wwPDB X-ray Structure Validation Summary Report (i)

Sep 26, 2023 – 04:24 PM EDT

PDB ID	:	6CQQ
Title	:	Crystal structure of F24 TCR -DR15-RQ13 peptide complex
Authors	:	Farenc, C.; Gras, S.; Rossjohn, J.
Deposited on	:	2018-03-16
Resolution	:	2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

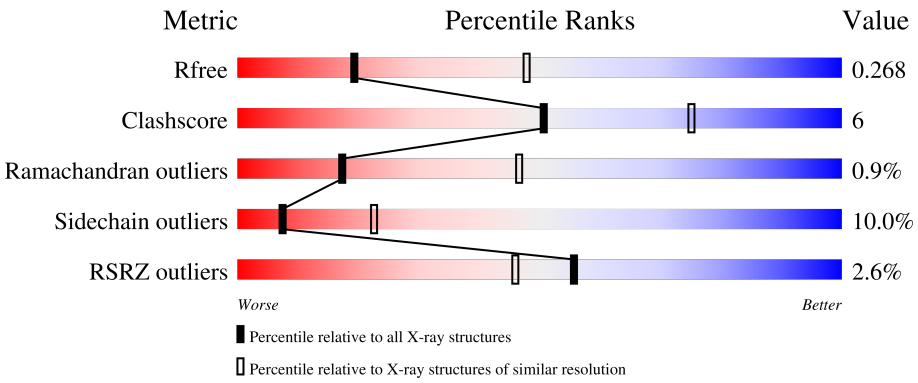
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=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	182	75% 22% • •
1	F	182	3% 81% 16% • •
2	B	190	6% 67% 28% • •
2	G	190	6% 72% 24% • •
3	C	13	85% 8% 8%

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Mol	Chain	Length	Quality of chain
3	H	13	8% 77% 15% 8%
4	D	205	% 80% 17%
4	I	205	3% 77% 19%
5	E	245	% 83% 16%
5	J	245	84% 15%

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	NAG	G	201	-	-	-	X

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 13785 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 II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1464	949	238	272	5	0	0	0
1	F	178	1464	949	238	272	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	THR	ALA	conflict	UNP P01903
F	182	THR	ALA	conflict	UNP P01903

- Molecule 2 is a protein called HLA-DRB1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	188	1545	976	274	289	6	0	0	0
2	G	189	1554	981	276	291	6	0	0	0

- Molecule 3 is a protein called Peptide from Capsid protein p24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	13	113	70	22	21	0	0	0
3	H	13	113	70	22	21	0	0	0

- Molecule 4 is a protein called F24 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	200	1575	990	259	318	8	0	3	0

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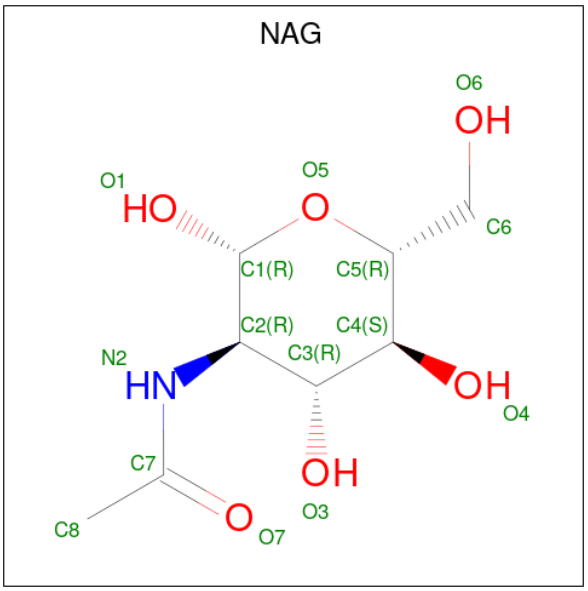
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	I	200	1575	990	259	318	8	0	3	0

- Molecule 5 is a protein called F24 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	244	1972	1250	336	378	8	0	0	0
			Total	C	N	O	S			
5	J	244	1972	1250	336	378	8	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

