



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:45 AM UTC

PDB ID : 4J6M / pdb_00004j6m
Title : Crystal structure of calcium²⁺-free wild-type CD23 lectin domain (crystal form D)
Authors : Dhaliwal, B.; Fabiane, S.M.; Sutton, B.J.
Deposited on : 2013-02-11
Resolution : 2.48 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

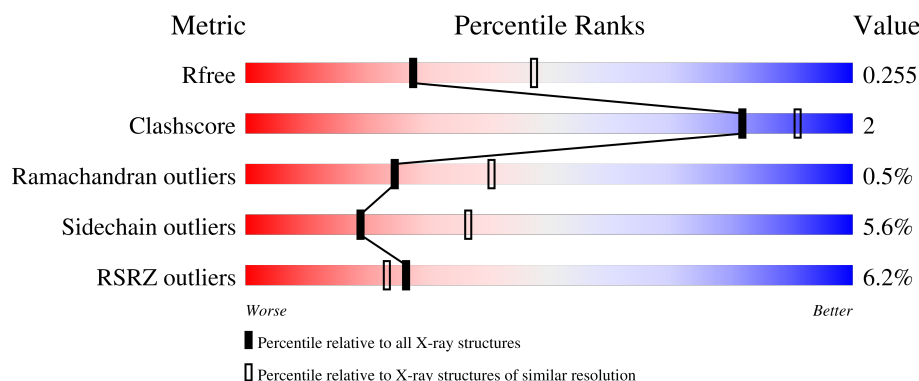
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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 $\leq 5\%$. 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	6% 83% 11% • 6%
1	B	143	5% 82% 10% • 6%
1	C	143	5% 80% 12% •• 6%
1	D	143	7% 81% 11% • 6%
1	E	143	9% 85% 8% • 6%

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Mol	Chain	Length	Quality of chain
1	F	143	3% 82% 9% 8%
1	G	143	7% 80% 8% 10%
1	H	143	5% 78% 11% 10%

2 Entry composition

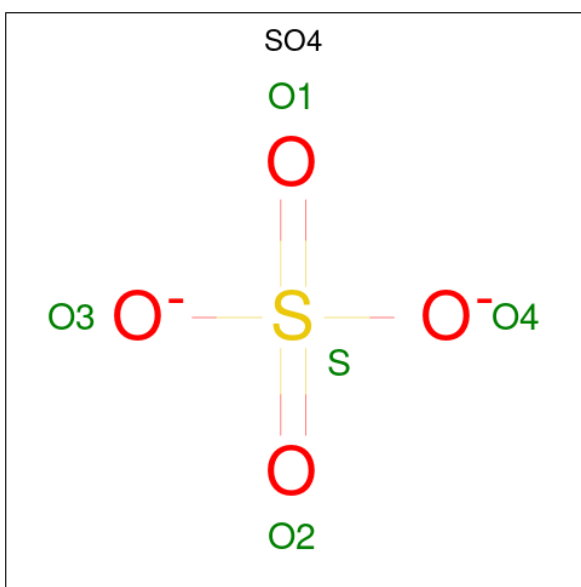
There are 3 unique types of molecules in this entry. The entry contains 8785 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	135	Total	C	N	O	S	0	0	0
			1082	679	193	199	11			
1	B	135	Total	C	N	O	S	0	0	0
			1082	679	193	199	11			
1	C	135	Total	C	N	O	S	0	0	0
			1082	679	193	199	11			
1	D	134	Total	C	N	O	S	0	0	0
			1075	674	192	198	11			
1	E	134	Total	C	N	O	S	0	0	0
			1075	674	192	198	11			
1	F	131	Total	C	N	O	S	0	0	0
			1053	661	188	193	11			
1	G	129	Total	C	N	O	S	0	0	0
			1039	649	187	192	11			
1	H	129	Total	C	N	O	S	0	0	0
			1039	649	187	192	11			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

