Full wwPDB X-ray Structure Validation Report (i)

Oct 9, 2023 – 04:28 PM EDT

PDB ID	:	8D5Q
Title	:	TCR TG6 in complex with Ld-HF10
Authors	:	Wang, Y.; Dai, S.
Deposited on	:	2022-06-05
Resolution	:	2.50 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

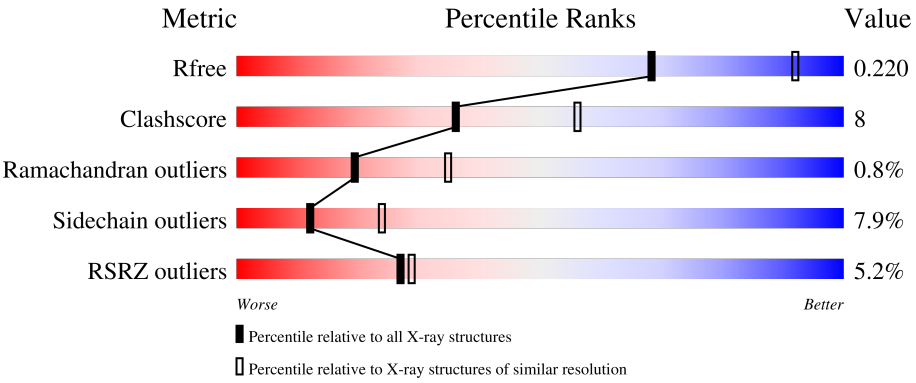
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 >=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 <=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	209	7% 75% 20%
2	B	244	6% 76% 22%
3	C	180	2% 82% 14%
4	E	10	10% 60% 30% 10%

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
6	MES	B	302	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5349 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 TCR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1600	1000	265	327	8			

- Molecule 2 is a protein called TCR-beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1967	1243	350	365	9			

- Molecule 3 is a protein called H-2 class I histocompatibility antigen, L-D alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	176	Total	C	N	O	S	0	1	0
			1470	923	261	279	7			

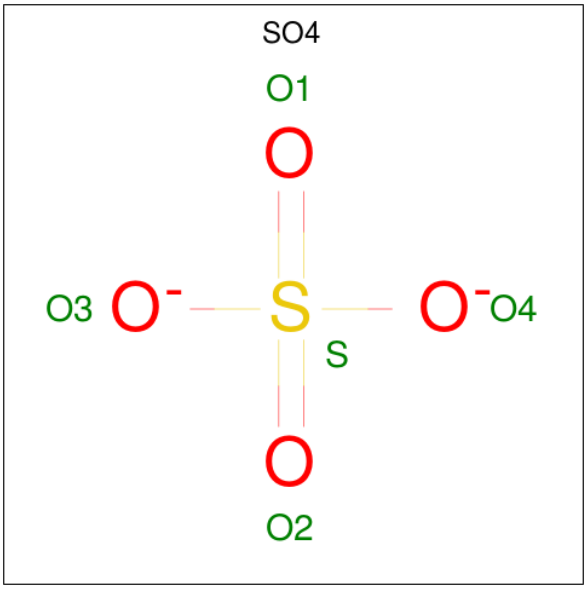
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	MET	-	initiating methionine	UNP P01897
C	8	TYR	PHE	conflict	UNP P01897
C	12	THR	VAL	conflict	UNP P01897
C	15	ARG	PRO	conflict	UNP P01897
C	23	THR	ILE	conflict	UNP P01897
C	30	ASP	ASN	conflict	UNP P01897
C	49	VAL	ALA	conflict	UNP P01897
C	66	VAL	ILE	conflict	UNP P01897
C	131	ARG	LYS	conflict	UNP P01897

- Molecule 4 is a protein called Dense granule protein 6, HF10 peptide.

