:ASN:H	1.47	0.62
1:A:231:VAL:CG2	1:A:244:TRP:CZ2	2.84	0.61
1:A:275:GLU:N	1:A:276:PRO:CD	2.63	0.61
5:E:63:ASN:C	5:E:64:LEU:HD12	2.21	0.61
1:A:218:GLN:HE22	1:A:222:GLU:C	2.02	0.61
4:D:191:ILE:O	4:D:191:ILE:HG22	2.01	0.61
5:E:22:GLU:OE2	5:E:73:GLN:NE2	2.34	0.60
1:A:74:HIS:CE1	1:A:97:ARG:HH21	2.19	0.60
4:D:123:ASP:HB3	5:E:128:PHE:CD2	2.36	0.60
1:A:215:LEU:CD1	1:A:245:ALA:CB	2.79	0.60
1:A:218:GLN:NE2	1:A:222:GLU:O	2.34	0.60
4:D:189:SER:O	4:D:190:ILE:HG13	2.01	0.60
5:E:224:THR:O	5:E:224:THR:HG22	2.01	0.59
1:A:197:HIS:O	1:A:198:GLU:C	2.39	0.59
4:D:186:PHE:O	4:D:188:ASN:ND2	2.36	0.59
1:A:215:LEU:HD11	1:A:245:ALA:CB	2.26	0.59
4:D:48:MET:HE1	4:D:61:PHE:C	2.22	0.59
2:B:54:LEU:CD1	2:B:64:LEU:HD11	2.32	0.59
6:A:301:TAM:O4	6:A:301:TAM:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:THR:O	1:A:181:ARG:HG2	2.03	0.59
5:E:45:GLN:NE2	8:E:414:HOH:O	2.33	0.58
1:A:75:ARG:HD2	5:E:53:PHE:CZ	2.38	0.58
1:A:235:PRO:HG2	2:B:65:LEU:HD22	1.86	0.58
4:D:195:THR:HG21	5:E:133:ALA:CB	2.33	0.58
4:D:187:ASN:ND2	4:D:187:ASN:O	2.37	0.58
5:E:13:GLN:NE2	5:E:18:PRO:O	2.38	0.56
4:D:1:LYS:HE2	8:E:414:HOH:O	2.03	0.56
1:A:205:ALA:C	1:A:206:LEU:HD22	2.25	0.56
1:A:253:GLN:H	1:A:253:GLN:NE2	2.03	0.56
1:A:201:LEU:CD1	1:A:217:TRP:CH2	2.84	0.56
4:D:116:PRO:HB2	4:D:192:PRO:HB3	1.87	0.56
1:A:231:VAL:HG23	1:A:244:TRP:CZ2	2.41	0.56
4:D:159:LEU:HD12	4:D:159:LEU:O	2.06	0.56
1:A:157:ARG:NH2	7:A:304:SO4:O1	2.39	0.56
5:E:138:THR:HG21	5:E:140:LYS:HE3	1.87	0.56
1:A:218:GLN:OE1	1:A:224:GLN:N	2.39	0.55
1:A:14:ARG:HB2	1:A:17:ARG:HD2	1.88	0.55
5:E:135:ILE:CD1	5:E:141:ALA:HB2	2.31	0.55
1:A:259:CYS:O	1:A:271:THR:HG22	2.06	0.55
1:A:208:PHE:CE2	1:A:242:GLN:HA	2.42	0.55
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.42	0.55
4:D:188:ASN:ND2	4:D:190:ILE:HD11	2.22	0.54
1:A:206:LEU:HD22	1:A:206:LEU:N	2.22	0.54
4:D:48:MET:CE	4:D:58:ASP:HB3	2.38	0.54
1:A:206:LEU:HD13	1:A:242:GLN:HB2	1.90	0.54
1:A:194:VAL:HG13	1:A:195:SER:N	2.17	0.53
1:A:270:LEU:C	1:A:270:LEU:HD23	2.28	0.53
1:A:231:VAL:HG21	1:A:244:TRP:CZ2	2.42	0.53
4:D:153:ILE:HD13	4:D:186:PHE:HE2	1.72	0.53
5:E:30:ASN:N	5:E:31:PRO:CD	2.71	0.53
4:D:153:ILE:HD12	4:D:154:THR:N	2.23	0.53
4:D:153:ILE:HD13	4:D:186:PHE:CE2	2.44	0.53
5:E:62:GLN:O	5:E:63:ASN:HB2	2.09	0.53
1:A:208:PHE:CD1	1:A:213:ILE:HD11	2.44	0.53
