



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:28 pm GMT

PDB ID : 4J6K
Title : Crystal structure of calcium²⁺-free wild-type CD23 lectin domain (crystal form B)
Authors : Dhaliwal, B.; Pang, M.O.Y.; Sutton, B.J.
Deposited on : 2013-02-11
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

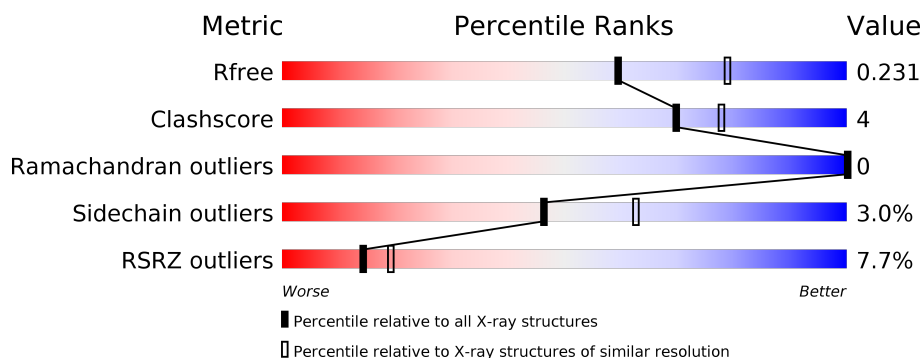
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	143	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>9%</div> <div>11%</div> </div> </div>
1	B	143	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>6%</div> <div>16%</div> </div> </div>
1	C	143	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>12%</div> </div> </div>
1	D	143	<div> <div>3%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>7%</div> </div> </div>
1	E	143	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>5%</div> <div>10%</div> </div> </div>
1	F	143	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>10%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	143	<div><div></div><div>6%</div><div>81%</div><div>10%</div><div>8%</div></div>
1	H	143	<div><div></div><div>25%</div><div>74%</div><div>13%</div><div>13%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8366 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 Low affinity immunoglobulin epsilon Fc receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			1025	640	184	190	11			
1	B	120	Total	C	N	O	S	0	0	0
			974	612	173	180	9			
1	C	126	Total	C	N	O	S	0	0	0
			1019	639	183	188	9			
1	D	133	Total	C	N	O	S	0	0	0
			1067	668	191	197	11			
1	E	129	Total	C	N	O	S	0	0	0
			1042	654	186	191	11			
1	F	129	Total	C	N	O	S	0	0	0
			1040	651	187	192	10			
1	G	131	Total	C	N	O	S	0	0	0
			1055	662	189	194	10			
1	H	124	Total	C	N	O	S	0	0	0
			997	625	177	185	10			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

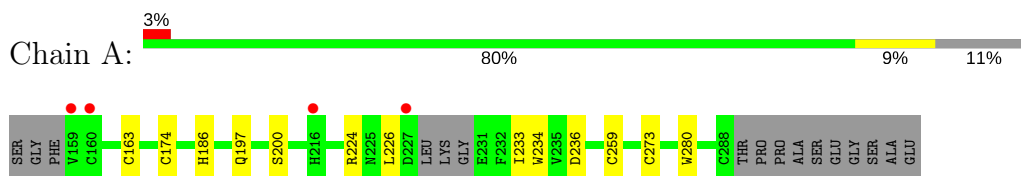
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	34	Total	O	0	0
			34	34		
3	B	13	Total	O	0	0
			13	13		
3	C	6	Total	O	0	0
			6	6		
3	D	24	Total	O	0	0
			24	24		
3	E	11	Total	O	0	0
			11	11		
3	F	8	Total	O	0	0
			8	8		
3	G	20	Total	O	0	0
			20	20		
3	H	11	Total	O	0	0
			11	11		

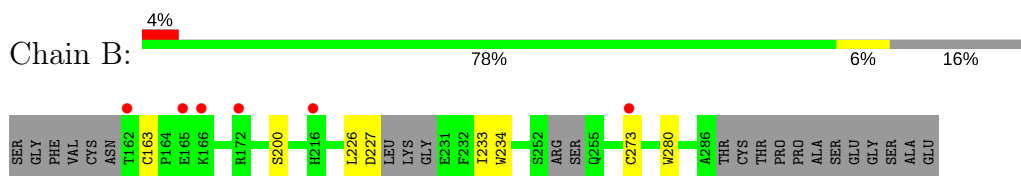
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