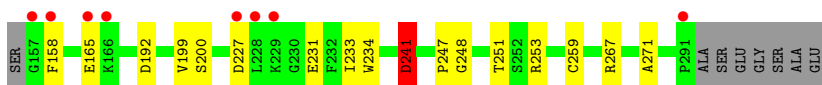
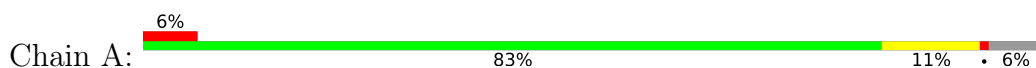
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		
3	B	33	Total	O	0	0
			33	33		
3	C	39	Total	O	0	0
			39	39		
3	D	35	Total	O	0	0
			35	35		
3	E	19	Total	O	0	0
			19	19		
3	F	35	Total	O	0	0
			35	35		
3	G	22	Total	O	0	0
			22	22		
3	H	24	Total	O	0	0
			24	24		

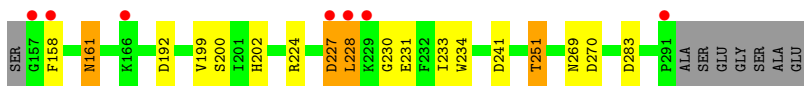
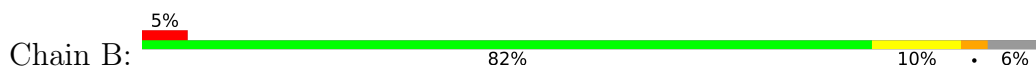
3 Residue-property plots [i](#)

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.

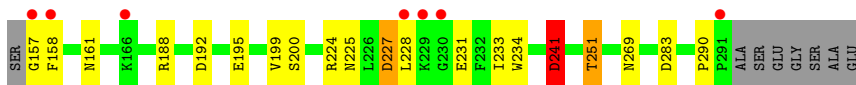
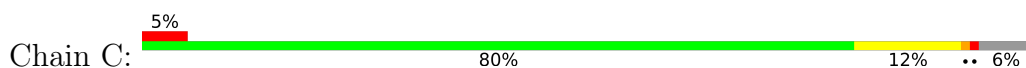
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



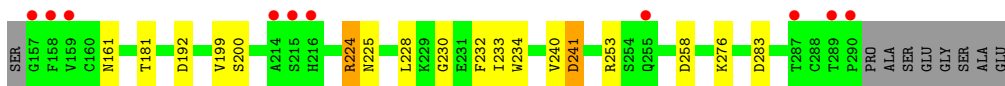
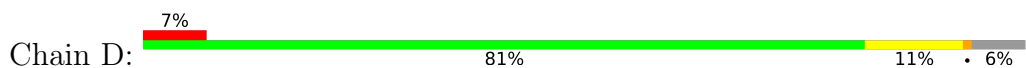
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



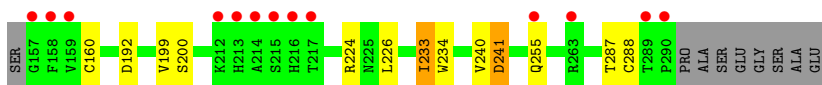
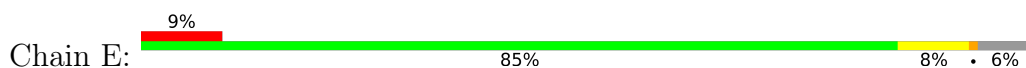
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



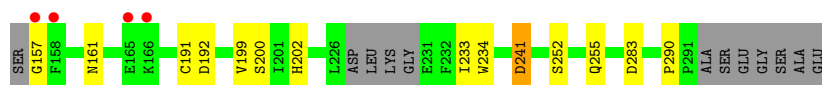
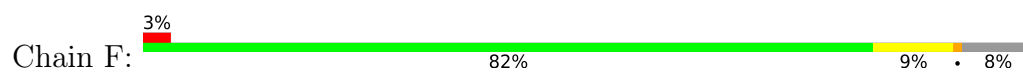
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



