Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 09:59 pm GMT

PDB ID	:	2XN9
Title	:	Crystal structure of the ternary complex between human T cell receptor, staphylococcal enterotoxin H and human major histocompatibility complex class II
Authors	:	Saline, M.; Rodstrom, K.E.J.; Fischer, G.; Orekhov, V.Y.; Karlsson, B.G.; Lindkvist-Petersson, K.
Deposited on	:	2010-07-31
Resolution	:	2.30 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:

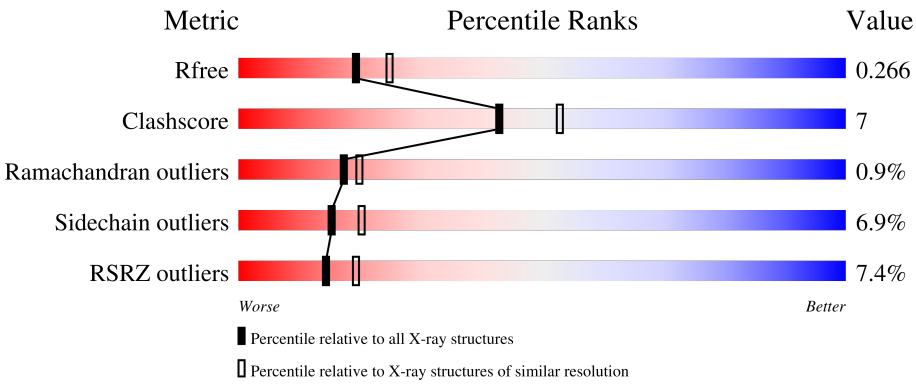
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	204	3% 79% 16% • •
2	B	244	4% 82% 14% • • •
3	C	217	2% 82% 15% • •
4	D	182	21% 80% 15% • •

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Mol	Chain	Length	Quality of chain
5	E	190	10% 76% 18%
6	F	13	77% 23%

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	GOL	B	1246	-	-	X	-

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 8711 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 T CELL RECEPTOR ALPHA CHAIN C REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	199	1570	986	265	312	7	0	6	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	158	CYS	THR	engineered mutation	UNP P01848

- Molecule 2 is a protein called T CELL RECEPTOR BETA-1 CHAIN C REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	242	1960	1234	339	381	6	0	3	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	118	LYS	ASN	conflict	UNP P01850
B	119	ASN	LYS	conflict	UNP P01850
B	151	TYR	PHE	conflict	UNP P01850
B	171	CYS	SER	engineered mutation	UNP P01850
B	189	SER	CYS	conflict	UNP P01850

- Molecule 3 is a protein called ENTEROTOXIN H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	215	1757	1108	287	359	3	0	1	0

- Molecule 4 is a protein called HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR ALPHA CHAIN,.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	178	1480	956	241	278	5	0	3	0

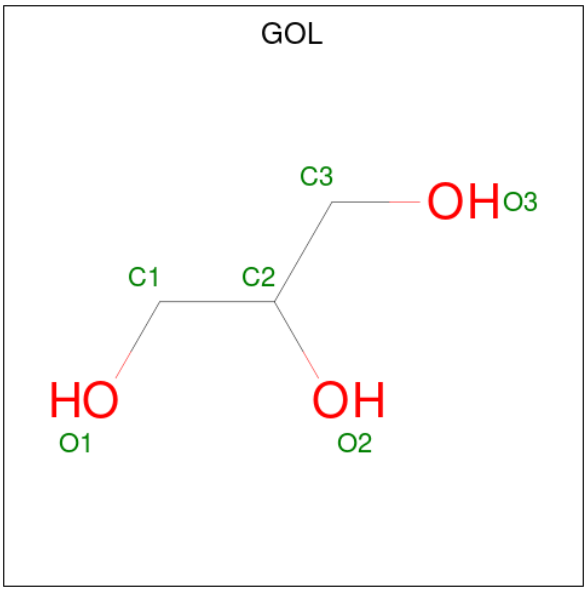
- Molecule 5 is a protein called MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	188	1534	963	274	291	6	0	2	0

- Molecule 6 is a protein called HEMAGGLUTININ.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
6	F	13	105	69	18	18	0	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
8	C	1	1	1	0	0

- Molecule 9 is water.

