Full wwPDB X-ray Structure Validation Report (i)

Nov 4, 2026 – 02:16 PM JST

PDB ID	:	44JB / pdb_000044jb
Title	:	KIR2DS2 bound to HLA-C*05:01 presenting the RecA peptide
Authors	:	Faoro, C.; Rossjohn, J.
Deposited on	:	2026-07-31
Resolution	:	2.40 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 (1)) were used in the production of this report:

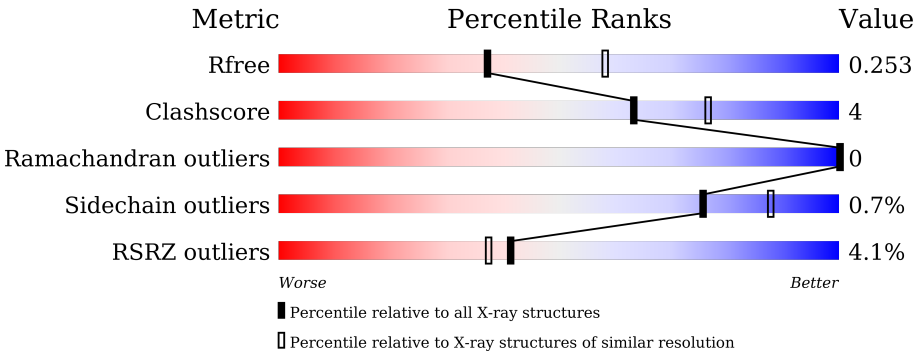
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	279	3% 87% 12%
1	E	279	2% 89% 9%
2	B	100	87% 13%
2	F	100	2% 89% 11%
3	C	9	11% 78% 22%
3	G	9	11% 89% 11%

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Mol	Chain	Length	Quality of chain
4	D	202	
4	H	202	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9497 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, C alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2226	1390	411	418	7			
1	E	275	Total	C	N	O	S	0	0	0
			2246	1401	413	425	7			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P10321
A	1	MET	-	expression tag	UNP P10321
A	9	TYR	ASP	variant	UNP P10321
A	24	ALA	SER	variant	UNP P10321
A	35	GLN	ARG	variant	UNP P10321
A	73	THR	ALA	variant	UNP P10321
A	77	ASN	SER	variant	UNP P10321
A	80	LYS	ASN	variant	UNP P10321
A	90	ALA	ASP	variant	UNP P10321
A	99	TYR	SER	variant	UNP P10321
A	114	ASN	ASP	variant	UNP P10321
A	116	PHE	SER	variant	UNP P10321
A	138	LYS	THR	variant	UNP P10321
A	147	TRP	LEU	variant	UNP P10321
A	152	GLU	ALA	variant	UNP P10321
A	156	ARG	LEU	variant	UNP P10321
A	177	LYS	GLU	variant	UNP P10321
A	184	HIS	PRO	variant	UNP P10321
A	194	VAL	LEU	variant	UNP P10321
A	253	GLU	GLN	variant	UNP P10321
A	261	VAL	MET	variant	UNP P10321
A	267	PRO	GLN	variant	UNP P10321
A	273	ARG	SER	variant	UNP P10321
A	275	GLY	GLU	variant	UNP P10321
E	0	MET	-	initiating methionine	UNP P10321

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	MET	-	expression tag	UNP P10321
E	9	TYR	ASP	variant	UNP P10321
E	24	ALA	SER	variant	UNP P10321
E	35	GLN	ARG	variant	UNP P10321
E	73	THR	ALA	variant	UNP P10321
E	77	ASN	SER	variant	UNP P10321
E	80	LYS	ASN	variant	UNP P10321
E	90	ALA	ASP	variant	UNP P10321
E	99	TYR	SER	variant	UNP P10321
E	114	ASN	ASP	variant	UNP P10321
E	116	PHE	SER	variant	UNP P10321
E	138	LYS	THR	variant	UNP P10321
E	147	TRP	LEU	variant	UNP P10321
E	152	GLU	ALA	variant	UNP P10321
E	156	ARG	LEU	variant	UNP P10321
E	177	LYS	GLU	variant	UNP P10321
E	184	HIS	PRO	variant	UNP P10321
E	194	VAL	LEU	variant	UNP P10321
E	253	GLU	GLN	variant	UNP P10321
E	261	VAL	MET	variant	UNP P10321
E	267	PRO	GLN	variant	UNP P10321
E	273	ARG	SER	variant	UNP P10321
E	275	GLY	GLU	variant	UNP P10321