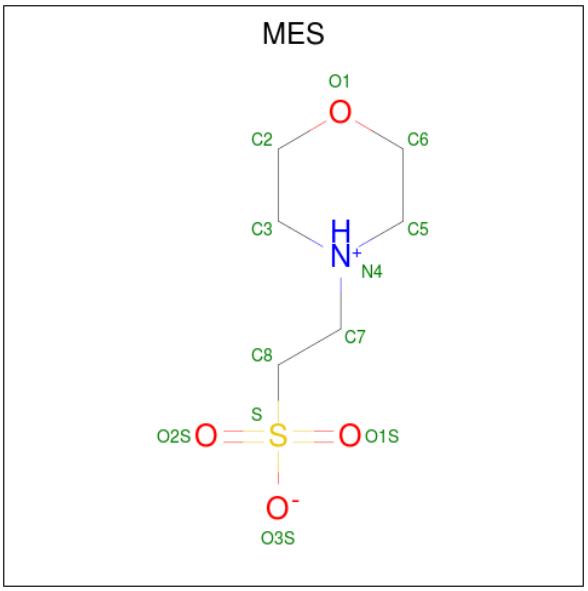
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	10	Total	C	N	O	0	0	0
			82	52	13	17			

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C N O S 12 6 1 4 1	0	0

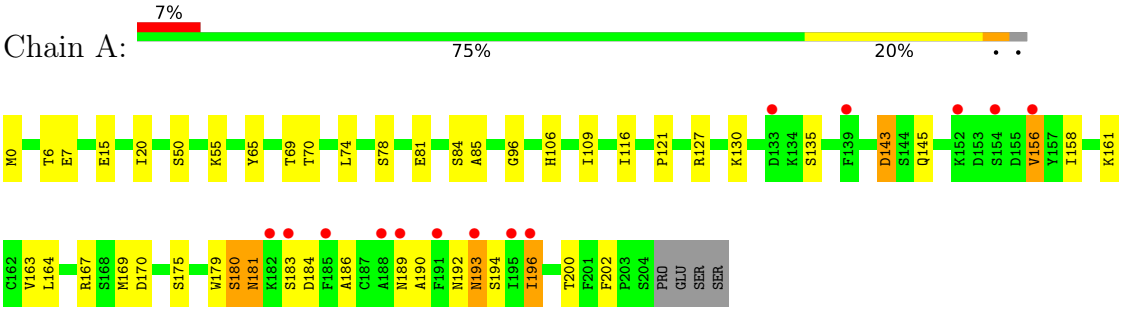
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	66	Total O 66 66	0	0
7	B	71	Total O 71 71	0	0
7	C	65	Total O 65 65	0	0
7	E	6	Total O 6 6	0	0

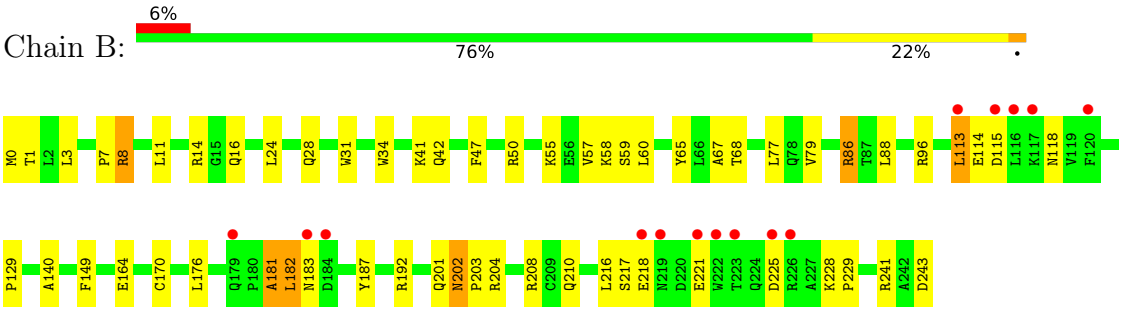
3 Residue-property plots (i)

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.