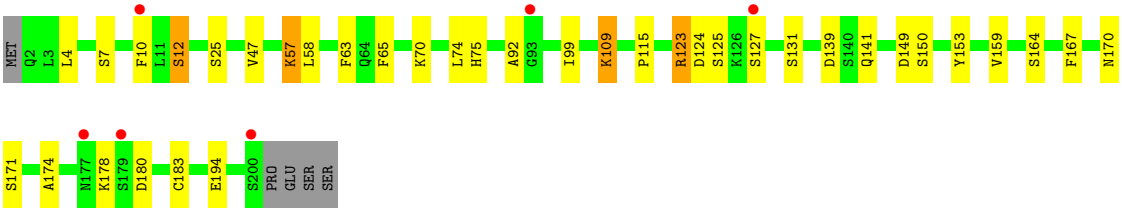
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	92	92	92	0	0
			Total	O		
9	B	74	74	74	0	0
			Total	O		
9	C	67	67	67	0	0
			Total	O		
9	D	25	25	25	0	0
			Total	O		
9	E	17	17	17	0	0
			Total	O		
9	F	5	5	5	0	0

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.

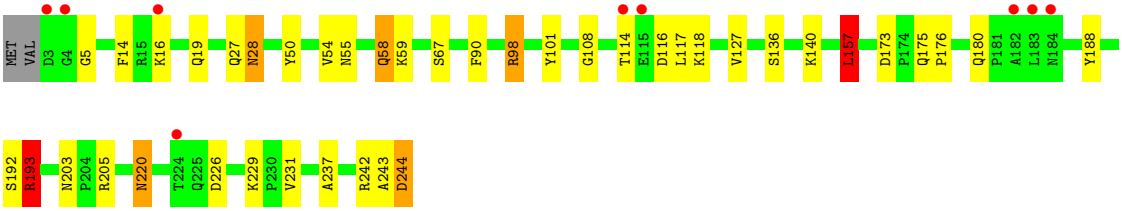
• Molecule 1: T CELL RECEPTOR ALPHA CHAIN C REGION

Chain A:



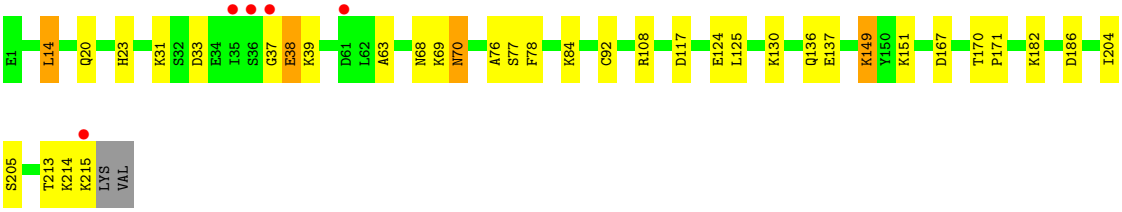
• Molecule 2: T CELL RECEPTOR BETA-1 CHAIN C REGION

Chain B:



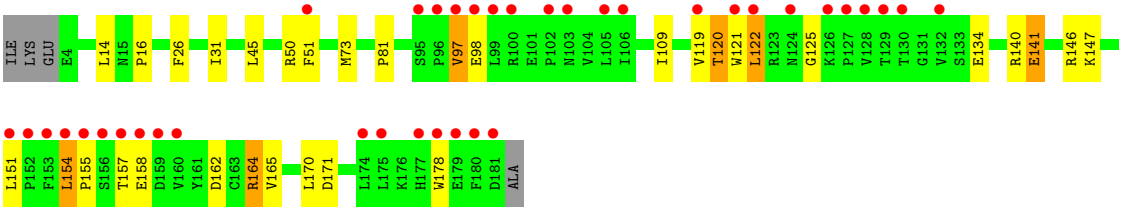
• Molecule 3: ENTEROTOXIN H

Chain C:



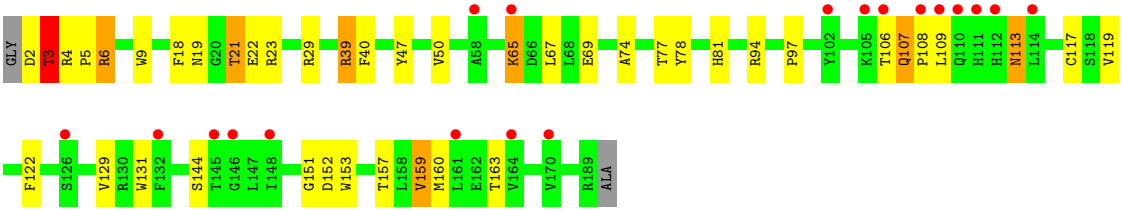
• Molecule 4: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR ALPHA CHAIN,

Chain D:



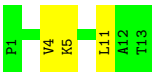
- Molecule 5: MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II BETA CHAIN

Chain E:



- Molecule 6: HEMAGGLUTININ

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	191.18Å 48.89Å 166.72Å 90.00° 113.55° 90.00°	Depositor
Resolution (Å)	152.50 – 2.30 42.16 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.2 (152.50-2.30) 97.2 (42.16-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.10 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.222 , 0.272 0.217 , 0.266	Depositor DCC
R_{free} test set	3148 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	35.8	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8711	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NA

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	0.78	1/1601 (0.1%)	0.76	0/2167
2	B	0.67	0/2013	0.75	3/2739 (0.1%)
3	C	0.63	0/1784	0.70	1/2399 (0.0%)
4	D	0.56	0/1525	0.64	0/2081
5	E	0.56	0/1573	0.71	0/2141
6	F	0.50	0/106	0.73	0/141
All	All	0.65	1/8602 (0.0%)	0.72	4/11668 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	183	CYS	CB-SG	5.35	1.91	1.82

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	193	ARG	NE-CZ-NH2	-7.39	116.60	120.30
2	B	157	LEU	CA-CB-CG	7.16	131.77	115.30
2	B	193	ARG	NE-CZ-NH1	5.97	123.28	120.30
3	C	14	LEU	CA-CB-CG	5.29	127.47	115.30