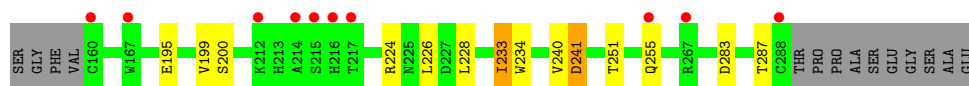
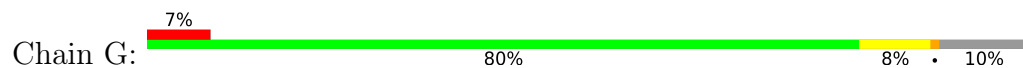
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



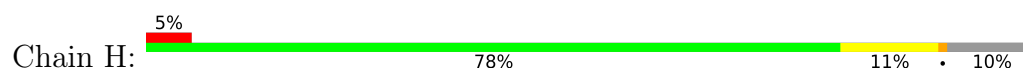
- Molecule 1: Low affinity immunoglobulin epsilon Fc receptor



- 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	52.29Å 65.10Å 106.78Å 95.26° 88.88° 89.62°	Depositor
Resolution (Å)	36.31 – 2.48 36.31 – 2.48	Depositor EDS
% Data completeness (in resolution range)	94.6 (36.31-2.48) 94.5 (36.31-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.48Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.208 , 0.243 0.218 , 0.255	Depositor DCC
R_{free} test set	2377 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.128 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8785	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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

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	0.84	0/1116	1.29	2/1512 (0.1%)
1	B	0.83	0/1116	1.29	9/1512 (0.6%)
1	C	0.80	0/1116	1.31	8/1512 (0.5%)
1	D	0.81	0/1108	1.36	5/1500 (0.3%)
1	E	0.76	0/1108	1.30	2/1500 (0.1%)
1	F	0.80	0/1086	1.29	7/1471 (0.5%)
1	G	0.82	0/1070	1.33	5/1447 (0.3%)
1	H	0.84	0/1070	1.35	3/1447 (0.2%)
All	All	0.81	0/8790	1.32	41/11901 (0.3%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	283	ASP	CA-CB-CG	7.67	120.27	112.60
1	G	251	THR	N-CA-C	-7.51	100.61	110.53
1	H	199	VAL	N-CA-C	7.01	118.49	109.30
1	G	199	VAL	N-CA-C	6.85	118.27	109.30
1	F	199	VAL	N-CA-C	6.78	118.18	109.30
1	E	199	VAL	N-CA-C	6.75	118.14	109.30
1	D	199	VAL	N-CA-C	6.71	118.09	109.30
1	B	199	VAL	N-CA-C	6.56	117.89	109.30
1	D	283	ASP	CA-CB-CG	6.50	119.10	112.60
1	A	199	VAL	N-CA-C	6.45	117.75	109.30
1	C	199	VAL	N-CA-C	6.21	117.43	109.30
1	C	225	ASN	CA-CB-CG	6.18	118.78	112.60
1	C	283	ASP	CA-CB-CG	6.00	118.60	112.60
1	C	241	ASP	CA-CB-CG	5.72	118.32	112.60
1	B	283	ASP	CA-CB-CG	5.68	118.28	112.60
1	F	241	ASP	CA-CB-CG	5.67	118.27	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	258	ASP	N-CA-C	5.64	120.86	113.30
1	G	283	ASP	CA-CB-CG	5.60	118.20	112.60
1	A	241	ASP	CA-CB-CG	5.56	118.16	112.60
1	B	158	PHE	CA-CB-CG	5.50	119.30	113.80
1	D	161	ASN	CA-CB-CG	5.48	118.08	112.60
1	B	161	ASN	CA-CB-CG	5.42	118.02	112.60
1	D	258	ASP	N-CA-C	5.41	120.55	113.30
1	F	161	ASN	CA-CB-CG	5.41	118.01	112.60
1	C	251	THR	CB-CA-C	5.40	118.65	109.84
1	G	241	ASP	CA-CB-CG	5.38	117.98	112.60
1	E	241	ASP	N-CA-C	-5.37	102.86	111.02
1	D	241	ASP	N-CA-C	-5.35	102.89	111.02
1	B	251	THR	CB-CA-C	5.34	118.43	109.89
1	F	283	ASP	CA-CB-CG	5.31	117.91	112.60
1	G	241	ASP	N-CA-C	-5.29	102.97	111.02
1	C	269	ASN	CA-CB-CG	5.24	117.84	112.60
1	B	270	ASP	CA-CB-CG	5.22	117.82	112.60
1	C	161	ASN	CA-CB-CG	5.19	117.79	112.60
1	F	241	ASP	N-CA-C	-5.18	103.14	111.02
1	B	227	ASP	CA-C-N	5.18	131.43	121.54
1	B	227	ASP	C-N-CA	5.18	131.43	121.54
1	C	241	ASP	N-CA-C	-5.11	103.26	111.02
1	B	269	ASN	CA-CB-CG	5.04	117.64	112.60
1	F	191	CYS	CA-C-N	5.01	126.95	120.44
1	F	191	CYS	C-N-CA	5.01	126.95	120.44