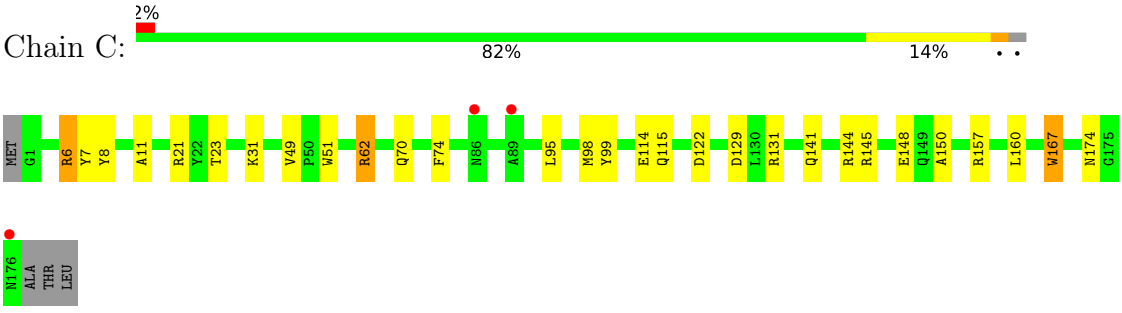
• Molecule 1: TCR-alpha



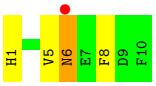
• Molecule 2: TCR-beta



• Molecule 3: H-2 class I histocompatibility antigen, L-D alpha chain



• Molecule 4: Dense granule protein 6, HF10 peptide


H1
V5
N6
E7
F8
D9
F10

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	89.96Å 89.96Å 105.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.02 – 2.50 44.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.02-2.50) 99.9 (44.98-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.24 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.169 , 0.222 0.174 , 0.220	Depositor DCC
R_{free} test set	1493 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	61.9	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 44.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.040 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5349	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MES, 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	0.84	1/1639 (0.1%)	1.02	0/2223
2	B	0.80	1/2020 (0.0%)	1.05	3/2751 (0.1%)
3	C	0.91	1/1512 (0.1%)	1.11	8/2049 (0.4%)
4	E	1.01	0/85	0.84	0/113
All	All	0.85	3/5256 (0.1%)	1.06	11/7136 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	114	GLU	CD-OE1	8.68	1.35	1.25
1	A	7	GLU	CD-OE1	6.17	1.32	1.25
2	B	164	GLU	CD-OE2	5.03	1.31	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	86	ARG	NE-CZ-NH1	-10.78	114.91	120.30
3	C	6	ARG	NE-CZ-NH2	-8.95	115.83	120.30
2	B	86	ARG	NE-CZ-NH2	6.97	123.79	120.30
3	C	157	ARG	NE-CZ-NH2	-6.33	117.14	120.30
3	C	6	ARG	NE-CZ-NH1	5.92	123.26	120.30
2	B	8	ARG	CG-CD-NE	-5.43	100.39	111.80
3	C	62	ARG	CB-CA-C	5.24	120.88	110.40
3	C	167	TRP	CA-CB-CG	-5.22	103.78	113.70
3	C	23	THR	CA-CB-OG1	-5.21	98.06	109.00
3	C	21	ARG	NE-CZ-NH1	-5.10	117.75	120.30
3	C	174	ASN	CB-CA-C	-5.04	100.32	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1600	0	1487	30	0
2	B	1967	0	1903	45	0
3	C	1470	0	1352	11	0
4	E	82	0	67	5	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
6	B	12	0	13	7	0
7	A	66	0	0	1	0
7	B	71	0	0	2	0
7	C	65	0	0	0	0
7	E	6	0	0	0	0
All	All	5349	0	4822	80	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 8.

