



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:16 PM UTC

PDB ID : 4K71 / pdb_00004k71
Title : Crystal structure of a high affinity Human Serum Albumin variant bound to the Neonatal Fc Receptor
Authors : Schmidt, M.M.; Townson, S.A.; Andreucci, A.; Dombrowski, C.; Erbe, D.V.; King, B.; Kovalchin, J.T.; Masci, A.; Murillo, A.; Schirmer, E.B.; Furfine, E.S.; Barnes, T.M.
Deposited on : 2013-04-16
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 ⓘ 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

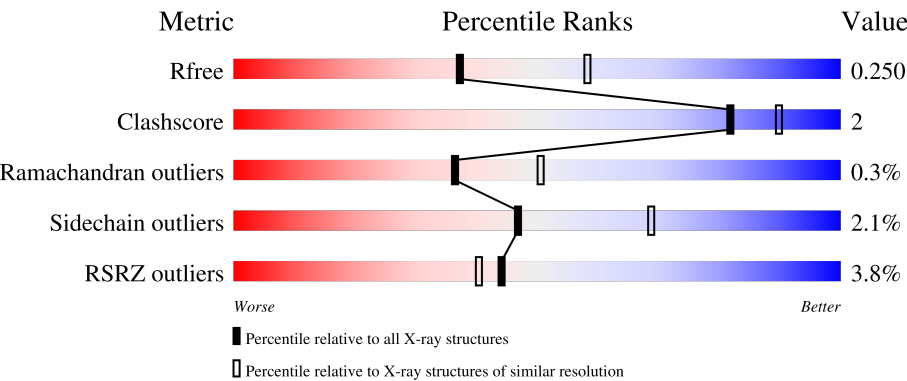
1 Overall quality at a glance i

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 $\leq 5\%$. 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	585	2% 91% 8% .
1	D	585	8% 91% 8% .
2	B	274	% 88% 7% .
2	E	274	2% 89% 7% .

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Mol	Chain	Length	Quality of chain
3	C	99	% 95% 5%
3	F	99	3% 94% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15259 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 Serum albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	583	Total	C	N	O	S	48	0	0
			4631	2923	784	882	42			
1	D	579	Total	C	N	O	S	107	0	0
			4597	2903	778	874	42			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	418	MET	VAL	engineered mutation	UNP P02768
A	420	ALA	THR	engineered mutation	UNP P02768
A	505	GLY	GLU	engineered mutation	UNP P02768
A	547	ALA	VAL	engineered mutation	UNP P02768
D	418	MET	VAL	engineered mutation	UNP P02768
D	420	ALA	THR	engineered mutation	UNP P02768
D	505	GLY	GLU	engineered mutation	UNP P02768
D	547	ALA	VAL	engineered mutation	UNP P02768

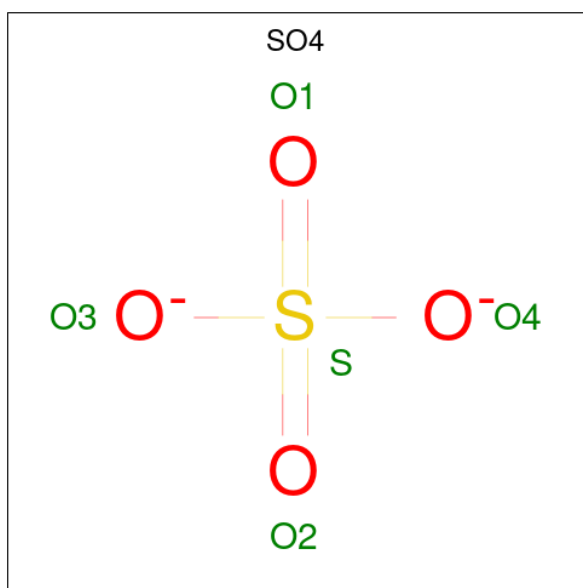
- Molecule 2 is a protein called IgG receptor FcRn large subunit p51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	264	Total	C	N	O	S	23	0	0
			2078	1329	358	383	8			
2	E	264	Total	C	N	O	S	10	0	0
			2078	1329	358	383	8			

- Molecule 3 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	99	Total	C	N	O	S	23	0	0
			829	528	140	158	3			
3	F	99	Total	C	N	O	S	3	0	0
			829	528	140	158	3			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