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	1082	0	994	13	0
1	B	1082	0	994	5	0
1	C	1082	0	994	6	0
1	D	1075	0	987	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1075	0	987	12	0
1	F	1053	0	962	4	0
1	G	1039	0	952	3	0
1	H	1039	0	952	4	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	F	5	0	0	0	0
3	A	31	0	0	0	0
3	B	33	0	0	1	0
3	C	39	0	0	0	0
3	D	35	0	0	2	0
3	E	19	0	0	1	0
3	F	35	0	0	0	0
3	G	22	0	0	0	0
3	H	24	0	0	0	0
All	All	8785	0	7822	41	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 2.

All (41) 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:267:ARG:HH22	1:E:255:GLN:CD	1.42	1.27
1:A:267:ARG:NH2	1:E:255:GLN:CD	2.03	1.14
1:A:267:ARG:NH2	1:E:255:GLN:OE1	1.83	1.08
1:A:247:PRO:HD2	1:E:255:GLN:HE22	1.50	0.76
3:E:316:HOH:O	1:F:255:GLN:HB3	1.87	0.74
1:B:161:ASN:HB3	3:B:406:HOH:O	1.85	0.74
1:A:247:PRO:HD2	1:E:255:GLN:NE2	2.10	0.67
1:C:157:GLY:HA2	1:C:290:PRO:HA	1.77	0.66
1:F:157:GLY:HA2	1:F:290:PRO:HA	1.79	0.63
1:A:247:PRO:CD	1:E:255:GLN:HE22	2.16	0.58
1:D:253:ARG:NH1	3:D:310:HOH:O	2.35	0.58
1:A:165:GLU:H	1:A:165:GLU:CD	2.12	0.57
1:C:195:GLU:OE2	1:H:276:LYS:NZ	2.38	0.57
1:G:226:LEU:CD1	1:G:233:ILE:HG12	2.41	0.50
1:B:200:SER:HA	1:B:234:TRP:CE3	2.47	0.50
1:G:200:SER:HA	1:G:234:TRP:CE3	2.49	0.48
1:H:200:SER:HA	1:H:234:TRP:CE3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:226:LEU:CD1	1:H:233:ILE:HG12	2.43	0.48
1:D:200:SER:HA	1:D:234:TRP:CE3	2.49	0.48
1:A:259:CYS:O	1:A:271:ALA:N	2.46	0.47
1:F:200:SER:HA	1:F:234:TRP:CE3	2.49	0.47
1:D:181:THR:CG2	1:D:276:LYS:HE2	2.44	0.47
1:E:200:SER:HA	1:E:234:TRP:CE3	2.50	0.47
1:A:200:SER:HA	1:A:234:TRP:CE3	2.50	0.47
1:C:200:SER:HA	1:C:234:TRP:CE3	2.50	0.46
1:D:225:ASN:OD1	1:D:230:GLY:HA2	2.16	0.46
1:B:228:LEU:HD13	1:C:188:ARG:HH12	1.80	0.46
1:D:181:THR:HG22	1:D:276:LYS:HE2	1.97	0.46
1:C:227:ASP:HB3	1:C:231:GLU:OE2	2.16	0.45
1:E:226:LEU:CD1	1:E:233:ILE:HG12	2.48	0.44
1:A:241:ASP:HB2	1:B:202:HIS:O	2.18	0.43
1:B:227:ASP:HB3	1:B:231:GLU:OE2	2.18	0.43
1:C:241:ASP:HB2	1:F:202:HIS:O	2.19	0.43
1:A:247:PRO:HG2	1:E:255:GLN:HE22	1.83	0.42
1:D:224:ARG:CD	3:D:305:HOH:O	2.67	0.42
1:E:160:CYS:HA	1:E:288:CYS:HA	2.01	0.42
1:A:247:PRO:CG	1:E:255:GLN:HE22	2.33	0.42
1:A:248:GLY:O	1:G:255:GLN:NE2	2.54	0.41
1:E:226:LEU:HD12	1:E:233:ILE:HG12	2.03	0.41
1:D:225:ASN:HB2	1:D:232:PHE:CZ	2.56	0.40
1:H:223:LEU:HD23	1:H:260:VAL:HG21	2.02	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	133/143 (93%)	126 (95%)	7 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	133/143 (93%)	122 (92%)	9 (7%)	2 (2%)	8	14
1	C	133/143 (93%)	124 (93%)	8 (6%)	1 (1%)	16	28
1	D	132/143 (92%)	125 (95%)	7 (5%)	0	100	100
1	E	132/143 (92%)	125 (95%)	7 (5%)	0	100	100
1	F	127/143 (89%)	120 (94%)	7 (6%)	0	100	100
1	G	127/143 (89%)	121 (95%)	6 (5%)	0	100	100
1	H	127/143 (89%)	120 (94%)	5 (4%)	2 (2%)	7	13
All	All	1044/1144 (91%)	983 (94%)	56 (5%)	5 (0%)	24	40