All (80) 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:175:SER:OG	2:B:192:ARG:HD3	1.76	0.85
1:A:116:ILE:HD11	1:A:143:ASP:HA	1.59	0.84
1:A:106:HIS:HA	2:B:42:GLN:HE22	1.42	0.83
2:B:202:ASN:C	2:B:202:ASN:HD22	1.88	0.77
2:B:202:ASN:ND2	2:B:204:ARG:H	1.85	0.73
2:B:8:ARG:HB2	6:B:302:MES:C6	2.25	0.67
3:C:167:TRP:CE2	4:E:1:HIS:CE1	2.86	0.64
6:B:302:MES:H32	6:B:302:MES:O3S	2.00	0.61
2:B:202:ASN:HD22	2:B:203:PRO:N	2.00	0.60
1:A:181:ASN:ND2	1:A:181:ASN:N	2.51	0.58
2:B:8:ARG:HB2	6:B:302:MES:H61	1.86	0.57
2:B:181:ALA:O	2:B:182:LEU:C	2.43	0.56
1:A:116:ILE:CD1	1:A:143:ASP:HA	2.31	0.56
3:C:70:GLN:HE22	4:E:6:ASN:H	1.52	0.56
1:A:116:ILE:HD11	1:A:143:ASP:CA	2.34	0.56
1:A:181:ASN:N	1:A:181:ASN:HD22	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:ILE:HD11	2:B:41:LYS:HE2	1.88	0.56
1:A:175:SER:OG	2:B:192:ARG:CD	2.50	0.55
1:A:186:ALA:O	1:A:190:ALA:HB2	2.06	0.55
2:B:201:GLN:HA	2:B:241:ARG:O	2.08	0.54
3:C:129:ASP:O	3:C:131[B]:ARG:HG3	2.08	0.53
2:B:202:ASN:HD22	2:B:204:ARG:H	1.55	0.53
6:B:302:MES:O3S	6:B:302:MES:C3	2.56	0.53
2:B:55:LYS:HG3	2:B:68:THR:HG23	1.92	0.52
1:A:156:VAL:HA	1:A:180:SER:HB2	1.92	0.51
1:A:192:ASN:C	1:A:194:SER:H	2.13	0.51
2:B:115:ASP:HB3	2:B:118:ASN:HD22	1.74	0.51
1:A:181:ASN:HD22	1:A:181:ASN:H	1.58	0.50
1:A:106:HIS:HA	2:B:42:GLN:NE2	2.18	0.50
2:B:8:ARG:HB2	6:B:302:MES:H62	1.93	0.50
1:A:156:VAL:O	1:A:156:VAL:HG23	2.12	0.50
1:A:96:GLY:O	4:E:5:VAL:HG23	2.12	0.50
1:A:156:VAL:O	1:A:156:VAL:CG2	2.59	0.50
1:A:15:GLU:HA	1:A:78:SER:OG	2.12	0.50
2:B:8:ARG:H	6:B:302:MES:H52	1.77	0.50
2:B:208:ARG:NH1	2:B:210:GLN:OE1	2.40	0.49
1:A:81:GLU:OE1	1:A:163:VAL:HG11	2.13	0.49
2:B:65:TYR:OH	2:B:86:ARG:HD3	2.12	0.49
2:B:31:TRP:CZ2	2:B:96:ARG:HG2	2.48	0.49
2:B:11:LEU:HD21	2:B:113:LEU:CD1	2.43	0.48
2:B:31:TRP:CZ3	2:B:50:ARG:HB2	2.49	0.48
2:B:3:LEU:HD23	2:B:24:LEU:HA	1.96	0.46
3:C:8:TYR:CE2	3:C:98:MET:HG3	2.51	0.46
1:A:116:ILE:CG1	1:A:143:ASP:HA	2.46	0.46
2:B:47:PHE:CD2	2:B:67:ALA:HB2	2.52	0.45