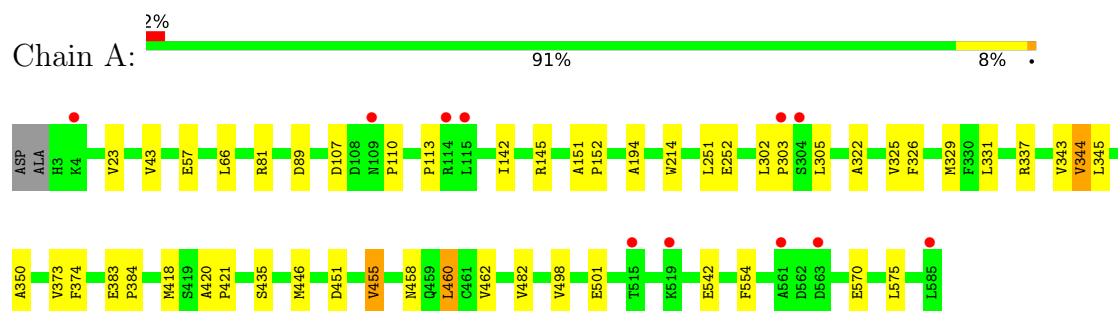
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	39	Total	O	0	0
			39	39		
5	B	28	Total	O	0	0
			28	28		
5	C	7	Total	O	0	0
			7	7		
5	D	30	Total	O	0	0
			30	30		
5	E	12	Total	O	0	0
			12	12		
5	F	6	Total	O	0	0
			6	6		

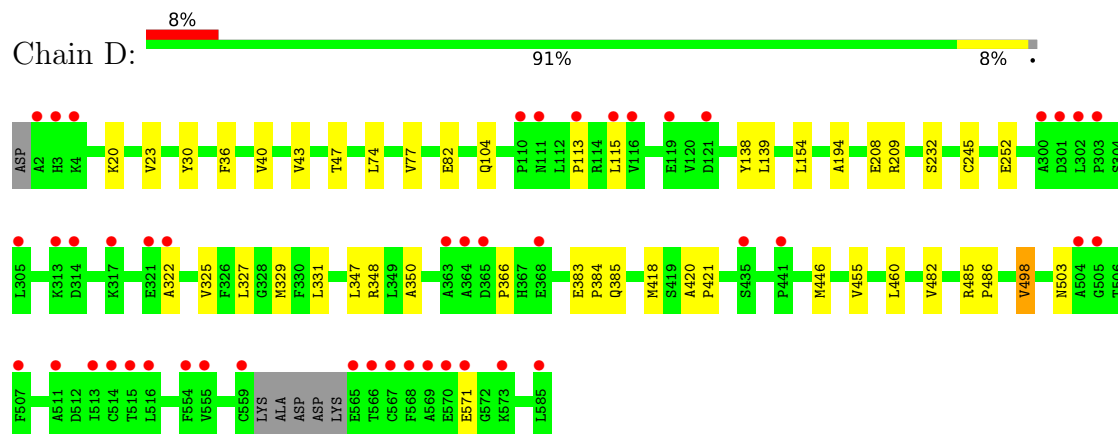
3 Residue-property plots [i](#)

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.