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	1570	0	1508	19	0
2	B	1960	0	1834	24	0
3	C	1757	0	1712	22	0
4	D	1480	0	1394	20	0
5	E	1534	0	1428	33	0
6	F	105	0	121	2	0
7	A	6	0	8	1	0
7	B	18	0	24	5	0
8	C	1	0	0	0	0
9	A	92	0	0	1	0
9	B	74	0	0	0	0
9	C	67	0	0	1	0
9	D	25	0	0	0	0
9	E	17	0	0	0	0
9	F	5	0	0	0	0
All	All	8711	0	8029	112	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 (112) 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:194[B]:GLU:H	1:A:194[B]:GLU:CD	1.56	0.97
5:E:129:VAL:HG11	5:E:159:VAL:HG21	1.57	0.86
5:E:23[B]:ARG:HH11	5:E:23[B]:ARG:HG3	1.43	0.83
3:C:213:THR:HG22	3:C:215:LYS:H	1.45	0.82
2:B:203:ASN:HD21	2:B:205:ARG:HH21	1.31	0.79
5:E:23[B]:ARG:HH11	5:E:23[B]:ARG:CG	1.98	0.75
1:A:171:SER:OG	2:B:193:ARG:HD3	1.89	0.72
5:E:129:VAL:CG1	5:E:159:VAL:HG21	2.19	0.71
5:E:117:CYS:HB3	5:E:159:VAL:HG23	1.75	0.69
5:E:129:VAL:HG11	5:E:159:VAL:CG2	2.23	0.68
5:E:81:HIS:CD2	6:F:4:VAL:HG23	2.28	0.67
1:A:194[B]:GLU:CD	1:A:194[B]:GLU:N	2.38	0.66
4:D:141[A]:GLU:O	4:D:141[A]:GLU:OE2	2.14	0.64
5:E:151:GLY:O	5:E:153:TRP:N	2.29	0.64
1:A:159:VAL:HG22	1:A:170:ASN:OD1	1.98	0.63
3:C:76:ALA:H	3:C:136:GLN:NE2	1.98	0.61
2:B:229:LYS:HG3	2:B:231:VAL:HG13	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2:ASP:OD2	5:E:4:ARG:HD3	2.01	0.61
2:B:173:ASP:OD1	2:B:193:ARG:NH2	2.29	0.61
3:C:124:GLU:OE2	3:C:149:LYS:HE2	2.01	0.61
3:C:170:THR:HB	3:C:171:PRO:CD	2.32	0.60
4:D:120:THR:HB	4:D:164:ARG:HG2	1.85	0.58
2:B:50:TYR:CZ	2:B:58:GLN:HG3	2.39	0.58
2:B:188:TYR:HE1	7:B:1246:GOL:H31	1.68	0.58
4:D:140:ARG:HG2	4:D:146:ARG:HD2	1.86	0.57
4:D:81:PRO:HB3	5:E:5:PRO:HB2	1.86	0.57
4:D:134:GLU:OE2	4:D:147:LYS:NZ	2.37	0.57
3:C:213:THR:HG23	9:C:2067:HOH:O	2.05	0.56
1:A:194[B]:GLU:N	1:A:194[B]:GLU:OE2	2.38	0.55
2:B:28:ASN:HD22	2:B:28:ASN:H	1.53	0.55
1:A:123[B]:ARG:HD2	1:A:124:ASP:O	2.06	0.55
5:E:2:ASP:CG	5:E:6:ARG:HH22	2.10	0.55
3:C:130:LYS:HE2	3:C:137:GLU:OE1	2.07	0.54
5:E:23[B]:ARG:CG	5:E:23[B]:ARG:NH1	2.62	0.54
2:B:5:GLY:H	2:B:28:ASN:ND2	2.06	0.54
5:E:119:VAL:CG2	5:E:157:THR:HG22	2.39	0.53
3:C:37:GLY:O	3:C:38:GLU:HG2	2.09	0.53
5:E:97:PRO:HB3	5:E:122:PHE:HB3	1.91	0.52
2:B:98:ARG:H	2:B:98:ARG:HD2	1.74	0.52
1:A:149:ASP:OD1	1:A:149:ASP:C	2.48	0.52
1:A:57:LYS:O	1:A:58:LEU:HD13	2.08	0.52
1:A:74[B]:LEU:HD22	1:A:75:HIS:N	2.25	0.51
3:C:167:ASP:O	3:C:205:SER:HB3	2.10	0.51
2:B:188:TYR:CE1	7:B:1246:GOL:H31	2.47	0.49
3:C:170:THR:HB	3:C:171:PRO:HD2	1.95	0.49
2:B:14:PHE:CZ	2:B:114:THR:HB	2.48	0.49
4:D:122:LEU:HB2	4:D:162:ASP:HB2	1.94	0.49
5:E:2:ASP:OD2	5:E:6:ARG:NH2	2.45	0.49
3:C:117:ASP:OD2	3:C:213:THR:HB	2.13	0.49
5:E:2:ASP:O	5:E:3:THR:HG22	2.12	0.49
4:D:109:ILE:HD11	4:D:119:VAL:HG21	1.94	0.49
3:C:108:ARG:NH2	3:C:204:ILE:O	2.42	0.48
5:E:29:ARG:HH12	5:E:39:ARG:NH1	2.11	0.48
3:C:39:LYS:O	3:C:63:ALA:HB2	2.13	0.48
4:D:73:MET:HG2	6:F:11:LEU:CD1	2.44	0.48