2:B:202:ASN:C	2:B:202:ASN:ND2	2.60	0.45
1:A:106:HIS:CD2	7:A:340:HOH:O	2.70	0.45
2:B:14:ARG:NH1	2:B:114:GLU:HB2	2.32	0.45
2:B:34:TRP:CE2	2:B:77:LEU:HB2	2.52	0.45
1:A:175:SER:HG	2:B:192:ARG:HD3	1.81	0.45
2:B:58:LYS:HD3	2:B:60:LEU:HD11	2.00	0.44
3:C:150:ALA:HB1	4:E:8:PHE:CE1	2.53	0.44
1:A:106:HIS:ND1	2:B:42:GLN:OE1	2.51	0.44
1:A:196:ILE:CG2	1:A:200:THR:HG21	2.48	0.44
2:B:11:LEU:HD21	2:B:113:LEU:HD13	2.00	0.43
2:B:216:LEU:HD12	2:B:229:PRO:HG2	2.00	0.43
3:C:11:ALA:CB	3:C:74:PHE:HB3	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:141:GLN:HB3	3:C:145:ARG:NH2	2.34	0.43
2:B:42:GLN:NE2	7:B:407:HOH:O	2.51	0.43
2:B:129:PRO:CG	2:B:140:ALA:HB1	2.49	0.43
2:B:218:GLU:HA	2:B:228:LYS:NZ	2.33	0.43
1:A:121:PRO:HB2	1:A:200:THR:HG22	2.00	0.42
2:B:113:LEU:HD23	2:B:113:LEU:O	2.19	0.42
2:B:7:PRO:HA	6:B:302:MES:H81	2.01	0.42
3:C:7:TYR:HB2	3:C:99:TYR:CZ	2.53	0.42
3:C:167:TRP:CD2	4:E:1:HIS:CD2	3.07	0.42
2:B:149:PHE:O	2:B:187:TYR:N	2.46	0.42
2:B:86:ARG:NH1	7:B:402:HOH:O	2.48	0.42
2:B:31:TRP:CH2	2:B:96:ARG:HG2	2.55	0.41
1:A:69:THR:O	1:A:70:THR:C	2.57	0.41
2:B:47:PHE:CE2	2:B:67:ALA:HB2	2.55	0.41
1:A:20:ILE:HD12	1:A:74:LEU:HD23	2.02	0.41
3:C:144:ARG:HD3	3:C:148:GLU:OE1	2.20	0.41
3:C:49:VAL:HG21	3:C:51:TRP:CE2	2.56	0.41
2:B:86:ARG:HG3	2:B:88:LEU:CD2	2.51	0.41
1:A:84:SER:O	1:A:85:ALA:HB2	2.21	0.40
2:B:221:GLU:HA	2:B:221:GLU:OE1	2.20	0.40
2:B:59:SER:C	2:B:60:LEU:HD12	2.41	0.40
1:A:164:LEU:HB3	2:B:170:CYS:HB2	2.02	0.40
1:A:200:THR:HG1	1:A:202:PHE:HE2	1.65	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	203/209 (97%)	182 (90%)	18 (9%)	3 (2%)	10	18
2	B	242/244 (99%)	231 (96%)	9 (4%)	2 (1%)	19	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	C	175/180 (97%)	167 (95%)	8 (5%)	0	100 100
4	E	8/10 (80%)	8 (100%)	0	0	100 100
All	All	628/643 (98%)	588 (94%)	35 (6%)	5 (1%)	19 35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	181	ALA
2	B	182	LEU
1	A	161	LYS
1	A	170	ASP
1	A	193	ASN