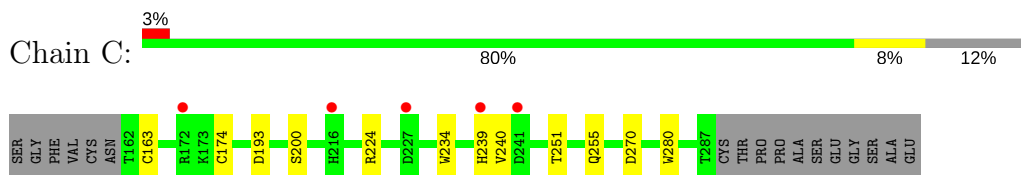
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



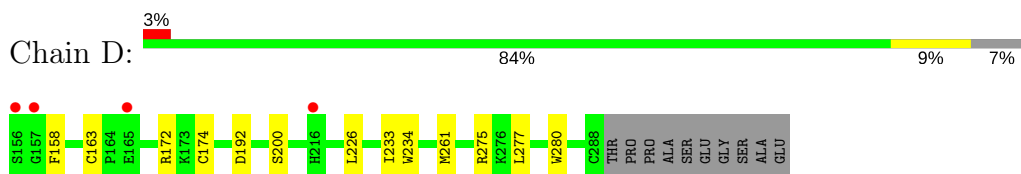
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



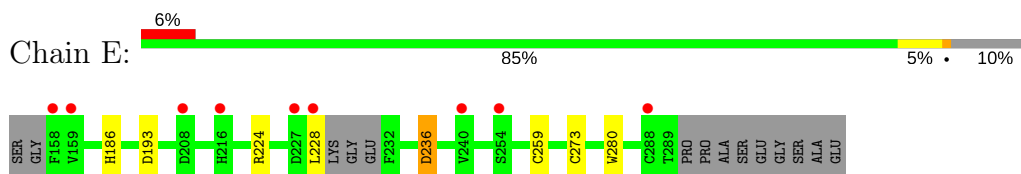
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



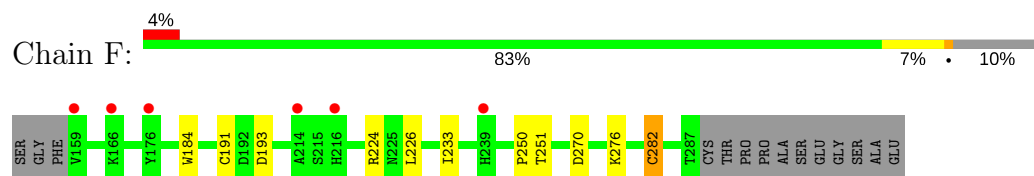
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



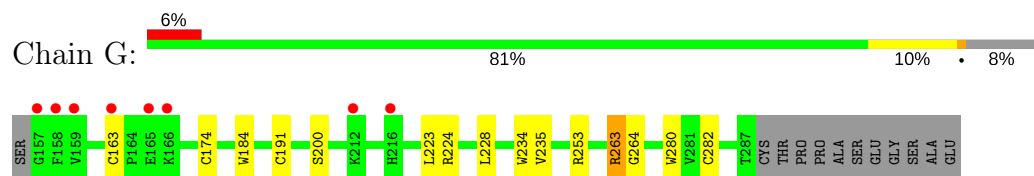
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



