



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 09:53 PM EDT

PDB ID : 2PMS
Title : Crystal structure of the complex of human lactoferrin N-lobe and lactoferrin-binding domain of pneumococcal surface protein A
Authors : Chattopadhyay, D.; Senkovich, O.; Cook, W.J.
Deposited on : 2007-04-23
Resolution : 2.91 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

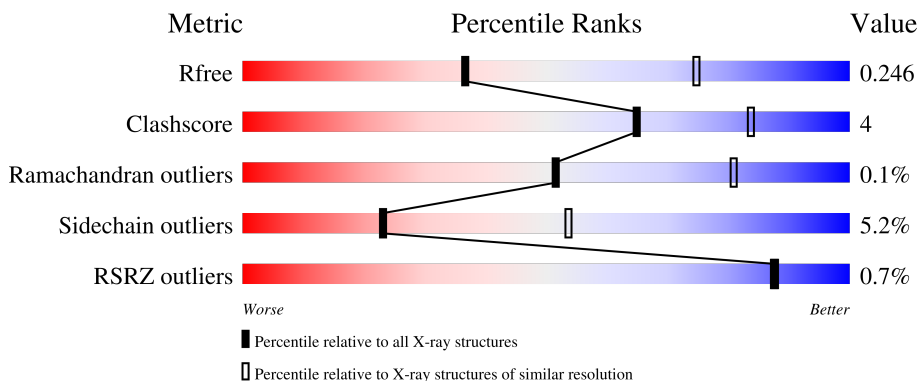
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


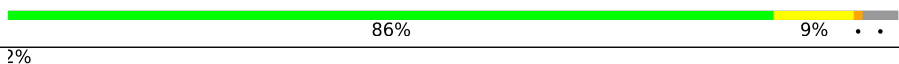
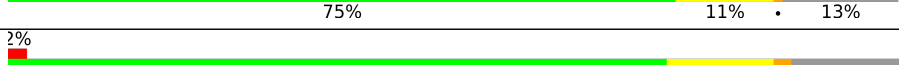

The reported resolution of this entry is 2.91 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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	344	 83% 12% . .
1	B	344	 86% 9% . .
2	C	125	 2% 75% 11% . 13%
2	D	125	 2% 74% 12% . 13%

2 Entry composition i

There are 8 unique types of molecules in this entry. The entry contains 6996 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 Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	331	2591	1634	471	473	13	0	0	0
1	B	331	2591	1634	471	473	13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	THR	ASN	conflict	UNP Q5EK51
B	123	THR	ASN	conflict	UNP Q5EK51

- Molecule 2 is a protein called PNEUMOCOCCAL SURFACE PROTEIN A (PSPA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	109	860	533	140	186	1	0	0	0
2	D	109	860	533	140	186	1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	164	GLY	-	expression tag	UNP Q8DRI0
C	165	SER	-	expression tag	UNP Q8DRI0
C	166	HIS	-	expression tag	UNP Q8DRI0
C	167	MET	-	expression tag	UNP Q8DRI0
D	164	GLY	-	expression tag	UNP Q8DRI0
D	165	SER	-	expression tag	UNP Q8DRI0
D	166	HIS	-	expression tag	UNP Q8DRI0
D	167	MET	-	expression tag	UNP Q8DRI0

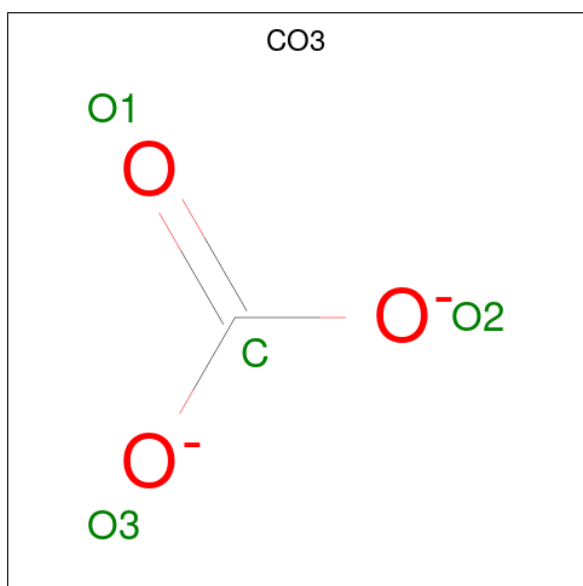
- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:

C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	14	8	1	5	0	0
3	B	1	14	8	1	5	0	0

- Molecule 4 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	4	1	3	0	0

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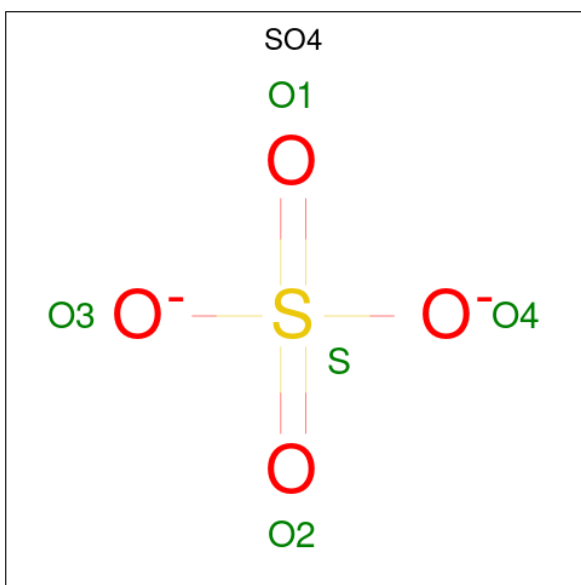
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	1	3		

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Fe	0	0
			1	1		
5	B	1	Total	Fe	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total 1	Zn 1	0	0
7	D	1	Total 1	Zn 1	0	0


- Molecule 8 is water.