2:B:127:VAL:HG23	2:B:237:ALA:HB3	1.96	0.47
5:E:108:PRO:HA	5:E:109:LEU:HA	1.77	0.47
4:D:26:PHE:HB2	4:D:31:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:5:GLY:H	2:B:28:ASN:HD21	1.62	0.47
2:B:243:ALA:N	2:B:244:ASP:HA	2.30	0.47
3:C:213:THR:HG22	3:C:214:LYS:N	2.30	0.46
3:C:77:SER:HA	3:C:92:CYS:O	2.15	0.46
5:E:74:ALA:HA	5:E:77:THR:OG1	2.16	0.46
4:D:51:PHE:N	4:D:51:PHE:CD2	2.83	0.46
5:E:74:ALA:O	5:E:78:TYR:HB3	2.15	0.46
2:B:14:PHE:CE1	2:B:114:THR:HB	2.51	0.46
2:B:176:PRO:HG2	7:B:1246:GOL:H32	1.97	0.46
2:B:101:TYR:HH	3:C:23:HIS:CE1	2.34	0.46
2:B:175:GLN:NE2	7:B:1246:GOL:O2	2.49	0.46
3:C:20:GLN:HE21	3:C:76:ALA:HB1	1.81	0.46
4:D:14:LEU:HD11	5:E:6:ARG:HB3	1.98	0.45
5:E:19:ASN:ND2	5:E:22:GLU:OE1	2.49	0.45
5:E:144:SER:HB2	5:E:159:VAL:HG12	1.97	0.45
1:A:167:PHE:CD2	2:B:140:LYS:HE2	2.53	0.44
7:A:1201:GOL:O3	7:B:1245:GOL:H12	2.17	0.44
1:A:12:SER:OG	1:A:109[B]:LYS:HE2	2.18	0.44
5:E:117:CYS:HB2	5:E:131:TRP:CZ2	2.53	0.44
1:A:153:TYR:O	1:A:174:ALA:HA	2.17	0.44
1:A:109[A]:LYS:HE3	1:A:109[A]:LYS:HB2	1.42	0.43
3:C:213:THR:CG2	3:C:214:LYS:N	2.80	0.43
5:E:113:ASN:HB3	5:E:163:THR:OG1	2.19	0.43
4:D:16:PRO:HD2	5:E:6:ARG:HD3	2.00	0.43
2:B:28:ASN:HD22	2:B:28:ASN:N	2.15	0.43
5:E:65:LYS:O	5:E:69:GLU:HG3	2.18	0.43
1:A:10[B]:PHE:CD1	1:A:10[B]:PHE:C	2.92	0.43
3:C:39:LYS:HE3	3:C:39:LYS:HB2	1.81	0.43
4:D:97:VAL:HG21	4:D:178:TRP:HZ2	1.84	0.43
3:C:182:LYS:HD3	3:C:182:LYS:HA	1.86	0.42
3:C:33:ASP:OD1	3:C:68:ASN:HB2	2.19	0.42
2:B:54:VAL:O	2:B:55:ASN:HB2	2.20	0.42
4:D:119:VAL:HG22	4:D:165:VAL:HG22	2.01	0.42
1:A:4:LEU:HD23	1:A:25:SER:HB2	2.01	0.42
3:C:78:PHE:HB3	3:C:186:ASP:HB3	2.02	0.42
1:A:178:LYS:HE2	1:A:180:ASP:HB3	2.02	0.42
4:D:109:ILE:CD1	4:D:119:VAL:HG21	2.51	0.41
4:D:154:LEU:HA	4:D:155:PRO:HD3	1.89	0.41
4:D:51:PHE:N	4:D:51:PHE:HD2	2.18	0.41
4:D:140:ARG:CG	4:D:146:ARG:HD2	2.50	0.41
1:A:139:ASP:C	1:A:139:ASP:OD2	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:16:LYS:HE3	2:B:117:LEU:HG	2.03	0.41
2:B:90:PHE:CZ	2:B:108:GLY:HA3	2.56	0.41
2:B:157:LEU:HD11	2:B:192:SER:CB	2.51	0.41
4:D:121:TRP:CE2	4:D:151:LEU:HB2	2.56	0.41
5:E:18:PHE:HB2	5:E:23[B]:ARG:HB3	2.02	0.41
5:E:40:PHE:HB2	5:E:47:TYR:CE2	2.56	0.41
1:A:92:ALA:O	9:A:2050:HOH:O	2.22	0.40
3:C:31:LYS:HD3	3:C:70:ASN:HD22	1.87	0.40
5:E:18:PHE:HB2	5:E:23[A]:ARG:HB3	2.03	0.40
1:A:47:VAL:HG11	1:A:63:PHE:CG	2.56	0.40
4:D:73:MET:HG3	5:E:9:TRP:CZ3	2.57	0.40
5:E:21:THR:HG23	5:E:21:THR:O	2.22	0.40
5:E:119:VAL:O	5:E:119:VAL:HG23	2.22	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	203/204 (100%)	193 (95%)	9 (4%)	1 (0%)	29	35
2	B	243/244 (100%)	231 (95%)	9 (4%)	3 (1%)	13	14
3	C	214/217 (99%)	203 (95%)	10 (5%)	1 (0%)	29	35
4	D	179/182 (98%)	168 (94%)	10 (6%)	1 (1%)	25	31
5	E	188/190 (99%)	173 (92%)	11 (6%)	4 (2%)	7	5
6	F	11/13 (85%)	11 (100%)	0	0	100	100
All	All	1038/1050 (99%)	979 (94%)	49 (5%)	10 (1%)	17	17