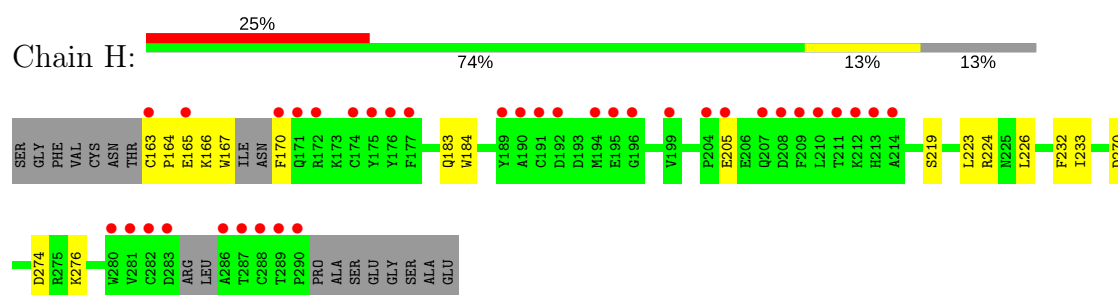
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.56Å 56.13Å 108.52Å 79.79° 84.85° 70.22°	Depositor
Resolution (Å)	45.42 – 2.30 45.42 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.2 (45.42-2.30) 87.7 (45.42-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.191 , 0.218 0.201 , 0.231	Depositor DCC
R_{free} test set	2390 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8366	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: 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	0.57	0/1055	0.69	0/1427
1	B	0.54	0/1003	0.73	0/1355
1	C	0.47	0/1050	0.67	0/1420
1	D	0.57	0/1099	0.71	0/1486
1	E	0.46	0/1073	0.69	0/1452
1	F	0.47	0/1071	0.67	0/1449
1	G	0.55	0/1087	0.71	0/1470
1	H	0.51	0/1027	0.71	0/1387
All	All	0.52	0/8465	0.70	0/11446

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	1025	0	941	5	0
1	B	974	0	890	3	0
1	C	1019	0	944	6	0
1	D	1067	0	986	7	0
1	E	1042	0	962	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1040	0	964	8	0
1	G	1055	0	974	9	0
1	H	997	0	913	11	0
2	D	5	0	0	0	0
2	F	5	0	0	0	0
2	G	5	0	0	0	0
2	H	5	0	0	0	0
3	A	34	0	0	0	0
3	B	13	0	0	1	0
3	C	6	0	0	0	0
3	D	24	0	0	0	0
3	E	11	0	0	0	0
3	F	8	0	0	2	0
3	G	20	0	0	2	0
3	H	11	0	0	1	0
All	All	8366	0	7574	49	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 (49) 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:163:CYS:HG	1:A:174:CYS:HG	1.20	0.88
1:G:163:CYS:HG	1:G:174:CYS:HG	1.15	0.88
1:G:253:ARG:NH2	3:G:417:HOH:O	2.18	0.76
1:D:163:CYS:HG	1:D:174:CYS:HG	1.23	0.71
1:B:273:CYS:SG	3:B:307:HOH:O	2.28	0.71
1:F:184:TRP:CH2	1:F:224:ARG:HD2	2.30	0.67
1:F:191:CYS:HG	1:F:282:CYS:HG	1.36	0.67
1:C:163:CYS:HG	1:C:174:CYS:HG	1.34	0.66
1:C:255:GLN:HG3	1:H:274:ASP:HB3	1.77	0.65
1:H:184:TRP:CH2	1:H:224:ARG:HD2	2.33	0.64
1:F:184:TRP:CZ2	1:F:224:ARG:HD2	2.32	0.64
1:H:184:TRP:CZ2	1:H:224:ARG:HD2	2.33	0.64
1:G:263:ARG:HE	1:G:264:GLY:H	1.54	0.55
1:A:200:SER:HA	1:A:234:TRP:CE3	2.42	0.54
1:D:200:SER:HA	1:D:234:TRP:CE3	2.42	0.54
1:G:235:VAL:HG22	3:G:412:HOH:O	2.07	0.53
1:A:226:LEU:HD12	1:A:233:ILE:HD12	1.91	0.52
1:D:261:MET:HE1	1:D:275:ARG:CZ	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:270:ASP:HB2	3:F:406:HOH:O	2.12	0.49
1:H:165:GLU:O	1:H:167:TRP:HD1	1.96	0.49
1:G:184:TRP:CH2	1:G:224:ARG:HD3	2.48	0.48
1:D:226:LEU:HD12	1:D:233:ILE:HD12	1.95	0.47
1:A:259:CYS:HG	1:A:273:CYS:HG	0.53	0.47
1:D:163:CYS:HG	1:D:174:CYS:CB	2.27	0.47
1:G:263:ARG:HE	1:G:264:GLY:N	2.12	0.47
1:A:197:GLN:OE1	1:A:236:ASP:HB3	2.16	0.46
1:C:193:ASP:HA	1:F:276:LYS:HE2	1.97	0.45
1:G:200:SER:HA	1:G:234:TRP:CE3	2.52	0.45
1:H:226:LEU:HD12	1:H:233:ILE:HD12	1.98	0.45
1:E:259:CYS:HG	1:E:273:CYS:CB	2.28	0.45
1:F:191:CYS:HG	1:F:282:CYS:CB	2.29	0.45
1:C:163:CYS:HG	1:C:174:CYS:CB	2.31	0.44
1:C:239:HIS:CD2	1:C:240:VAL:H	2.36	0.44
1:E:193:ASP:HA	1:H:276:LYS:HE2	1.99	0.44
1:G:223:LEU:HB2	1:G:234:TRP:CZ3	2.53	0.44
1:B:200:SER:HA	1:B:234:TRP:CE3	2.53	0.43
1:E:193:ASP:OD1	1:H:183:GLN:HG3	2.19	0.43
1:D:261:MET:HE1	1:D:277:LEU:HD21	1.99	0.43
1:H:224:ARG:HD3	3:H:402:HOH:O	2.19	0.42
1:F:250:PRO:HA	3:F:406:HOH:O	2.19	0.42
1:B:226:LEU:O	1:B:227:ASP:HB2	2.20	0.42
1:E:236:ASP:N	1:E:236:ASP:OD2	2.51	0.42
1:H:170:PHE:HZ	1:H:205:GLU:HB3	1.85	0.42
1:D:158:PHE:HB3	1:D:172:ARG:HH22	1.84	0.41
1:F:226:LEU:HD12	1:F:233:ILE:HD12	2.01	0.41
1:G:191:CYS:HG	1:G:282:CYS:HG	0.41	0.41
1:H:223:LEU:HD11	1:H:232:PHE:HB3	2.03	0.41
1:C:200:SER:HA	1:C:234:TRP:CE3	2.57	0.40
1:H:163:CYS:HA	1:H:164:PRO:HD3	1.98	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	123/143 (86%)	116 (94%)	7 (6%)	0	100	100
1	B	114/143 (80%)	110 (96%)	4 (4%)	0	100	100
1	C	124/143 (87%)	119 (96%)	5 (4%)	0	100	100
1	D	131/143 (92%)	126 (96%)	5 (4%)	0	100	100
1	E	125/143 (87%)	119 (95%)	6 (5%)	0	100	100
1	F	127/143 (89%)	123 (97%)	4 (3%)	0	100	100
1	G	129/143 (90%)	125 (97%)	4 (3%)	0	100	100
1	H	118/143 (82%)	110 (93%)	8 (7%)	0	100	100
All	All	991/1144 (87%)	948 (96%)	43 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	109/120 (91%)	106 (97%)	3 (3%)	49	65
1	B	102/120 (85%)	99 (97%)	3 (3%)	48	64
1	C	107/120 (89%)	103 (96%)	4 (4%)	39	53
1	D	113/120 (94%)	111 (98%)	2 (2%)	64	79
1	E	111/120 (92%)	106 (96%)	5 (4%)	32	44
1	F	110/120 (92%)	107 (97%)	3 (3%)	50	67
1	G	111/120 (92%)	108 (97%)	3 (3%)	50	67
1	H	105/120 (88%)	102 (97%)	3 (3%)	48	64
All	All	868/960 (90%)	842 (97%)	26 (3%)	46	63