4:D:164:MET:O	4:D:164:MET:HG2	2.09	0.53
5:E:157:LEU:HD23	5:E:158:SER:N	2.24	0.53
2:B:40:LEU:HD23	2:B:45:ARG:HA	1.92	0.53
1:A:249:VAL:HB	1:A:250:PRO:HD2	1.91	0.52
2:B:99:MET:HG2	2:B:99:MET:OXT	2.09	0.52
1:A:253:GLN:N	1:A:253:GLN:NE2	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:C	1:A:201:LEU:CD1	2.77	0.52
1:A:253:GLN:H	1:A:253:GLN:HE21	1.58	0.52
4:D:190:ILE:HB	4:D:192:PRO:HD3	1.92	0.51
2:B:54:LEU:HD12	2:B:64:LEU:HD11	1.92	0.51
4:D:158:VAL:HG22	4:D:169:ASN:OD1	2.10	0.51
5:E:57:SER:HB2	5:E:59:GLU:OE1	2.10	0.51
5:E:37:ARG:CB	5:E:47:LEU:HD21	2.40	0.51
5:E:138:THR:HG21	5:E:140:LYS:CE	2.41	0.51
1:A:111:ARG:CD	1:A:113:TYR:CZ	2.88	0.50
5:E:3:THR:HG21	5:E:5:HIS:HE1	1.71	0.50
1:A:189:MET:HG2	1:A:272:LEU:HD23	1.94	0.50
5:E:35:TRP:CD1	5:E:74:PHE:CE2	2.99	0.50
5:E:177:LEU:HD12	5:E:177:LEU:O	2.12	0.49
2:B:12:ARG:NH1	2:B:13:HIS:ND1	2.61	0.49
1:A:234:ARG:HD2	2:B:10:TYR:CE2	2.48	0.49
5:E:120:VAL:HG21	5:E:217:LEU:HD21	1.95	0.49
1:A:35:ARG:HD3	2:B:53:ASP:OD2	2.13	0.49
5:E:157:LEU:HD23	5:E:157:LEU:C	2.33	0.49
4:D:188:ASN:ND2	4:D:189:SER:H	2.11	0.48
5:E:177:LEU:HD12	5:E:177:LEU:C	2.34	0.48
1:A:254:GLU:OE1	1:A:274:TRP:CD1	2.67	0.48
4:D:176:ASN:HD22	4:D:176:ASN:N	2.06	0.48
2:B:12:ARG:HG2	2:B:12:ARG:HH11	1.77	0.48
4:D:152:TYR:O	4:D:173:ALA:HA	2.14	0.48
5:E:16:GLY:HA2	5:E:80:LYS:HG3	1.95	0.48
4:D:138:ASP:OD1	4:D:139:SER:N	2.46	0.47
4:D:176:ASN:ND2	4:D:176:ASN:H	2.09	0.47
5:E:33:LEU:HD23	5:E:74:PHE:HB2	1.96	0.47
1:A:219:ARG:HG2	1:A:219:ARG:O	2.15	0.47
4:D:49:PHE:C	4:D:49:PHE:CD2	2.87	0.47
5:E:34:TYR:CE1	5:E:49:TYR:CD1	3.03	0.47
1:A:219:ARG:CG	1:A:219:ARG:O	2.62	0.47
1:A:215:LEU:C	1:A:215:LEU:CD1	2.82	0.47
4:D:124:SER:O	4:D:125:LYS:C	2.53	0.47
1:A:75:ARG:HD2	5:E:53:PHE:CE1	2.51	0.46
2:B:12:ARG:HG2	2:B:12:ARG:NH1	2.31	0.46
1:A:226:GLN:HG3	1:A:226:GLN:O	2.15	0.46
4:D:123:ASP:HB3	5:E:128:PHE:HD2	1.79	0.46
4:D:195:THR:CG2	5:E:133:ALA:HB1	2.43	0.46
1:A:255:GLN:HB2	1:A:257:TYR:HE2	1.79	0.46
4:D:191:ILE:N	4:D:192:PRO:HD3	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:224:THR:O	5:E:224:THR:CG2	2.63	0.46
4:D:189:SER:C	4:D:190:ILE:CD1	2.85	0.45
5:E:167:HIS:N	7:E:304:SO4:O1	2.48	0.45
1:A:255:GLN:HB2	1:A:257:TYR:CE2	2.52	0.45
1:A:202:ARG:HA	1:A:245:ALA:O	2.17	0.45
5:E:171:CYS:HB3	5:E:193:ARG:HD3	1.99	0.45
5:E:99:GLY:O	5:E:100:MET:HE2	2.17	0.44