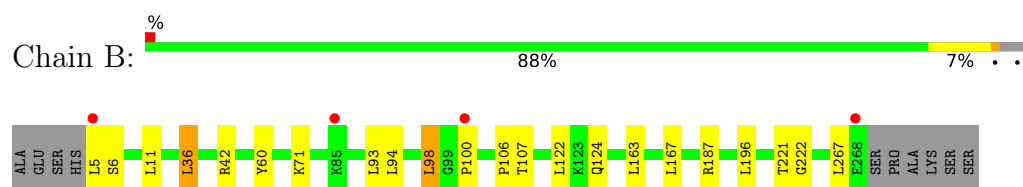
- Molecule 1: Serum albumin



- Molecule 1: Serum albumin



- Molecule 2: IgG receptor FcRn large subunit p51

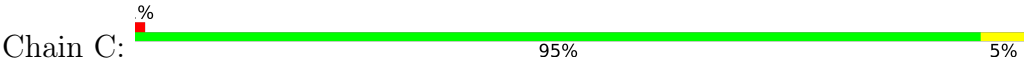


- Molecule 2: IgG receptor FcRn large subunit p51

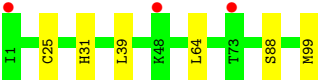




● Molecule 3: Beta-2-microglobulin



● Molecule 3: Beta-2-microglobulin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	127.89Å 203.54Å 100.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.29 – 2.40 108.29 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (108.29-2.40) 99.7 (108.29-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.255 0.212 , 0.250	Depositor DCC
R_{free} test set	5144 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15259	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 3.48% 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	0.82	0/4721	0.91	0/6364
1	D	0.77	0/4686	0.93	1/6317 (0.0%)
2	B	0.82	0/2143	0.87	0/2912
2	E	0.78	0/2143	0.84	0/2912
3	C	0.78	0/852	0.83	0/1152
3	F	0.73	0/852	0.81	0/1152
All	All	0.79	0/15397	0.89	1/20809 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	503	ASN	N-CA-C	5.57	117.18	107.49

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	4631	0	4554	28	0
1	D	4597	0	4519	21	0
2	B	2078	0	1989	13	0
2	E	2078	0	1989	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	829	0	794	3	0
3	F	829	0	794	2	0
4	A	35	0	0	1	0
4	B	10	0	0	0	0
4	C	10	0	0	0	0
4	D	30	0	0	0	0
4	E	5	0	0	0	0
4	F	5	0	0	0	0
5	A	39	0	0	1	0
5	B	28	0	0	0	0
5	C	7	0	0	0	0
5	D	30	0	0	0	0
5	E	12	0	0	0	0
5	F	6	0	0	1	0
All	All	15259	0	14639	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 2.