- 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
			833	530	140	159	4			
2	F	100	Total	C	N	O	S	0	0	0
			828	526	139	159	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
F	0	MET	-	initiating methionine	UNP P61769

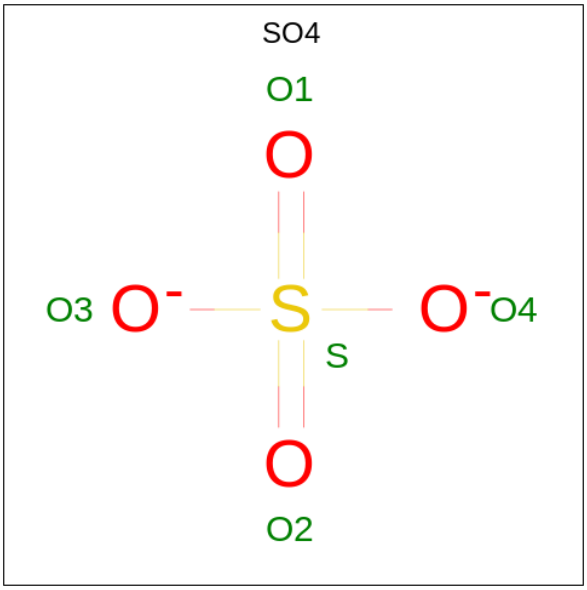
- Molecule 3 is a protein called RecA peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			73	49	11	13			
3	G	9	Total	C	N	O	0	0	0
			73	49	11	13			

- Molecule 4 is a protein called Killer cell immunoglobulin-like receptor 2DS2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	195	Total	C	N	O	S	0	0	0
			1491	943	258	283	7			
4	H	195	Total	C	N	O	S	0	0	0
			1495	944	258	286	7			

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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

- Molecule 6 is water.

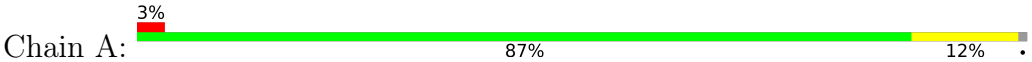
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	36	Total O 36 36	0	0
6	B	11	Total O 11 11	0	0
6	C	4	Total O 4 4	0	0
6	D	21	Total O 21 21	0	0
6	E	50	Total O 50 50	0	0
6	F	20	Total O 20 20	0	0
6	G	6	Total O 6 6	0	0
6	H	19	Total O 19 19	0	0

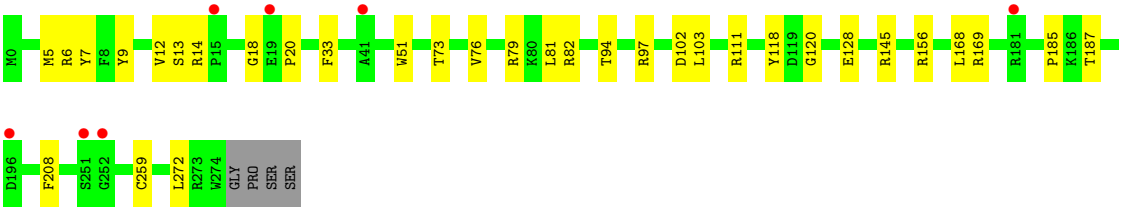
3 Residue-property plots (i)

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 I histocompatibility antigen, C alpha chain

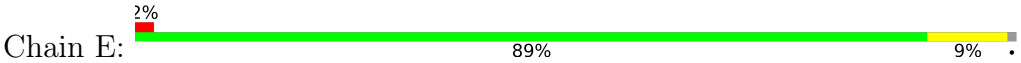
Chain A:

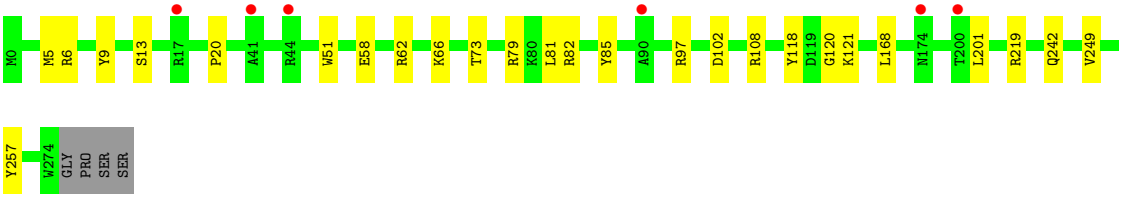




• Molecule 1: HLA class I histocompatibility antigen, C alpha chain

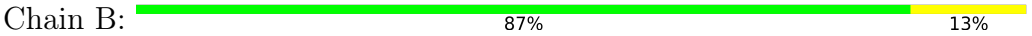
Chain E:

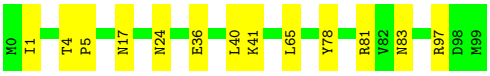




• Molecule 2: Beta-2-microglobulin

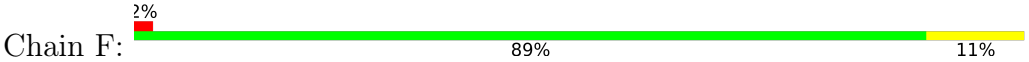
Chain B:





• Molecule 2: Beta-2-microglobulin

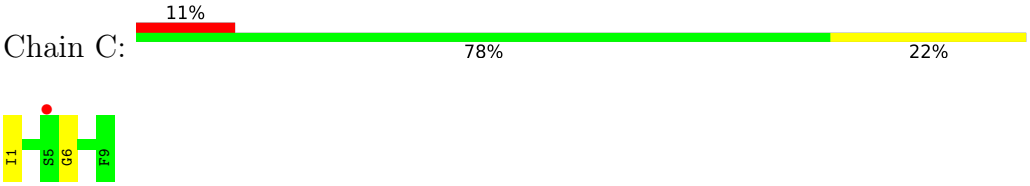
Chain F:





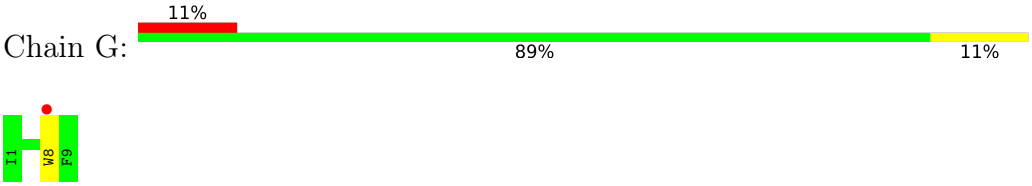
• Molecule 3: RecA peptide

Chain C:



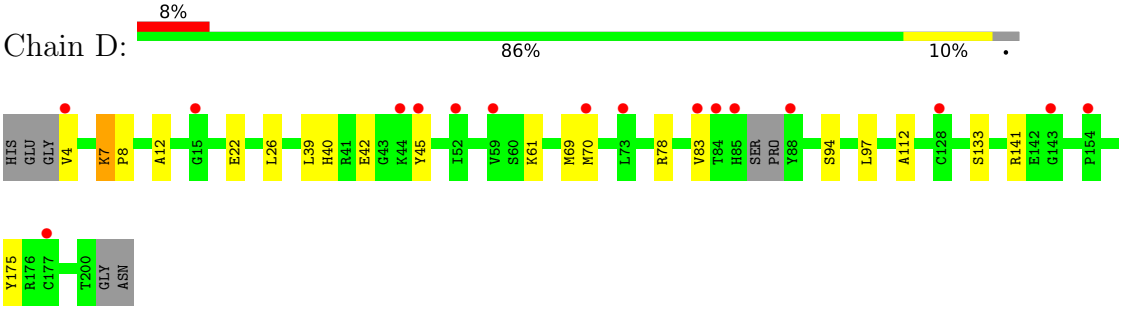
• Molecule 3: RecA peptide

Chain G:



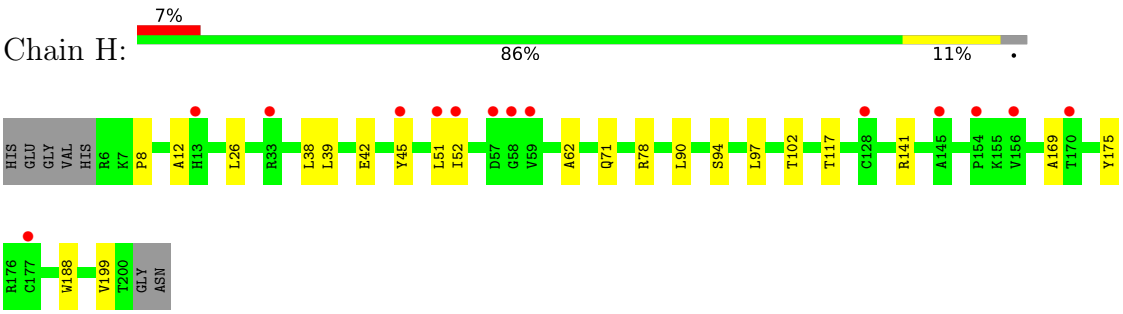
• Molecule 4: Killer cell immunoglobulin-like receptor 2DS2

Chain D:



• Molecule 4: Killer cell immunoglobulin-like receptor 2DS2

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	48.05Å 70.24Å 228.68Å 90.00° 94.51° 90.00°	Depositor
Resolution (Å)	47.91 – 2.40 47.91 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.7 (47.91-2.40) 97.6 (47.91-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.63 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5058	Depositor
R, R_{free}	0.228 , 0.253 0.228 , 0.253	Depositor DCC
R_{free} test set	1984 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å^2)	41.7	Xtriage
Anisotropy	0.877	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 45.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.052 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	9497	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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: 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	0.07	0/2288	0.22	0/3109
1	E	0.07	0/2308	0.22	0/3133
2	B	0.07	0/856	0.23	0/1158
2	F	0.07	0/851	0.24	0/1152
3	C	0.12	0/75	0.30	0/99
3	G	0.13	0/75	0.30	0/99
4	D	0.10	0/1534	0.32	0/2085
4	H	0.10	0/1538	0.29	0/2091
All	All	0.08	0/9525	0.25	0/12926

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

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	2226	0	2074	26	0
1	E	2246	0	2103	19	0
2	B	833	0	792	7	0
2	F	828	0	780	6	0
3	C	73	0	71	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	73	0	71	1	0
4	D	1491	0	1409	11	0
4	H	1495	0	1425	12	0
5	A	20	0	0	1	0
5	B	5	0	0	0	0
5	D	25	0	0	1	0
5	E	5	0	0	0	0
5	H	10	0	0	0	0
6	A	36	0	0	0	0
6	B	11	0	0	0	0
6	C	4	0	0	1	0
6	D	21	0	0	1	0
6	E	50	0	0	0	0
6	F	20	0	0	0	0
6	G	6	0	0	0	0
6	H	19	0	0	0	0
All	All	9497	0	8725	73	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 4.