5:E:207:HIS:CE1	7:E:303:SO4:O4	2.71	0.44
1:A:219:ARG:H	1:A:219:ARG:HD2	1.83	0.44
4:D:121:LEU:HD21	5:E:144:VAL:HG23	1.98	0.44
1:A:51:TRP:CE2	1:A:179:LEU:HD11	2.52	0.44
5:E:49:TYR:HB3	5:E:57:SER:HB3	1.99	0.44
5:E:8:PRO:O	5:E:109:SER:OG	2.26	0.44
5:E:153:ASP:HB3	5:E:188:TYR:CE2	2.51	0.44
4:D:190:ILE:HG22	4:D:191:ILE:N	2.29	0.44
2:B:30:PHE:HZ	2:B:64:LEU:CD1	2.28	0.44
5:E:33:LEU:HD22	5:E:68:ARG:CZ	2.47	0.44
1:A:222:GLU:O	1:A:224:GLN:N	2.50	0.44
1:A:169:ARG:NH2	7:A:305:SO4:O3	2.50	0.44
4:D:151:VAL:HG12	4:D:177:LYS:NZ	2.33	0.44
1:A:200:THR:O	1:A:201:LEU:HB2	2.18	0.43
5:E:3:THR:CG2	5:E:4:ILE:N	2.81	0.43
1:A:141:GLN:O	1:A:145:HIS:CD2	2.71	0.43
1:A:194:VAL:HG22	1:A:195:SER:N	2.33	0.43
1:A:138:MET:CE	1:A:138:MET:HA	2.48	0.43
5:E:30:ASN:N	5:E:31:PRO:HD3	2.33	0.43
5:E:63:ASN:ND2	5:E:82:LEU:CD1	2.49	0.43
3:C:9:THR:CG2	5:E:96:THR:CG2	2.97	0.43
5:E:58:SER:CB	7:E:305:SO4:O1	2.67	0.43
4:D:15:GLU:OE2	4:D:167:LYS:NZ	2.52	0.43
5:E:7:TRP:HB2	5:E:8:PRO:HA	2.00	0.43
1:A:81:LEU:HD13	1:A:118:TYR:CD1	2.54	0.43
6:A:301:TAM:H42	6:A:301:TAM:O5	2.18	0.43
4:D:134:PHE:HZ	4:D:190:ILE:HG21	1.84	0.43
1:A:230:LEU:HD23	1:A:230:LEU:N	2.34	0.43
1:A:73:THR:HG22	5:E:97:GLY:HA2	2.00	0.42
4:D:48:MET:CE	4:D:61:PHE:O	2.61	0.42
1:A:235:PRO:CG	2:B:65:LEU:HD22	2.48	0.42
2:B:59:ASP:O	2:B:60:TRP:HB2	2.18	0.42
5:E:98:LEU:HD22	5:E:98:LEU:N	2.33	0.42
4:D:190:ILE:CD1	4:D:190:ILE:N	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:HIS:HA	7:A:304:SO4:O4	2.19	0.42
4:D:195:THR:O	4:D:196:PHE:HB2	2.20	0.42
1:A:243:LYS:HG2	1:A:244:TRP:N	2.34	0.42
2:B:46:ILE:HG22	2:B:47:GLU:O	2.18	0.42
1:A:215:LEU:HD13	1:A:245:ALA:HB3	2.02	0.42
2:B:51:HIS:HB3	2:B:66:TYR:CD2	2.55	0.42
5:E:37:ARG:HD3	5:E:89:TYR:CZ	2.55	0.42
1:A:165:VAL:O	1:A:169:ARG:HG3	2.19	0.42
3:C:7:ILE:C	3:C:8:LEU:HD12	2.40	0.41
2:B:73:THR:OG1	2:B:74:GLU:N	2.53	0.41
5:E:173:ASP:HB2	5:E:190:LEU:HD12	2.00	0.41
2:B:41:LYS:HD3	2:B:78:TYR:CE1	2.55	0.41
5:E:2:GLN:HG2	5:E:2:GLN:H	1.74	0.41
1:A:45:MET:CE	3:C:2:LEU:HD11	2.50	0.41
4:D:48:MET:HE2	4:D:58:ASP:N	2.35	0.41
3:C:9:THR:CG2	5:E:96:THR:HG21	2.49	0.41
4:D:189:SER:C	4:D:190:ILE:CG1	2.88	0.41
5:E:58:SER:HB2	7:E:305:SO4:O1	2.21	0.41
4:D:159:LEU:HD11	4:D:168:SER:HB3	2.03	0.41
4:D:55:ASP:OD1	4:D:64:GLN:HG2	2.20	0.41
4:D:159:LEU:HD12	4:D:159:LEU:C	2.42	0.41