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	186	HIS
1	A	224	ARG
1	A	280	TRP
1	B	163	CYS
1	B	233	ILE
1	B	280	TRP
1	C	224	ARG
1	C	251	THR
1	C	270	ASP
1	C	280	TRP
1	D	192	ASP
1	D	280	TRP
1	E	186	HIS
1	E	224	ARG
1	E	228	LEU
1	E	236	ASP
1	E	280	TRP
1	F	193	ASP
1	F	251	THR
1	F	282	CYS
1	G	228	LEU
1	G	263	ARG
1	G	280	TRP
1	H	166	LYS
1	H	219	SER
1	H	270	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	239	HIS
1	D	161	ASN
1	D	216	HIS
1	E	202	HIS
1	G	183	GLN
1	G	269	ASN
1	H	216	HIS

5.3.3 RNA ⓘ

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
2	SO4	D	301	-	4,4,4	0.18	0	6,6,6	0.50	0
2	SO4	F	301	-	4,4,4	0.23	0	6,6,6	0.37	0
2	SO4	G	301	-	4,4,4	0.26	0	6,6,6	0.24	0
2	SO4	H	301	-	4,4,4	0.32	0	6,6,6	0.26	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
2	SO4	D	301	-	-	0/0/0/0	0/0/0/0
2	SO4	F	301	-	-	0/0/0/0	0/0/0/0
2	SO4	G	301	-	-	0/0/0/0	0/0/0/0
2	SO4	H	301	-	-	0/0/0/0	0/0/0/0