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	152	ASP
3	C	38	GLU
2	B	226[A]	ASP
2	B	226[B]	ASP
4	D	125	GLY
1	A	127	SER
2	B	220	ASN
5	E	3	THR
5	E	106	THR
5	E	107	GLN

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	176/180 (98%)	160 (91%)	16 (9%)	9	11
2	B	212/215 (99%)	196 (92%)	16 (8%)	13	17
3	C	194/197 (98%)	187 (96%)	7 (4%)	35	49
4	D	163/166 (98%)	149 (91%)	14 (9%)	10	12
5	E	165/171 (96%)	153 (93%)	12 (7%)	14	18
6	F	12/12 (100%)	11 (92%)	1 (8%)	11	14
All	All	922/941 (98%)	856 (93%)	66 (7%)	15	18

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	SER
1	A	12	SER
1	A	57	LYS
1	A	65	PHE
1	A	70	LYS
1	A	99	ILE
1	A	109[A]	LYS
1	A	109[B]	LYS
1	A	115	PRO

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Mol	Chain	Res	Type
1	A	123[A]	ARG
1	A	123[B]	ARG
1	A	125	SER
1	A	131	SER
1	A	141	GLN
1	A	150	SER
1	A	164	SER
2	B	19	GLN
2	B	27	GLN
2	B	28	ASN
2	B	58	GLN
2	B	59	LYS
2	B	67	SER
2	B	98	ARG
2	B	116	ASP
2	B	118	LYS
2	B	136	SER
2	B	157	LEU
2	B	180	GLN
2	B	193	ARG
2	B	220	ASN
2	B	242	ARG
2	B	244	ASP
3	C	14	LEU
3	C	69	LYS
3	C	70	ASN
3	C	84	LYS
3	C	125	LEU
3	C	149	LYS
3	C	151	LYS
4	D	45	LEU
4	D	50	ARG
4	D	97	VAL
4	D	98	GLU
4	D	120	THR
4	D	122	LEU
4	D	141[A]	GLU
4	D	141[B]	GLU
4	D	154	LEU
4	D	157	THR
4	D	158	GLU
4	D	164	ARG

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Mol	Chain	Res	Type
4	D	170	LEU
4	D	171	ASP
5	E	3	THR
5	E	6	ARG
5	E	21	THR
5	E	39	ARG
5	E	50	VAL
5	E	65	LYS
5	E	67	LEU
5	E	94	ARG
5	E	107	GLN
5	E	113	ASN
5	E	159	VAL
5	E	160	MET
6	F	5	LYS

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

Mol	Chain	Res	Type
2	B	27	GLN
2	B	28	ASN
2	B	167	HIS
2	B	175	GLN
2	B	184	ASN
2	B	233	GLN
3	C	20	GLN
3	C	29	ASN
3	C	70	ASN
3	C	136	GLN
4	D	149	HIS
5	E	113	ASN
6	F	6	GLN
6	F	7	ASN