1:A:208:PHE:CE1	1:A:213:ILE:CD1	3.04	0.41
4:D:145:GLN:NE2	4:D:145:GLN:H	2.20	0.41
1:A:108:ARG:HA	7:A:305:SO4:O3	2.21	0.40
4:D:187:ASN:HD22	4:D:187:ASN:N	2.19	0.40
1:A:208:PHE:CE1	1:A:213:ILE:HD11	2.56	0.40
4:D:161:MET:CE	5:E:140:LYS:HD2	2.49	0.40
1:A:242:GLN:NE2	2:B:10:TYR:CD1	2.90	0.40
1:A:82:ARG:HA	1:A:87:GLN:HG2	2.04	0.40
2:B:57:SER:HB2	8:B:110:HOH:O	2.21	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	274/276 (99%)	250 (91%)	19 (7%)	5 (2%)	11	9
2	B	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
3	C	8/10 (80%)	8 (100%)	0	0	100	100
4	D	194/196 (99%)	179 (92%)	10 (5%)	5 (3%)	7	4
5	E	243/245 (99%)	229 (94%)	14 (6%)	0	100	100
All	All	817/827 (99%)	760 (93%)	47 (6%)	10 (1%)	16	17

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASP
4	D	148	ASP
1	A	194	VAL
1	A	198	GLU
1	A	197	HIS
4	D	125	LYS
4	D	190	ILE
4	D	162	ARG
4	D	188	ASN
1	A	269	PRO

### 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	232/232 (100%)	223 (96%)	9 (4%)	39	54
2	B	95/95 (100%)	91 (96%)	4 (4%)	36	51
3	C	7/7 (100%)	7 (100%)	0	100	100
4	D	174/174 (100%)	162 (93%)	12 (7%)	19	25
5	E	211/211 (100%)	205 (97%)	6 (3%)	51	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	719/719 (100%)	688 (96%)	31 (4%)	35 50

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	14	ARG
1	A	111	ARG
1	A	115	GLN
1	A	202	ARG
1	A	215	LEU
1	A	219	ARG
1	A	224	GLN
1	A	253	GLN
2	B	4	THR
2	B	12	ARG
2	B	47	GLU
2	B	83	ASN
4	D	4	VAL
4	D	11	LEU
4	D	88	LEU
4	D	103	THR
4	D	110	ASN
4	D	145	GLN
4	D	151	VAL
4	D	153	ILE
4	D	176	ASN
4	D	187	ASN
4	D	188	ASN
4	D	190	ILE
5	E	33	LEU
5	E	49	TYR
5	E	98	LEU
5	E	107	GLU
5	E	193	ARG
5	E	213	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	HIS

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Mol	Chain	Res	Type
1	A	74	HIS
1	A	86	ASN
1	A	93	HIS
1	A	115	GLN
1	A	141	GLN
1	A	145	HIS
1	A	174	ASN
1	A	224	GLN
1	A	242	GLN
1	A	253	GLN
1	A	262	GLN
2	B	17	ASN
2	B	83	ASN
4	D	38	GLN
4	D	110	ASN
4	D	145	GLN
4	D	176	ASN
4	D	187	ASN
4	D	188	ASN
5	E	5	HIS
5	E	6	GLN
5	E	13	GLN
5	E	38	GLN
5	E	63	ASN
5	E	119	ASN
5	E	154	HIS
5	E	207	HIS

### 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

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
6	TAM	A	301	-	7,10,10	0.92	0	9,12,12	2.61	6 (66%)
7	SO4	A	302	-	4,4,4	0.40	0	6,6,6	0.22	0