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	228	LEU
1	C	228	LEU
1	H	252	SER
1	B	230	GLY
1	H	216	HIS

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	115/120 (96%)	107 (93%)	8 (7%)	14	27
1	B	115/120 (96%)	110 (96%)	5 (4%)	26	48
1	C	115/120 (96%)	108 (94%)	7 (6%)	17	33
1	D	114/120 (95%)	108 (95%)	6 (5%)	20	39
1	E	114/120 (95%)	108 (95%)	6 (5%)	20	39
1	F	112/120 (93%)	108 (96%)	4 (4%)	31	55
1	G	110/120 (92%)	103 (94%)	7 (6%)	16	31
1	H	110/120 (92%)	102 (93%)	8 (7%)	13	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	905/960 (94%)	854 (94%)	51 (6%)	19	37

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	PHE
1	A	192	ASP
1	A	227	ASP
1	A	231	GLU
1	A	233	ILE
1	A	241	ASP
1	A	251	THR
1	A	253	ARG
1	B	192	ASP
1	B	224	ARG
1	B	233	ILE
1	B	241	ASP
1	B	251	THR
1	C	158	PHE
1	C	192	ASP
1	C	224	ARG
1	C	227	ASP
1	C	233	ILE
1	C	241	ASP
1	C	251	THR
1	D	192	ASP
1	D	224	ARG
1	D	228	LEU
1	D	233	ILE
1	D	240	VAL
1	D	241	ASP
1	E	192	ASP
1	E	224	ARG
1	E	233	ILE
1	E	240	VAL
1	E	241	ASP
1	E	287	THR
1	F	192	ASP
1	F	233	ILE
1	F	241	ASP
1	F	252	SER
1	G	195	GLU

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Mol	Chain	Res	Type
1	G	224	ARG
1	G	228	LEU
1	G	233	ILE
1	G	240	VAL
1	G	241	ASP
1	G	287	THR
1	H	216	HIS
1	H	224	ARG
1	H	233	ILE
1	H	240	VAL
1	H	241	ASP
1	H	251	THR
1	H	270	ASP
1	H	288	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	GLN
1	A	225	ASN
1	B	197	GLN
1	B	225	ASN
1	C	197	GLN
1	D	197	GLN
1	E	186	HIS
1	E	197	GLN
1	E	255	GLN
1	F	197	GLN
1	F	216	HIS
1	F	225	ASN
1	F	255	GLN
1	G	186	HIS
1	G	197	GLN
1	H	171	GLN
1	H	197	GLN
1	H	269	ASN