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.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	127/143 (88%)	0.15	4 (3%)	49	56	17, 34, 58, 106	0
1	B	120/143 (83%)	0.32	6 (5%)	30	36	18, 43, 85, 102	0
1	C	126/143 (88%)	0.42	5 (3%)	39	46	30, 57, 89, 109	0
1	D	133/143 (93%)	0.20	4 (3%)	51	58	19, 39, 78, 102	0
1	E	129/143 (90%)	0.57	9 (6%)	17	23	35, 60, 92, 124	0
1	F	129/143 (90%)	0.53	6 (4%)	32	39	32, 58, 102, 130	0
1	G	131/143 (91%)	0.35	8 (6%)	22	28	21, 39, 82, 126	0
1	H	124/143 (86%)	1.44	36 (29%)	1	1	32, 67, 110, 185	0
All	All	1019/1144 (89%)	0.49	78 (7%)	14	19	17, 49, 92, 185	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	157	GLY	10.4
1	H	163	CYS	7.5
1	H	290	PRO	7.0
1	H	175	TYR	6.8
1	H	212	LYS	6.7
1	C	227	ASP	5.8
1	H	289	THR	5.5
1	E	158	PHE	5.4
1	H	176	TYR	5.3
1	H	196	GLY	5.2
1	H	204	PRO	5.2
1	D	156	SER	5.1
1	H	205	GLU	4.9
1	F	166	LYS	4.9
1	G	158	PHE	4.8
1	H	211	THR	4.7

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Mol	Chain	Res	Type	RSRZ
1	E	228	LEU	4.7
1	H	214	ALA	4.6
1	F	159	VAL	4.5
1	A	159	VAL	4.4
1	H	286	ALA	4.2
1	H	283	ASP	4.1
1	H	207	GLN	3.7
1	H	192	ASP	3.7
1	H	165	GLU	3.7
1	H	170	PHE	3.7
1	C	239	HIS	3.6
1	D	157	GLY	3.6
1	H	171	GLN	3.5
1	B	172	ARG	3.4
1	C	172	ARG	3.4
1	H	208	ASP	3.3
1	E	240	VAL	3.3
1	B	273	CYS	3.2
1	D	216	HIS	3.2
1	H	287	THR	3.2
1	H	177	PHE	3.2
1	G	166	LYS	3.2
1	E	159	VAL	3.2
1	H	191	CYS	3.1
1	H	199	VAL	3.0
1	H	194	MET	2.9
1	A	227	ASP	2.9
1	B	165	GLU	2.9
1	G	163	CYS	2.9
1	A	160	CYS	2.9
1	H	288	CYS	2.9
1	F	176	TYR	2.9
1	G	165	GLU	2.8
1	E	216	HIS	2.7
1	B	166	LYS	2.7
1	H	280	TRP	2.6
1	G	216	HIS	2.5
1	A	216	HIS	2.5
1	G	159	VAL	2.5
1	H	210	LEU	2.5
1	H	281	VAL	2.4
1	E	227	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	172	ARG	2.4
1	C	216	HIS	2.4
1	B	216	HIS	2.4
1	D	165	GLU	2.4
1	H	282	CYS	2.4
1	G	212	LYS	2.3
1	F	214	ALA	2.3
1	C	241	ASP	2.3
1	H	174	CYS	2.2
1	H	190	ALA	2.2
1	F	239	HIS	2.2
1	H	213	HIS	2.2
1	B	162	THR	2.1
1	H	195	GLU	2.1
1	E	288	CYS	2.1
1	E	208	ASP	2.1
1	F	216	HIS	2.1
1	H	209	PHE	2.1
1	H	189	TYR	2.0
1	E	254	SER	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	G	301	5/5	0.98	0.17	1.03	48,50,52,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	F	301	5/5	0.94	0.16	-0.09	50,53,56,59	0
2	SO4	H	301	5/5	0.98	0.14	-0.35	45,46,50,52	0
2	SO4	D	301	5/5	0.99	0.13	-0.97	31,35,38,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.