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)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	$\#\|Z\| > 2$
7	GOL	A	1201	-	5,5,5	0.51	0	5,5,5	0.47	0
7	GOL	B	1245	-	5,5,5	0.47	0	5,5,5	0.62	0
7	GOL	B	1246	-	5,5,5	0.40	0	5,5,5	0.27	0
7	GOL	B	1247	-	5,5,5	0.38	0	5,5,5	0.20	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
7	GOL	A	1201	-	-	4/4/4/4	-
7	GOL	B	1245	-	-	1/4/4/4	-
7	GOL	B	1246	-	-	2/4/4/4	-
7	GOL	B	1247	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1201	GOL	O1-C1-C2-C3
7	A	1201	GOL	C1-C2-C3-O3
7	A	1201	GOL	O2-C2-C3-O3
7	B	1247	GOL	O1-C1-C2-C3
7	A	1201	GOL	O1-C1-C2-O2
7	B	1247	GOL	O1-C1-C2-O2
7	B	1245	GOL	O1-C1-C2-C3
7	B	1246	GOL	O1-C1-C2-C3
7	B	1246	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1201	GOL	1	0
7	B	1245	GOL	1	0
7	B	1246	GOL	4	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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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	199/204 (97%)	0.20	6 (3%) 50 57	12, 24, 46, 55	0
2	B	242/244 (99%)	0.19	9 (3%) 41 48	10, 32, 53, 67	0
3	C	215/217 (99%)	0.02	5 (2%) 60 67	23, 37, 52, 60	0
4	D	178/182 (97%)	0.92	38 (21%) 0 1	29, 49, 81, 86	0
5	E	188/190 (98%)	0.57	19 (10%) 7 9	29, 50, 71, 86	0
6	F	13/13 (100%)	0.07	0 100 100	30, 34, 41, 43	0
All	All	1035/1050 (98%)	0.35	77 (7%) 14 19	10, 38, 71, 86	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	111	HIS	6.9
5	E	109	LEU	6.5
4	D	160	VAL	6.3
4	D	180	PHE	5.9
4	D	157	THR	5.3
4	D	129	THR	5.1
5	E	108	PRO	4.9
4	D	155	PRO	4.9
2	B	182	ALA	4.7
4	D	97	VAL	4.6
2	B	3	ASP	4.1
4	D	127	PRO	4.1
4	D	156	SER	4.1
4	D	153	PHE	4.1
1	A	127	SER	4.0
4	D	154	LEU	4.0
4	D	128	VAL	3.9
4	D	95	SER	3.8
4	D	158	GLU	3.6

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Mol	Chain	Res	Type	RSRZ
4	D	96	PRO	3.5
4	D	181	ASP	3.5
4	D	105	LEU	3.4
5	E	105	LYS	3.3
4	D	98	GLU	3.3
3	C	35	ILE	3.3
2	B	115	GLU	3.1
4	D	121	TRP	3.1
4	D	178	TRP	3.1
5	E	170	VAL	3.0
5	E	106	THR	3.0
5	E	110	GLN	3.0
4	D	151	LEU	3.0
5	E	145	THR	3.0
5	E	146	GLY	3.0
2	B	4	GLY	2.9
4	D	51	PHE	2.9
4	D	179	GLU	2.9
1	A	93	GLY	2.8
2	B	183	LEU	2.8
3	C	61	ASP	2.8
1	A	200	SER	2.8
2	B	224	THR	2.8
4	D	152	PRO	2.8
5	E	102	TYR	2.7
4	D	130	THR	2.7
5	E	148	ILE	2.6
5	E	112	HIS	2.6
5	E	161	LEU	2.6
1	A	179	SER	2.6
4	D	99	LEU	2.6
4	D	102	PRO	2.6
4	D	106	ILE	2.6
4	D	177	HIS	2.6
4	D	159	ASP	2.6
5	E	132	PHE	2.5
4	D	122	LEU	2.5
4	D	124	ASN	2.5
1	A	177	ASN	2.5
4	D	126	LYS	2.4
3	C	215	LYS	2.4
4	D	119	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	114	THR	2.3
4	D	103	ASN	2.3
5	E	58	ALA	2.2
5	E	164	VAL	2.2
2	B	184	ASN	2.2
4	D	100	ARG	2.1
4	D	175	LEU	2.1
4	D	132	VAL	2.1
5	E	126	SER	2.1
5	E	65	LYS	2.0
3	C	36	SER	2.0
2	B	16	LYS	2.0
4	D	174	LEU	2.0
5	E	114	LEU	2.0
1	A	10[A]	PHE	2.0
3	C	37	GLY	2.0

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

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

6.3 Carbohydrates (i)

There are no 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, 95th 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
7	GOL	B	1247	6/6	0.76	0.27	77,78,79,79	0
7	GOL	A	1201	6/6	0.80	0.22	42,49,51,51	0
7	GOL	B	1246	6/6	0.81	0.26	69,69,70,70	0
7	GOL	B	1245	6/6	0.87	0.18	34,38,40,40	0
8	NA	C	1216	1/1	0.99	0.09	22,22,22,22	0

6.5 Other polymers (i)

There are no such residues in this entry.