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 oligosaccharides 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	A	301	-	4,4,4	0.29	0	6,6,6	0.37	0
2	SO4	F	301	-	4,4,4	0.15	0	6,6,6	0.23	0
2	SO4	B	301	-	4,4,4	0.22	0	6,6,6	0.27	0
2	SO4	C	301	-	4,4,4	0.27	0	6,6,6	0.36	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 [i](#)

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	135/143 (94%)	0.32	8 (5%)	28	25	11, 27, 55, 77	0
1	B	135/143 (94%)	0.28	7 (5%)	33	29	13, 25, 61, 84	0
1	C	135/143 (94%)	0.36	7 (5%)	33	29	12, 26, 55, 86	0
1	D	134/143 (93%)	0.57	10 (7%)	20	18	15, 30, 67, 101	0
1	E	134/143 (93%)	0.59	13 (9%)	13	11	16, 31, 66, 94	0
1	F	131/143 (91%)	0.16	4 (3%)	51	48	14, 25, 49, 62	0
1	G	129/143 (90%)	0.43	10 (7%)	19	16	11, 30, 61, 74	0
1	H	129/143 (90%)	0.45	7 (5%)	31	28	17, 31, 60, 67	0
All	All	1062/1144 (92%)	0.39	66 (6%)	26	23	11, 28, 61, 101	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	158	PHE	6.8
1	C	228	LEU	6.2
1	E	214	ALA	5.4
1	A	157	GLY	5.1
1	A	228	LEU	5.1
1	E	157	GLY	5.0
1	E	255	GLN	4.8
1	E	158	PHE	4.8
1	G	214	ALA	4.6
1	D	290	PRO	4.5
1	D	255	GLN	4.5
1	D	289	THR	4.4
1	B	228	LEU	4.4
1	E	290	PRO	4.3
1	G	288	CYS	4.2
1	E	212	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	F	158	PHE	4.1
1	C	157	GLY	4.0
1	B	158	PHE	4.0
1	H	255	GLN	4.0
1	D	157	GLY	4.0
1	C	229	LYS	3.9
1	E	289	THR	3.9
1	B	166	LYS	3.8
1	C	158	PHE	3.6
1	F	157	GLY	3.6
1	G	215	SER	3.5
1	E	215	SER	3.4
1	A	158	PHE	3.4
1	E	159	VAL	3.3
1	H	212	LYS	3.2
1	B	291	PRO	3.1
1	D	159	VAL	3.1
1	A	229	LYS	3.0
1	E	216	HIS	3.0
1	C	291	PRO	3.0
1	G	255	GLN	3.0
1	H	214	ALA	3.0
1	A	165	GLU	3.0
1	B	157	GLY	2.9
1	A	166	LYS	2.9
1	E	217	THR	2.7
1	H	216	HIS	2.7
1	B	227	ASP	2.7
1	A	291	PRO	2.6
1	H	215	SER	2.6
1	D	214	ALA	2.6
1	G	216	HIS	2.5
1	D	215	SER	2.4
1	B	229	LYS	2.4
1	F	166	LYS	2.4
1	C	166	LYS	2.4
1	C	230	GLY	2.3
1	D	216	HIS	2.3
1	A	227	ASP	2.3
1	H	251	THR	2.2
1	G	212	LYS	2.2
1	G	217	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	167	TRP	2.2
1	G	267	ARG	2.1
1	G	160	CYS	2.1
1	D	287	THR	2.1
1	E	263	ARG	2.1
1	F	165	GLU	2.1
1	E	213	HIS	2.1
1	H	288	CYS	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, 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($\text{\AA}^2$)	Q<0.9
2	SO4	C	301	5/5	0.96	0.07	31,35,38,38	0
2	SO4	A	301	5/5	0.97	0.06	33,33,34,36	0
2	SO4	B	301	5/5	0.98	0.06	33,34,36,36	0
2	SO4	F	301	5/5	0.98	0.07	29,33,35,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.