All (73) 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)
4:H:8:PRO:HG2	4:H:94:SER:HB3	1.76	0.68
1:A:14:ARG:HH11	1:A:18:GLY:HA3	1.64	0.63
4:D:112:ALA:O	1:E:108:ARG:NH2	2.32	0.63
1:E:5:MET:HB2	1:E:168:LEU:HD13	1.80	0.62
1:A:82:ARG:NH2	4:D:45:TYR:OH	2.33	0.61
4:H:141:ARG:NH1	4:H:175:TYR:OH	2.34	0.60
4:D:7:LYS:HG3	4:D:94:SER:HA	1.83	0.60
2:B:36:GLU:HB3	2:B:83:ASN:HB3	1.85	0.59
1:E:82:ARG:NH2	4:H:45:TYR:OH	2.36	0.58
4:H:26:LEU:HD12	4:H:39:LEU:HD21	1.86	0.57
1:E:73:THR:HG23	3:G:8:TRP:HD1	1.69	0.57
4:D:141:ARG:NH1	4:D:175:TYR:OH	2.37	0.56
1:E:62:ARG:HG2	1:E:66:LYS:HE2	1.87	0.56
1:E:9:TYR:HB2	1:E:97:ARG:HB3	1.86	0.56
2:B:40:LEU:HD21	2:B:81:ARG:HB2	1.87	0.56
4:H:38:LEU:HD12	4:H:90:LEU:HD21	1.88	0.56
1:A:120:GLY:HA3	2:B:1:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:40:HIS:NE2	5:D:305:SO4:O4	2.33	0.55
2:F:36:GLU:HB3	2:F:83:ASN:HB3	1.89	0.55
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.88	0.55
1:A:6:ARG:NH1	1:A:102:ASP:OD1	2.42	0.53
4:H:42:GLU:CD	4:H:78:ARG:HH12	2.17	0.53
1:E:242:GLN:NE2	2:F:12:ARG:O	2.43	0.52
4:D:26:LEU:HD12	4:D:39:LEU:HD21	1.93	0.51
1:E:120:GLY:HA3	2:F:1:ILE:HD11	1.92	0.51
3:C:6:GLY:N	6:C:101:HOH:O	2.39	0.51
1:A:13:SER:HA	1:A:20:PRO:HB3	1.92	0.51
1:A:187:THR:HB	1:A:272:LEU:HD11	1.93	0.51
1:A:12:VAL:HG22	1:A:94:THR:HG22	1.94	0.50
1:E:85:TYR:OH	1:E:121:LYS:NZ	2.38	0.48
4:D:8:PRO:HG2	4:D:94:SER:HB3	1.96	0.47
2:F:17:ASN:OD1	2:F:97:ARG:NH2	2.47	0.47
1:A:9:TYR:HB2	1:A:97:ARG:HB3	1.96	0.47
4:H:12:ALA:HB2	4:H:97:LEU:HD21	1.97	0.47
1:E:81:LEU:HD13	1:E:118:TYR:CD1	2.50	0.46
1:E:201:LEU:HD12	1:E:249:VAL:HG21	1.98	0.46
1:E:13:SER:HA	1:E:20:PRO:HB3	1.98	0.46
2:F:24:ASN:HB3	2:F:65:LEU:HD11	1.98	0.45
1:A:156:ARG:HH11	1:A:156:ARG:HA	1.81	0.45
1:A:185:PRO:HB3	1:A:208:PHE:HB3	1.98	0.45
4:D:12:ALA:HB2	4:D:97:LEU:HD21	1.99	0.45
1:A:5:MET:HE2	1:A:7:TYR:HE2	1.83	0.44
1:A:79:ARG:NH2	5:A:301:SO4:O2	2.51	0.44
1:E:9:TYR:CD2	1:E:97:ARG:HD3	2.52	0.44
1:A:51:TRP:CD1	1:A:51:TRP:H	2.35	0.44
2:F:96:ASP:HB3	2:F:99:MET:HB3	2.00	0.44