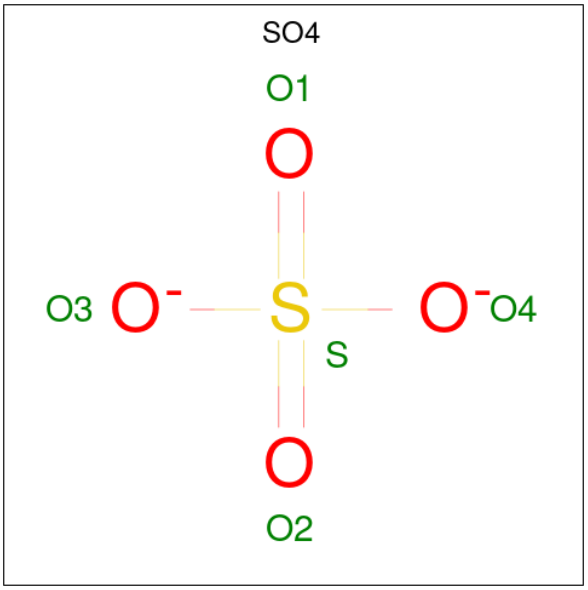


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	A	1	14	8	1	5	0	0
			Total	C	N	O		
6	F	1	14	8	1	5	0	0
			Total	C	N	O		
6	G	1	14	8	1	5	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

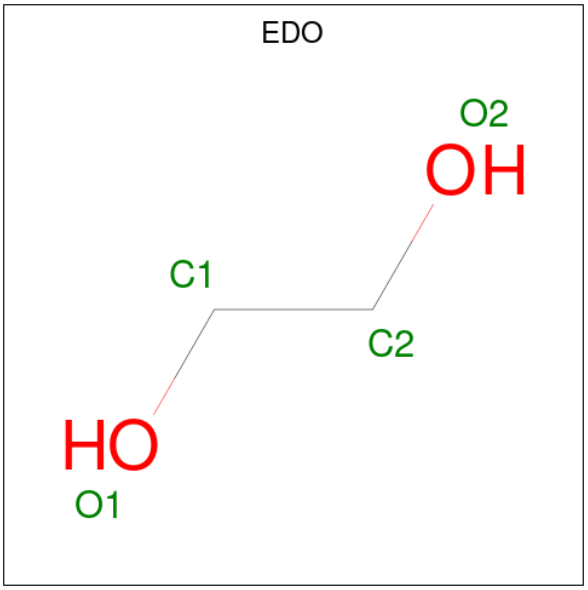
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Mg 1 1	0	0
7	C	1	Total Mg 1 1	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
9	J	1	4	2	2	0	0

- Molecule 10 is water.

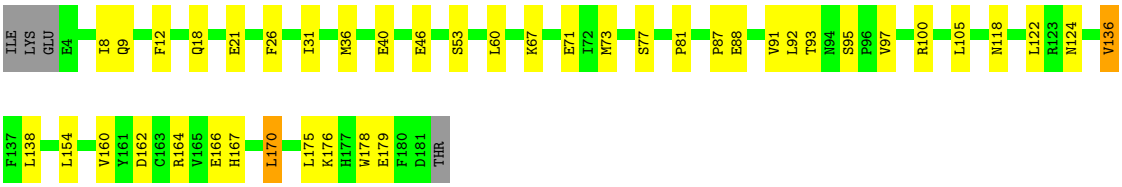
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	39	39	39	0	0
			Total	O		
10	B	23	23	23	0	0
			Total	O		
10	C	2	2	2	0	0
			Total	O		
10	D	45	45	45	0	0
			Total	O		
10	E	72	72	72	0	0
			Total	O		
10	F	30	30	30	0	0
			Total	O		
10	G	24	24	24	0	0
			Total	O		
10	H	6	6	6	0	0
			Total	O		
10	I	59	59	59	0	0
			Total	O		
10	J	85	85	85	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.

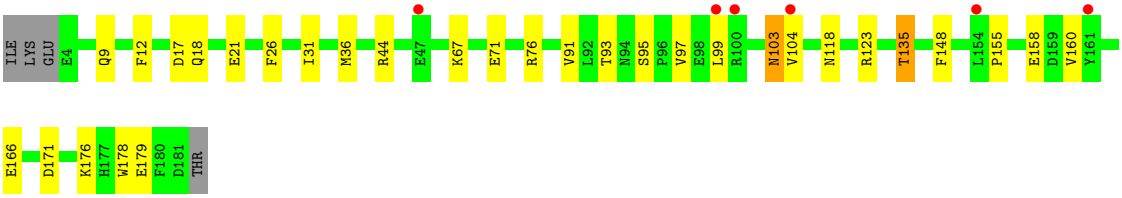
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain A:



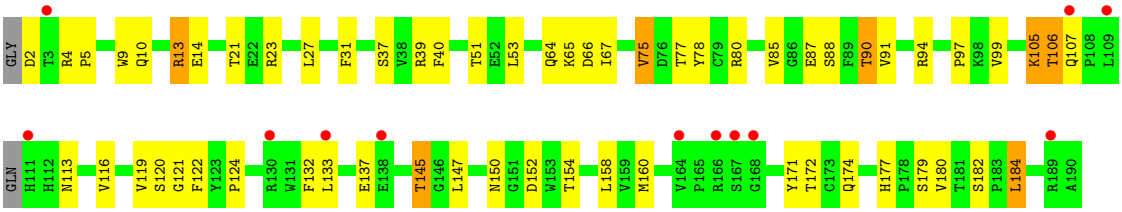
• Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

Chain F:



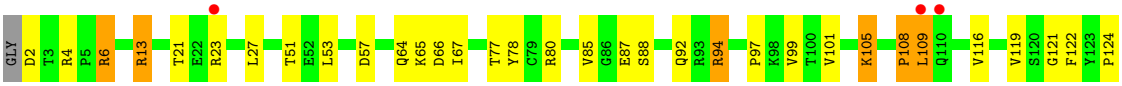
• Molecule 2: HLA-DRB1 protein

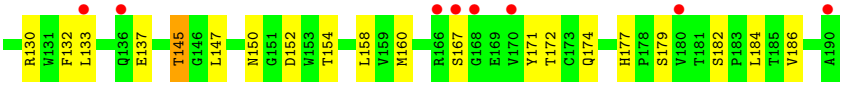
Chain B:



• Molecule 2: HLA-DRB1 protein

Chain G:





• Molecule 3: Peptide from Capsid protein p24

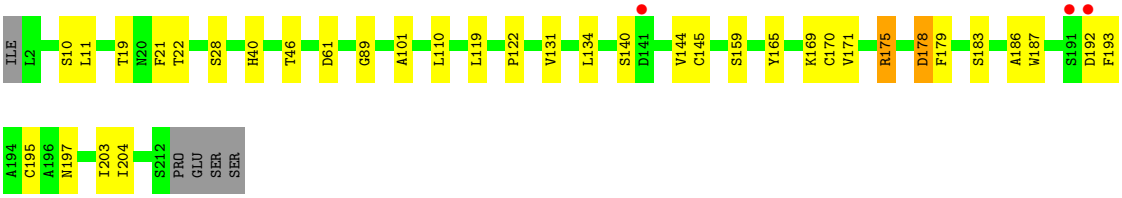
Chain C:

• Molecule 3: Peptide from Capsid protein p24

Chain H:

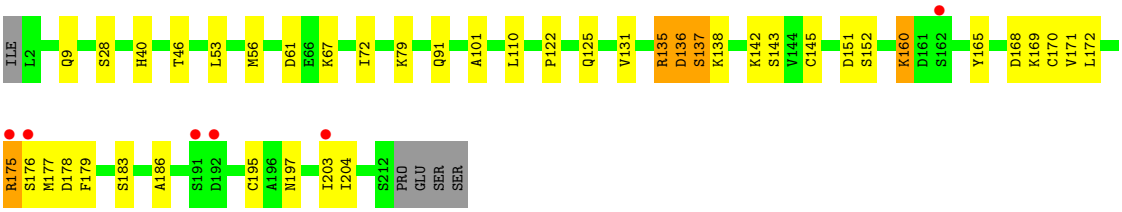
• Molecule 4: F24 alpha chain

Chain D:



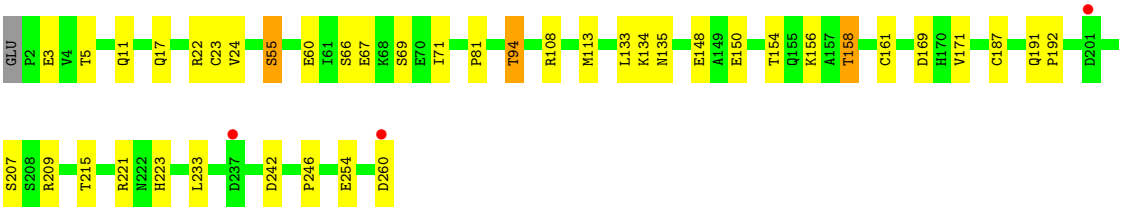
• Molecule 4: F24 alpha chain

Chain I:



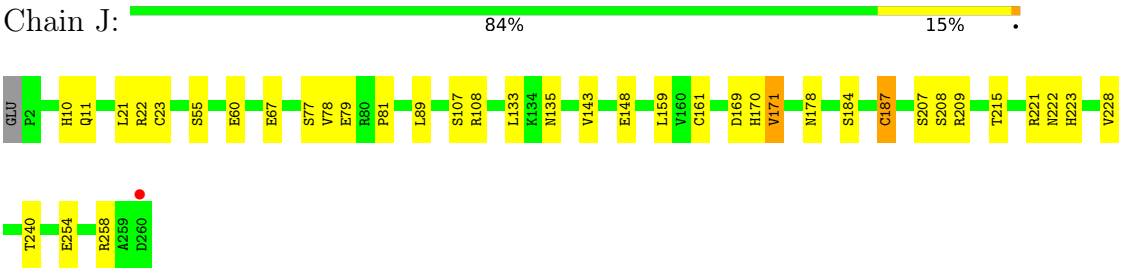
• Molecule 5: F24 beta chain

Chain E:



• Molecule 5: F24 beta chain

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.34Å 203.27Å 100.25Å 90.00° 109.16° 90.00°	Depositor
Resolution (Å)	40.99 – 2.80 40.23 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (40.99-2.80) 99.2 (40.23-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.33 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.207 , 0.254 0.216 , 0.268	Depositor DCC
R_{free} test set	3498 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	51.2	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 67.7	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	0.92	EDS
Total number of atoms	13785	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.76% 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: NAG, EDO, MG, 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	0/1509	0.76	0/2058
1	F	0.49	0/1509	0.73	0/2058
2	B	0.50	0/1587	0.74	0/2154
2	G	0.50	0/1597	0.72	0/2169
3	C	0.52	0/114	0.99	0/149
3	H	0.61	0/114	1.00	0/149
4	D	0.56	0/1621	0.81	0/2197
4	I	0.56	0/1621	0.80	0/2197
5	E	0.53	0/2026	0.76	0/2753
5	J	0.53	0/2026	0.77	0/2753
All	All	0.52	0/13724	0.77	0/18637

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (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	1464	0	1400	21	0
1	F	1464	0	1400	16	0
2	B	1545	0	1463	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	1554	0	1471	31	0
3	C	113	0	111	2	0
3	H	113	0	111	2	0
4	D	1575	0	1502	13	0
4	I	1575	0	1502	17	0
5	E	1972	0	1872	17	0
5	J	1972	0	1872	17	0
6	A	14	0	13	1	0
6	F	14	0	13	0	0
6	G	14	0	13	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
8	E	5	0	0	0	0
9	J	4	0	6	0	0
10	A	39	0	0	0	0
10	B	23	0	0	0	0
10	C	2	0	0	0	0
10	D	45	0	0	0	0
10	E	72	0	0	0	0
10	F	30	0	0	0	0
10	G	24	0	0	0	0
10	H	6	0	0	0	0
10	I	59	0	0	2	0
10	J	85	0	0	0	0
All	All	13785	0	12749	147	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 6.

The worst 5 of 147 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)
2:G:121:GLY:HA2	2:G:154:THR:HG23	1.52	0.91
2:G:150:ASN:HD22	2:G:154:THR:HG22	1.39	0.87
4:I:170:CYS:HG	5:J:187:CYS:HG	0.99	0.87
5:E:150:GLU:O	5:E:154:THR:HG22	1.77	0.84
1:F:135:THR:HG22	1:F:148:PHE:H	1.43	0.83

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	176/182 (97%)	173 (98%)	3 (2%)	0	100	100
1	F	176/182 (97%)	170 (97%)	6 (3%)	0	100	100
2	B	184/190 (97%)	171 (93%)	10 (5%)	3 (2%)	9	31
2	G	187/190 (98%)	171 (91%)	13 (7%)	3 (2%)	9	31
3	C	11/13 (85%)	11 (100%)	0	0	100	100
3	H	11/13 (85%)	11 (100%)	0	0	100	100
4	D	201/205 (98%)	188 (94%)	8 (4%)	5 (2%)	5	19
4	I	201/205 (98%)	185 (92%)	14 (7%)	2 (1%)	15	44
5	E	242/245 (99%)	232 (96%)	9 (4%)	1 (0%)	34	66
5	J	242/245 (99%)	230 (95%)	11 (4%)	1 (0%)	34	66
All	All	1631/1670 (98%)	1542 (94%)	74 (4%)	15 (1%)	17	46