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)
1:D:418:MET:HE1	1:D:460:LEU:HD11	1.63	0.79
2:B:5:LEU:HD23	2:B:167:LEU:HD21	1.69	0.75
1:D:331:LEU:HD13	1:D:350:ALA:HB2	1.70	0.73
1:A:81:ARG:NH2	1:A:89:ASP:OD1	2.27	0.67
2:B:98:LEU:HD13	2:B:163:LEU:HD23	1.78	0.66
1:A:498:VAL:HG23	2:B:42:ARG:NH1	2.11	0.66
1:A:305:LEU:HD11	1:A:337:ARG:HD2	1.82	0.62
1:A:331:LEU:HD13	1:A:350:ALA:HB2	1.83	0.61
1:D:418:MET:CE	1:D:460:LEU:HD11	2.31	0.60
1:A:214:TRP:CD1	1:A:343:VAL:HG11	2.35	0.60
1:D:385:GLN:HG3	1:D:446:MET:HE2	1.84	0.59
3:F:31:HIS:ND1	5:F:205:HOH:O	2.28	0.58
2:B:106:PRO:HG2	2:B:122:LEU:HD13	1.86	0.58
1:D:23:VAL:HG12	1:D:43:VAL:HG22	1.86	0.56
1:A:345:LEU:HD22	1:A:446:MET:HE1	1.87	0.56
1:A:326:PHE:HA	1:A:329:MET:HE3	1.87	0.55
1:A:498:VAL:HG23	2:B:42:ARG:HH12	1.70	0.55
1:D:20:LYS:HE3	1:D:47:THR:HG21	1.89	0.54
1:D:322:ALA:HB1	1:D:325:VAL:HB	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:498:VAL:HG13	2:E:42:ARG:HH12	1.72	0.53
1:A:303:PRO:O	1:A:337:ARG:NH2	2.37	0.53
3:F:25:CYS:HB2	3:F:39:LEU:HD21	1.91	0.52
1:D:498:VAL:HG13	2:E:42:ARG:NH1	2.24	0.52
1:A:66:LEU:HD13	1:A:251:LEU:HD12	1.92	0.51
1:A:305:LEU:HD11	1:A:337:ARG:CD	2.40	0.51
1:A:194:ALA:HB1	1:A:455:VAL:HG13	1.92	0.51
1:D:383:GLU:HB3	1:D:384:PRO:HD3	1.93	0.50
1:A:498:VAL:HG22	5:A:714:HOH:O	2.10	0.50
2:B:221:THR:HG23	2:B:222:GLY:O	2.12	0.50
1:D:30:TYR:CD2	1:D:74:LEU:HD11	2.47	0.50
1:D:325:VAL:HG12	1:D:329:MET:HE2	1.94	0.50
1:A:418:MET:HE1	1:A:460:LEU:CD1	2.42	0.49
1:A:420:ALA:HB3	1:A:421:PRO:HD3	1.95	0.48
1:A:325:VAL:HG12	1:A:329:MET:HE2	1.96	0.48
2:B:11:LEU:HD13	2:B:94:LEU:HD13	1.95	0.48
1:A:151:ALA:HB3	1:A:152:PRO:HD3	1.96	0.48
2:B:5:LEU:HD12	2:B:6:SER:H	1.79	0.48
2:E:60:TYR:C	2:E:60:TYR:CD1	2.92	0.48
1:D:194:ALA:HB1	1:D:455:VAL:CG1	2.44	0.47
1:A:418:MET:HE1	1:A:460:LEU:HD13	1.96	0.47
1:D:331:LEU:HD21	1:D:347:LEU:CD2	2.44	0.47
2:B:98:LEU:HD13	2:B:163:LEU:CD2	2.43	0.47
1:D:20:LYS:CE	1:D:47:THR:HG21	2.44	0.47
2:E:186:ALA:HB2	2:E:196:LEU:CD1	2.45	0.46
1:D:36:PHE:CZ	1:D:40:VAL:HG21	2.51	0.46
1:A:113:PRO:O	1:A:145:ARG:NH1	2.48	0.45
2:E:54:GLU:OE2	2:E:166:HIS:ND1	2.38	0.44
1:A:458:ASN:O	1:A:462:VAL:HG13	2.17	0.44
1:D:209:ARG:NH2	1:D:327:LEU:HD13	2.32	0.44
2:E:36:LEU:C	2:E:36:LEU:HD23	2.42	0.44
2:B:60:TYR:C	2:B:60:TYR:CD1	2.94	0.44
3:C:64:LEU:HD22	3:C:66:TYR:CD1	2.53	0.44
1:D:420:ALA:HB3	1:D:421:PRO:HD3	2.00	0.44
3:C:39:LEU:HD13	3:C:68:THR:HG22	2.00	0.44
1:A:482:VAL:HG23	4:A:606:SO4:O4	2.18	0.43
1:A:554:PHE:CD2	1:A:575:LEU:HD22	2.53	0.43
1:D:139:LEU:CD2	1:D:154:LEU:HG	2.48	0.43
2:E:106:PRO:HG3	2:E:122:LEU:HD22	2.01	0.43
1:A:373:VAL:HG13	1:A:374:PHE:CD1	2.54	0.43
2:B:36:LEU:C	2:B:36:LEU:HD23	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:64:LEU:HD23	3:C:65:LEU:N	2.34	0.43
2:E:71:LYS:HE3	2:E:94:LEU:HD23	2.01	0.43
2:E:127:TRP:O	2:E:138:SER:OG	2.37	0.43
2:E:167:LEU:HD23	2:E:174:LEU:CD1	2.50	0.42
1:A:107:ASP:OD2	1:A:110:PRO:HA	2.20	0.42
1:A:322:ALA:HB1	1:A:325:VAL:HB	2.02	0.41
1:D:485:ARG:HB3	1:D:486:PRO:HD3	2.02	0.41
2:B:267:LEU:H	2:B:267:LEU:HD12	1.85	0.41
2:B:93:LEU:C	2:B:94:LEU:HD12	2.45	0.41
1:A:344:VAL:HG23	1:A:451:ASP:OD1	2.21	0.41
1:A:23:VAL:HG12	1:A:43:VAL:HG22	2.03	0.40
1:A:383:GLU:HB3	1:A:384:PRO:HD3	2.02	0.40
1:D:348:ARG:HG3	1:D:482:VAL:CG1	2.51	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	581/585 (99%)	572 (98%)	9 (2%)	0	100	100
1	D	575/585 (98%)	556 (97%)	16 (3%)	3 (0%)	24	37
2	B	262/274 (96%)	253 (97%)	8 (3%)	1 (0%)	30	43
2	E	262/274 (96%)	254 (97%)	7 (3%)	1 (0%)	30	43
3	C	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
3	F	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
All	All	1874/1916 (98%)	1827 (98%)	42 (2%)	5 (0%)	36	50