7	SO4	A	303	-	4,4,4	0.47	0	6,6,6	0.10	0
7	SO4	A	304	-	4,4,4	0.25	0	6,6,6	0.28	0
7	SO4	A	305	-	4,4,4	0.42	0	6,6,6	0.15	0
7	SO4	A	306	-	4,4,4	0.27	0	6,6,6	0.10	0
7	SO4	E	301	-	4,4,4	0.31	0	6,6,6	0.18	0
7	SO4	E	302	-	4,4,4	0.30	0	6,6,6	0.12	0
7	SO4	E	303	-	4,4,4	0.16	0	6,6,6	0.08	0
7	SO4	E	304	-	4,4,4	0.32	0	6,6,6	0.18	0
7	SO4	E	305	-	4,4,4	0.57	0	6,6,6	0.22	0
7	SO4	E	306	-	4,4,4	0.26	0	6,6,6	0.12	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
6	TAM	A	301	-	-	0/12/12/12	0/0/0/0
7	SO4	A	302	-	-	0/0/0/0	0/0/0/0
7	SO4	A	303	-	-	0/0/0/0	0/0/0/0
7	SO4	A	304	-	-	0/0/0/0	0/0/0/0
7	SO4	A	305	-	-	0/0/0/0	0/0/0/0
7	SO4	A	306	-	-	0/0/0/0	0/0/0/0
7	SO4	E	301	-	-	0/0/0/0	0/0/0/0
7	SO4	E	302	-	-	0/0/0/0	0/0/0/0
7	SO4	E	303	-	-	0/0/0/0	0/0/0/0
7	SO4	E	304	-	-	0/0/0/0	0/0/0/0
7	SO4	E	305	-	-	0/0/0/0	0/0/0/0
7	SO4	E	306	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
6	A	301	TAM	C3-C-N	-3.31	101.44	108.28
6	A	301	TAM	C1-C-N	-2.99	102.10	108.28
6	A	301	TAM	C2-C-N	-2.77	102.55	108.28
6	A	301	TAM	C3-C-C2	2.98	115.27	110.50
6	A	301	TAM	C3-C-C1	3.38	115.90	110.50
6	A	301	TAM	C2-C-C1	3.54	116.15	110.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	301	TAM	2	0
7	A	302	SO4	1	0
7	A	303	SO4	4	0
7	A	304	SO4	2	0
7	A	305	SO4	2	0
7	E	303	SO4	1	0
7	E	304	SO4	1	0
7	E	305	SO4	3	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	276/276 (100%)	1.42	78 (28%) 1 0	26, 59, 196, 217	0
2	B	100/100 (100%)	0.51	8 (8%) 15 15	26, 66, 153, 169	0
3	C	10/10 (100%)	-0.14	0 100 100	25, 28, 34, 38	0
4	D	196/196 (100%)	0.66	24 (12%) 5 5	21, 49, 135, 163	0
5	E	245/245 (100%)	0.06	6 (2%) 62 65	24, 44, 107, 151	0
All	All	827/827 (100%)	0.71	116 (14%) 4 3	21, 52, 164, 217	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	LEU	10.9
1	A	196	ASP	10.6
1	A	249	VAL	10.4
1	A	248	VAL	8.7
1	A	250	PRO	8.6
1	A	251	SER	7.9
1	A	195	SER	7.8
2	B	99	MET	7.5
1	A	247	VAL	7.5
1	A	274	TRP	7.5
1	A	224	GLN	7.4
1	A	257	TYR	7.4
1	A	229	GLU	7.2
1	A	216	THR	7.2
1	A	228	THR	7.1
1	A	259	CYS	6.8
1	A	220	ASP	6.7
1	A	197	HIS	6.5
1	A	193	ALA	6.4
4	D	160	ASP	6.4

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Mol	Chain	Res	Type	RSRZ
1	A	276	PRO	6.3
1	A	189	MET	6.2
1	A	230	LEU	6.1
1	A	204	TRP	6.1
1	A	203	CYS	6.1
1	A	223	ASP	6.0
1	A	272	LEU	6.0