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	178	ASP
4	D	193	PHE
5	E	81	PRO
4	D	192	ASP
2	G	105	LYS

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	163/167 (98%)	150 (92%)	13 (8%)	12	34
1	F	163/167 (98%)	153 (94%)	10 (6%)	18	48
2	B	169/170 (99%)	147 (87%)	22 (13%)	4	13
2	G	170/170 (100%)	148 (87%)	22 (13%)	4	13
3	C	11/11 (100%)	10 (91%)	1 (9%)	9	27
3	H	11/11 (100%)	9 (82%)	2 (18%)	1	5
4	D	180/182 (99%)	165 (92%)	15 (8%)	11	32
4	I	180/182 (99%)	156 (87%)	24 (13%)	4	12
5	E	218/219 (100%)	198 (91%)	20 (9%)	9	27
5	J	218/219 (100%)	199 (91%)	19 (9%)	10	30
All	All	1483/1498 (99%)	1335 (90%)	148 (10%)	7	22

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	I	137	SER
5	J	209	ARG
4	I	152	SER
5	J	22	ARG
4	D	197	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	177	HIS
5	J	178	ASN
5	J	183	HIS
4	I	197	ASN
1	F	18	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\#\|Z\| > 2$
8	SO4	E	301	-	4,4,4	0.12	0	6,6,6	0.22	0
6	NAG	A	201	1	14,14,15	0.32	0	17,19,21	1.00	1 (5%)
6	NAG	G	201	2	14,14,15	0.29	0	17,19,21	1.00	1 (5%)
6	NAG	F	201	1	14,14,15	0.34	0	17,19,21	1.04	1 (5%)
9	EDO	J	301	-	3,3,3	0.56	0	2,2,2	0.50	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	NAG	G	201	2	-	1/6/23/26	0/1/1/1
6	NAG	F	201	1	-	2/6/23/26	0/1/1/1
6	NAG	A	201	1	-	0/6/23/26	0/1/1/1
9	EDO	J	301	-	-	0/1/1/1	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	F	201	NAG	O5-C1-C2	-3.49	105.78	111.29
6	A	201	NAG	C1-O5-C5	3.45	116.87	112.19
6	G	201	NAG	C1-O5-C5	3.16	116.48	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	201	NAG	O5-C5-C6-O6
6	F	201	NAG	C4-C5-C6-O6
6	G	201	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	201	NAG	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 (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	178/182 (97%)	-0.25	0	100	100	26, 49, 76, 98	0
1	F	178/182 (97%)	0.10	6 (3%)	45	35	32, 61, 94, 116	0
2	B	188/190 (98%)	0.29	12 (6%)	19	12	27, 60, 97, 122	1 (0%)
2	G	189/190 (99%)	0.38	11 (5%)	23	15	36, 65, 94, 116	1 (0%)
3	C	13/13 (100%)	-0.23	0	100	100	29, 37, 61, 86	0
3	H	13/13 (100%)	0.15	1 (7%)	13	7	33, 44, 75, 87	0
4	D	200/205 (97%)	-0.13	3 (1%)	73	68	24, 43, 85, 102	1 (0%)
4	I	200/205 (97%)	-0.08	6 (3%)	50	40	25, 45, 82, 94	1 (0%)
5	E	244/245 (99%)	-0.23	3 (1%)	79	73	22, 44, 81, 104	4 (1%)
5	J	244/245 (99%)	-0.33	1 (0%)	92	91	22, 43, 74, 103	3 (1%)
All	All	1647/1670 (98%)	-0.05	43 (2%)	56	46	22, 50, 88, 122	11 (0%)

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	110	GLN	7.8
2	G	109	LEU	5.1
2	B	109	LEU	5.0
2	B	107	GLN	4.7
2	B	111	HIS	4.6

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	MG	C	201	1/1	0.76	0.31	63,63,63,63	0
6	NAG	G	201	14/15	0.77	0.41	121,123,125,125	0
6	NAG	F	201	14/15	0.89	0.22	77,88,91,91	0
8	SO4	E	301	5/5	0.90	0.15	97,97,99,100	0
7	MG	B	201	1/1	0.91	0.59	50,50,50,50	0
6	NAG	A	201	14/15	0.94	0.28	79,84,88,88	0
9	EDO	J	301	4/4	0.95	0.11	42,44,50,53	0

6.5 Other polymers (i)

There are no such residues in this entry.