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	113	PRO
1	D	115	LEU
2	E	102	ASN
2	B	100	PRO
1	D	366	PRO

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	507/508 (100%)	496 (98%)	11 (2%)	45	67
1	D	503/508 (99%)	493 (98%)	10 (2%)	48	70
2	B	218/226 (96%)	211 (97%)	7 (3%)	34	56
2	E	218/226 (96%)	215 (99%)	3 (1%)	59	79
3	C	94/94 (100%)	94 (100%)	0	100	100
3	F	94/94 (100%)	91 (97%)	3 (3%)	34	56
All	All	1634/1656 (99%)	1600 (98%)	34 (2%)	47	69

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	GLU
1	A	142	ILE
1	A	252	GLU
1	A	302	LEU
1	A	344	VAL
1	A	435	SER
1	A	455	VAL
1	A	460	LEU
1	A	501	GLU
1	A	542	GLU
1	A	570	GLU
2	B	36	LEU
2	B	71	LYS
2	B	98	LEU

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Mol	Chain	Res	Type
2	B	107	THR
2	B	124	GLN
2	B	187	ARG
2	B	196	LEU
1	D	77	VAL
1	D	82	GLU
1	D	104	GLN
1	D	138	TYR
1	D	208	GLU
1	D	232	SER
1	D	245	CYS
1	D	252	GLU
1	D	498	VAL
1	D	571	GLU
2	E	5	LEU
2	E	133	GLU
2	E	143	GLN
3	F	64	LEU
3	F	88	SER
3	F	99	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	267	ASN
1	A	459	GLN
1	A	526	GLN
2	B	102	ASN
3	C	8	GLN
3	C	13	HIS
1	D	33	GLN
1	D	109	ASN
1	D	385	GLN
2	E	102	ASN
2	E	215	ASN
2	E	235	HIS
2	E	255	GLN

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](#)