1	A	187	THR	5.9
1	A	253	GLN	5.8
1	A	222	GLU	5.8
1	A	246	ALA	5.5
1	A	244	TRP	5.5
1	A	265	GLY	5.4
1	A	245	ALA	5.4
1	A	258	THR	5.3
1	A	273	ARG	5.1
1	A	227	ASP	5.0
4	D	163	SER	4.9
1	A	200	THR	4.7
1	A	194	VAL	4.7
1	A	226	GLN	4.6
4	D	190	ILE	4.6
1	A	267	PRO	4.6
1	A	198	GLU	4.6
1	A	214	THR	4.6
1	A	260	HIS	4.5
4	D	178	SER	4.5
1	A	199	ALA	4.5
5	E	0	MET	4.4
1	A	202	ARG	4.3
1	A	225	THR	4.3
4	D	143	VAL	4.2
4	D	192	PRO	4.2
1	A	188	HIS	4.2
1	A	271	THR	4.2
1	A	256	ARG	4.0
4	D	196	PHE	3.8
1	A	275	GLU	3.8
1	A	255	GLN	3.7
1	A	191	HIS	3.7
4	D	188	ASN	3.7
4	D	166	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	252	GLY	3.6
2	B	74	GLU	3.6
1	A	179	LEU	3.5
5	E	244	ASP	3.5
1	A	221	GLY	3.5
1	A	254	GLU	3.4
4	D	164	MET	3.4
1	A	215	LEU	3.4
1	A	217	TRP	3.4
1	A	241	PHE	3.3
4	D	195	THR	3.2
4	D	148	ASP	3.1
5	E	208	PHE	3.0
5	E	143	LEU	2.9
4	D	180	PHE	2.9
2	B	95	TRP	2.9
2	B	15	ALA	2.9
1	A	218	GLN	2.8
1	A	178	THR	2.8
2	B	75	LYS	2.8
4	D	144	SER	2.8
4	D	118	VAL	2.7
1	A	219	ARG	2.7
1	A	268	LYS	2.7
4	D	194	ASP	2.6
1	A	213	ILE	2.6
1	A	177	GLU	2.6
1	A	180	GLN	2.5
4	D	186	PHE	2.5
1	A	184	ALA	2.5
1	A	262	GLN	2.5
1	A	181	ARG	2.5
1	A	206	LEU	2.4
5	E	1	SER	2.3
1	A	207	SER	2.3
4	D	117	ALA	2.3
5	E	242	ARG	2.2
4	D	165	ASP	2.2
1	A	231	VAL	2.2
4	D	139	SER	2.2
2	B	41	LYS	2.2
1	A	266	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	185	PRO	2.2
4	D	111	ILE	2.2
2	B	98	ASP	2.2
4	D	150	ASP	2.1
1	A	176	LYS	2.1
1	A	261	VAL	2.1
1	A	208	PHE	2.0
2	B	97	ARG	2.0
4	D	122	ARG	2.0
1	A	190	THR	2.0
4	D	127	SER	2.0
1	A	238	ASP	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 ⓘ

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
7	SO4	E	306	5/5	0.88	0.27	7.19	31,34,46,54	5
7	SO4	E	302	5/5	0.83	0.22	2.29	36,44,52,62	5
7	SO4	E	301	5/5	0.93	0.19	1.86	63,76,80,80	1
7	SO4	E	305	5/5	0.93	0.21	1.09	35,39,47,53	5
7	SO4	A	305	5/5	0.94	0.15	-1.05	33,41,44,52	5
7	SO4	A	303	5/5	0.96	0.10	-2.37	41,64,76,77	0
7	SO4	A	304	5/5	0.99	0.10	-2.45	37,40,48,52	0
6	TAM	A	301	11/11	0.82	0.30	-	66,80,80,80	0
7	SO4	E	304	5/5	0.76	0.19	-	46,53,65,73	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	SO4	E	303	5/5	0.85	0.18	-	47,53,67,73	5
7	SO4	A	302	5/5	0.96	0.09	-	67,74,80,80	0
7	SO4	A	306	5/5	0.93	0.16	-	40,41,53,62	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.