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	179/183 (98%)	157 (88%)	22 (12%)	4 9
2	B	213/213 (100%)	200 (94%)	13 (6%)	18 36
3	C	146/148 (99%)	139 (95%)	7 (5%)	25 48
4	E	9/9 (100%)	8 (89%)	1 (11%)	6 11
All	All	547/553 (99%)	504 (92%)	43 (8%)	12 24

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	MET
1	A	6	THR
1	A	50	SER
1	A	55	LYS
1	A	65	TYR
1	A	127	ARG
1	A	130	LYS

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Mol	Chain	Res	Type
1	A	135	SER
1	A	143	ASP
1	A	145	GLN
1	A	156	VAL
1	A	158	ILE
1	A	167	ARG
1	A	169	MET
1	A	179	TRP
1	A	180	SER
1	A	181	ASN
1	A	183	SER
1	A	184	ASP
1	A	189	ASN
1	A	193	ASN
1	A	196	ILE
2	B	0	MET
2	B	1	THR
2	B	16	GLN
2	B	28	GLN
2	B	57	VAL
2	B	79	VAL
2	B	113	LEU
2	B	176	LEU
2	B	183	ASN
2	B	202	ASN
2	B	217	SER
2	B	225	ASP
2	B	243	ASP
3	C	6	ARG
3	C	31	LYS
3	C	62	ARG
3	C	95	LEU
3	C	115	GLN
3	C	122	ASP
3	C	160	LEU
4	E	6	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	80	GLN

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Mol	Chain	Res	Type
1	A	117	GLN
1	A	181	ASN
1	A	189	ASN
2	B	37	GLN
2	B	118	ASN
2	B	202	ASN
2	B	232	GLN
3	C	70	GLN
3	C	93	HIS
3	C	149	GLN
4	E	1	HIS
4	E	6	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 monosaccharides in this entry.

5.6 Ligand geometry

3 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	$\#\|Z\| > 2$
5	SO4	B	301	-	4,4,4	0.34	0	6,6,6	0.19	0
6	MES	B	302	-	12,12,12	0.75	0	14,16,16	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	SO4	C	201	-	4,4,4	0.32	0	6,6,6	0.08	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	MES	B	302	-	-	1/6/14/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	302	MES	N4-C7-C8-S

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	302	MES	7	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^{th} 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^2)	Q<0.9
1	A	205/209 (98%)	0.27	14 (6%) 17 17	42, 70, 127, 149	0
2	B	244/244 (100%)	0.33	15 (6%) 21 22	43, 64, 116, 136	0
3	C	176/180 (97%)	0.11	3 (1%) 70 72	44, 63, 103, 131	0
4	E	10/10 (100%)	0.58	1 (10%) 7 6	51, 54, 70, 88	0
All	All	635/643 (98%)	0.25	33 (5%) 27 29	42, 64, 121, 149	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	225	ASP	4.7
4	E	6	ASN	4.3
1	A	182	LYS	3.9
2	B	222	TRP	3.7
1	A	152	LYS	3.5
3	C	89	ALA	3.2
3	C	86	ASN	3.1
1	A	195	ILE	3.0
2	B	120	PHE	3.0
1	A	133	ASP	3.0
3	C	176	ASN	3.0
2	B	218	GLU	3.0
1	A	191	PHE	2.9
2	B	179	GLN	2.9
2	B	223	THR	2.8
2	B	221	GLU	2.7
1	A	188	ALA	2.7
1	A	154	SER	2.6
2	B	184	ASP	2.5
1	A	183	SER	2.5
1	A	196	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	226	ARG	2.4
1	A	139	PHE	2.3
1	A	156	VAL	2.2
1	A	189	ASN	2.2
2	B	219	ASN	2.2
2	B	117	LYS	2.2
2	B	183	ASN	2.2
2	B	113	LEU	2.2
1	A	185	PHE	2.1
2	B	115	ASP	2.0
1	A	193	ASN	2.0
2	B	116	LEU	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 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^{th} 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^2)	Q<0.9
6	MES	B	302	12/12	0.70	0.26	98,141,147,147	0
5	SO4	C	201	5/5	0.95	0.12	94,95,109,113	0
5	SO4	B	301	5/5	0.98	0.08	70,81,87,91	0

6.5 Other polymers (i)

There are no such residues in this entry.