19 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	$\# Z > 2$
4	SO4	A	601	-	4,4,4	0.29	0	6,6,6	0.20	0
4	SO4	A	605	-	4,4,4	0.28	0	6,6,6	0.73	0
4	SO4	A	602	-	4,4,4	0.31	0	6,6,6	0.20	0
4	SO4	D	606	-	4,4,4	0.34	0	6,6,6	0.33	0
4	SO4	A	604	-	4,4,4	0.25	0	6,6,6	0.18	0
4	SO4	C	102	-	4,4,4	0.26	0	6,6,6	0.36	0
4	SO4	B	302	-	4,4,4	0.30	0	6,6,6	0.20	0
4	SO4	C	101	-	4,4,4	0.32	0	6,6,6	0.18	0
4	SO4	B	301	-	4,4,4	0.32	0	6,6,6	0.23	0
4	SO4	D	604	-	4,4,4	0.24	0	6,6,6	0.54	0
4	SO4	A	603	-	4,4,4	0.21	0	6,6,6	0.29	0
4	SO4	A	607	-	4,4,4	0.27	0	6,6,6	0.48	0
4	SO4	D	603	-	4,4,4	0.29	0	6,6,6	0.40	0
4	SO4	D	605	-	4,4,4	0.28	0	6,6,6	0.20	0
4	SO4	E	301	-	4,4,4	0.32	0	6,6,6	0.47	0
4	SO4	D	601	-	4,4,4	0.31	0	6,6,6	0.14	0
4	SO4	A	606	-	4,4,4	0.34	0	6,6,6	0.67	0
4	SO4	D	602	-	4,4,4	0.34	0	6,6,6	0.29	0
4	SO4	F	101	-	4,4,4	0.31	0	6,6,6	0.37	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	606	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, 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	583/585 (99%)	-0.03	11 (1%) 66 62	27, 45, 78, 109	16 (2%)
1	D	579/585 (98%)	0.46	46 (7%) 18 15	27, 55, 104, 139	31 (5%)
2	B	264/274 (96%)	-0.11	4 (1%) 72 68	28, 41, 63, 98	7 (2%)
2	E	264/274 (96%)	-0.03	6 (2%) 61 57	28, 44, 68, 110	3 (1%)
3	C	99/99 (100%)	0.02	1 (1%) 79 76	29, 44, 69, 83	8 (8%)
3	F	99/99 (100%)	0.11	3 (3%) 52 48	34, 52, 79, 86	1 (1%)
All	All	1888/1916 (98%)	0.12	71 (3%) 44 40	27, 47, 87, 139	66 (3%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	565	GLU	6.7
1	D	569	ALA	6.3
1	D	115	LEU	5.0
1	D	566	THR	4.8
1	D	568	PHE	4.5
1	D	4	LYS	4.3
2	E	5	LEU	4.3
1	A	585	LEU	4.2
1	D	511	ALA	4.2
1	D	507	PHE	4.1
1	D	368	GLU	4.0
1	D	2	ALA	4.0
1	D	364	ALA	4.0
1	D	559	CYS	4.0
1	D	321	GLU	3.9
1	D	111	ASN	3.9
1	D	585	LEU	3.7
2	E	100	PRO	3.7
1	D	301	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	441	PRO	3.7
1	D	570	GLU	3.6
1	D	504	ALA	3.6
1	D	116	VAL	3.6
1	D	513	ILE	3.4
2	E	101	ASP	3.4
1	D	313	LYS	3.3
1	D	573	LYS	3.3
1	D	314	ASP	3.3
1	A	115	LEU	3.2
1	A	303	PRO	3.1
3	F	1	ILE	3.1
2	B	100	PRO	3.0
3	C	1	ILE	2.9
1	D	110	PRO	2.9
1	D	515	THR	2.9
1	D	119	GLU	2.8
1	A	114	ARG	2.8
1	D	303	PRO	2.8
2	B	268	GLU	2.8
1	D	300	ALA	2.7
1	D	121	ASP	2.7
1	D	554	PHE	2.7
2	B	5	LEU	2.7
1	A	304	SER	2.6
1	D	555	VAL	2.6
2	E	221	THR	2.6
1	D	505	GLY	2.5
1	D	317	LYS	2.5
1	D	516	LEU	2.5
1	A	561	ALA	2.5
2	E	168	GLU	2.4
1	A	4	LYS	2.4
1	D	567	CYS	2.4
1	A	109	ASN	2.3
3	F	73	THR	2.3
2	B	85	LYS	2.3
3	F	48	LYS	2.3
1	D	113	PRO	2.3
1	D	571	GLU	2.3
1	A	519	LYS	2.2
1	A	515	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	435	SER	2.2
1	D	305	LEU	2.2
1	D	514	CYS	2.2
2	E	248	HIS	2.1
1	D	302	LEU	2.1
1	D	365	ASP	2.1
1	D	322	ALA	2.1
1	D	3	HIS	2.1
1	D	363	ALA	2.0
1	A	563	ASP	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(Å ²)	Q<0.9
4	SO4	A	601	5/5	0.60	0.14	96,101,103,106	0
4	SO4	B	301	5/5	0.67	0.13	90,94,100,102	0
4	SO4	D	601	5/5	0.68	0.13	86,90,95,97	0
4	SO4	A	604	5/5	0.73	0.10	91,96,100,101	0
4	SO4	D	606	5/5	0.74	0.12	86,91,95,97	0
4	SO4	C	101	5/5	0.79	0.10	79,91,97,97	0
4	SO4	F	101	5/5	0.81	0.11	78,85,94,95	0
4	SO4	E	301	5/5	0.86	0.15	58,61,76,76	0
4	SO4	A	602	5/5	0.87	0.10	87,88,91,97	0
4	SO4	B	302	5/5	0.88	0.17	64,68,74,76	0
4	SO4	A	603	5/5	0.88	0.12	76,78,81,85	0
4	SO4	C	102	5/5	0.89	0.14	57,57,65,73	0
4	SO4	D	603	5/5	0.91	0.11	66,74,81,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	D	602	5/5	0.91	0.15	62,64,66,67	0
4	SO4	A	607	5/5	0.92	0.12	68,71,79,79	0
4	SO4	A	605	5/5	0.94	0.08	36,46,48,55	0
4	SO4	D	604	5/5	0.95	0.07	49,49,62,63	0
4	SO4	A	606	5/5	0.96	0.11	48,52,62,64	0
4	SO4	D	605	5/5	0.97	0.07	46,57,59,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.