1:A:5:MET:HE1	3:C:1:ILE:H2	1.83	0.43
4:H:102:THR:HG22	4:H:188:TRP:HB2	2.00	0.43
1:A:81:LEU:HD13	1:A:118:TYR:CD1	2.53	0.43
1:E:118:TYR:O	1:E:121:LYS:HG3	2.18	0.43
1:A:5:MET:HE3	1:A:33:PHE:HZ	1.84	0.43
1:A:145:ARG:NH2	6:D:401:HOH:O	2.52	0.43
1:E:6:ARG:NH1	1:E:102:ASP:OD1	2.52	0.42
4:H:51:LEU:HD23	4:H:62:ALA:HB1	2.00	0.42
2:B:41:LYS:NZ	2:B:78:TYR:OH	2.49	0.42
1:A:169:ARG:HH21	4:H:117:THR:HG22	1.84	0.42
1:E:51:TRP:CD1	1:E:51:TRP:H	2.37	0.42
1:E:79:ARG:NH1	4:H:71:GLN:OE1	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:GLU:H	1:E:58:GLU:CD	2.27	0.42
1:A:14:ARG:HD3	1:A:18:GLY:HA3	2.02	0.42
4:D:22:GLU:O	4:D:69:MET:N	2.52	0.42
4:H:169:ALA:HB1	4:H:199:VAL:HG22	2.02	0.42
1:A:103:LEU:HD13	1:A:168:LEU:HD23	2.02	0.41
1:A:259:CYS:HB3	1:A:272:LEU:HB2	2.03	0.41
1:E:219:ARG:HG3	1:E:257:TYR:CZ	2.56	0.41
4:D:42:GLU:OE2	4:D:78:ARG:NE	2.50	0.41
1:A:73:THR:O	1:A:76:VAL:HG22	2.20	0.41
1:A:145:ARG:NH2	4:D:133:SER:O	2.53	0.41
2:B:17:ASN:OD1	2:B:97:ARG:NH2	2.51	0.41
2:B:24:ASN:HB3	2:B:65:LEU:HD11	2.02	0.41
2:B:4:THR:HA	2:B:5:PRO:HD3	1.94	0.40
1:A:111:ARG:CZ	1:A:128:GLU:HG2	2.51	0.40
1:A:5:MET:HE2	1:A:7:TYR:CE2	2.57	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	273/279 (98%)	267 (98%)	6 (2%)	0	100	100
1	E	273/279 (98%)	267 (98%)	6 (2%)	0	100	100
2	B	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
2	F	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	G	7/9 (78%)	7 (100%)	0	0	100	100
4	D	191/202 (95%)	185 (97%)	6 (3%)	0	100	100
4	H	193/202 (96%)	187 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1140/1180 (97%)	1113 (98%)	27 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	223/234 (95%)	223 (100%)	0	100 100
1	E	228/234 (97%)	228 (100%)	0	100 100
2	B	94/95 (99%)	94 (100%)	0	100 100
2	F	93/95 (98%)	92 (99%)	1 (1%)	65 82
3	C	7/7 (100%)	7 (100%)	0	100 100
3	G	7/7 (100%)	7 (100%)	0	100 100
4	D	162/173 (94%)	157 (97%)	5 (3%)	35 57
4	H	164/173 (95%)	163 (99%)	1 (1%)	78 89
All	All	978/1018 (96%)	971 (99%)	7 (1%)	76 88

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	4	VAL
4	D	7	LYS
4	D	61	LYS
4	D	70	MET
4	D	83	VAL
2	F	75	LYS
4	H	52	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	HIS
2	B	13	HIS
4	D	13	HIS
2	F	13	HIS
4	H	13	HIS
4	H	27	GLN
4	H	55	HIS
4	H	63	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

13 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	H	302	-	4,4,4	0.59	0	6,6,6	0.05	0
5	SO4	D	302	-	4,4,4	0.60	0	6,6,6	0.05	0
5	SO4	E	301	-	4,4,4	0.59	0	6,6,6	0.08	0
5	SO4	D	303	-	4,4,4	0.59	0	6,6,6	0.06	0
5	SO4	A	302	-	4,4,4	0.60	0	6,6,6	0.05	0
5	SO4	H	301	-	4,4,4	0.59	0	6,6,6	0.04	0
5	SO4	D	304	-	4,4,4	0.58	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	SO4	A	303	-	4,4,4	0.59	0	6,6,6	0.05	0
5	SO4	A	301	-	4,4,4	0.59	0	6,6,6	0.05	0
5	SO4	A	304	-	4,4,4	0.59	0	6,6,6	0.05	0
5	SO4	D	305	-	4,4,4	0.59	0	6,6,6	0.05	0
5	SO4	D	301	-	4,4,4	0.60	0	6,6,6	0.05	0
5	SO4	B	101	-	4,4,4	0.59	0	6,6,6	0.05	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	301	SO4	1	0
5	D	305	SO4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{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	275/279 (98%)	0.36	7 (2%) 58 54	33, 53, 85, 104	0
1	E	275/279 (98%)	0.29	6 (2%) 62 58	27, 48, 84, 100	0
2	B	100/100 (100%)	0.37	0 100 100	37, 49, 84, 95	0
2	F	100/100 (100%)	0.30	2 (2%) 65 60	30, 49, 80, 95	0
3	C	9/9 (100%)	1.17	1 (11%) 10 7	46, 62, 70, 71	0
3	G	9/9 (100%)	0.87	1 (11%) 10 7	42, 44, 57, 60	0
4	D	195/202 (96%)	0.84	16 (8%) 17 14	37, 61, 96, 113	0
4	H	195/202 (96%)	0.68	14 (7%) 21 18	33, 56, 86, 103	0
All	All	1158/1180 (98%)	0.49	47 (4%) 41 37	27, 53, 88, 113	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	4	VAL	3.9
4	H	57	ASP	3.7
4	H	51	LEU	3.6
4	D	45	TYR	3.4
4	D	59	VAL	3.2
4	H	45	TYR	3.1
1	E	90	ALA	3.0
2	F	99	MET	2.9
1	A	181	ARG	2.8
4	H	145	ALA	2.8
3	C	5	SER	2.7
4	H	128	CYS	2.6
4	D	85	HIS	2.6
2	F	1	ILE	2.6
1	A	41	ALA	2.5
4	H	156	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
4	D	84	THR	2.5
4	D	52	ILE	2.4
1	A	19	GLU	2.4
4	D	15	GLY	2.4
4	D	128	CYS	2.4
1	A	252	GLY	2.3
4	H	177	CYS	2.3
4	D	83	VAL	2.3
4	D	143	GLY	2.3
4	H	13	HIS	2.3
4	D	154	PRO	2.3
1	A	196	ASP	2.2
4	H	170	THR	2.2
3	G	8	TRP	2.2
1	A	15	PRO	2.2
1	E	44	ARG	2.2
4	H	154	PRO	2.2
4	H	59	VAL	2.2
4	D	177	CYS	2.2
4	H	52	ILE	2.2
4	D	44	LYS	2.2
1	E	41	ALA	2.1
1	E	17	ARG	2.1
4	H	33	ARG	2.1
4	H	58	GLY	2.1
1	E	200	THR	2.1
4	D	70	MET	2.1
1	E	174	ASN	2.0
1	A	251	SER	2.0
4	D	73	LEU	2.0
4	D	88	TYR	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 oligosaccharides 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
5	SO4	B	101	5/5	0.37	0.12	114,120,128,130	0
5	SO4	D	305	5/5	0.49	0.15	90,93,113,116	0
5	SO4	A	304	5/5	0.69	0.08	101,107,117,121	0
5	SO4	D	304	5/5	0.73	0.18	65,73,89,91	0
5	SO4	A	303	5/5	0.79	0.09	74,80,99,105	0
5	SO4	A	301	5/5	0.84	0.11	99,101,106,112	0
5	SO4	A	302	5/5	0.85	0.08	78,79,96,107	0
5	SO4	E	301	5/5	0.87	0.08	71,76,95,97	0
5	SO4	D	303	5/5	0.90	0.12	66,69,75,76	0
5	SO4	H	301	5/5	0.91	0.14	57,58,80,89	0
5	SO4	D	301	5/5	0.92	0.09	55,57,70,74	0
5	SO4	H	302	5/5	0.92	0.12	57,65,71,74	0
5	SO4	D	302	5/5	0.93	0.14	57,60,66,68	0

6.5 Other polymers (i)

There are no such residues in this entry.