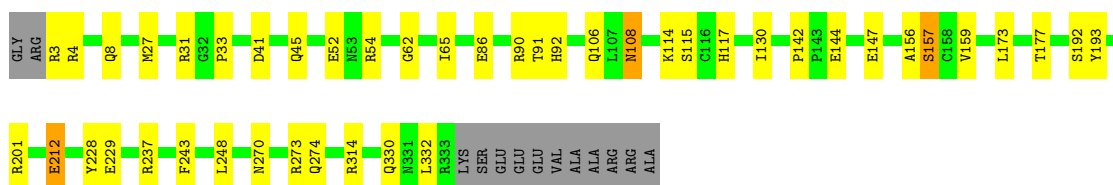
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total 8	O 8	0	0
8	B	10	Total 10	O 10	0	0
8	C	3	Total 3	O 3	0	0
8	D	3	Total 3	O 3	0	0

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.

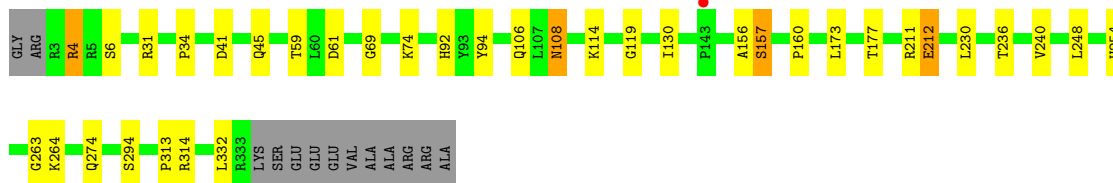
- Molecule 1: Lactotransferrin

Chain A: 




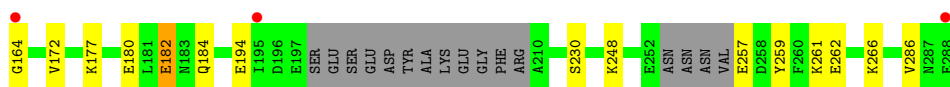
- Molecule 1: Lactotransferrin

Chain B: 




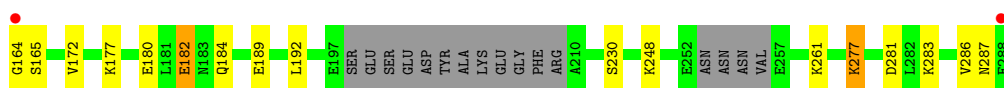
- Molecule 2: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)

Chain C: 



- Molecule 2: PNEUMOCOCCAL SURFACE PROTEIN A (PSPA)

Chain D: 



4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	130.18Å 130.18Å 80.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 2.91 15.00 – 2.91	Depositor EDS
% Data completeness (in resolution range)	95.2 (15.00-2.91) 95.2 (15.00-2.91)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.203 , 0.249 0.201 , 0.246	Depositor DCC
R_{free} test set	1694 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 8.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l 0.043 for h,-h-k,-l 0.043 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6996	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 3.21% 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: ZN, NAG, SO4, CO3, FE

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	0.46	0/2655	0.56	0/3591
1	B	0.47	0/2655	0.54	0/3591
2	C	0.53	0/863	0.60	0/1148
2	D	0.54	0/863	0.60	0/1148
All	All	0.48	0/7036	0.56	0/9478

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	2591	0	2534	30	0
1	B	2591	0	2534	20	1
2	C	860	0	862	5	1
2	D	860	0	862	10	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
5	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	1	0	0	0	0
6	A	15	0	0	1	0
6	B	15	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	8	0	0	0	0
8	B	10	0	0	0	0
8	C	3	0	0	1	0
8	D	3	0	0	1	0
All	All	6996	0	6818	56	1

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 (56) 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:92:HIS:HE2	2:D:164:GLY:N	1.52	1.08
1:A:330:GLN:HE22	1:B:294:SER:H	1.03	0.99
1:A:92:HIS:NE2	2:D:164:GLY:N	2.30	0.78
1:A:330:GLN:NE2	1:B:294:SER:H	1.86	0.66
1:A:114:LYS:HB3	1:A:173:LEU:HD11	1.77	0.66
2:D:182:GLU:HG3	8:D:403:HOH:O	1.96	0.65
1:A:4:ARG:HH11	1:A:8:GLN:NE2	1.98	0.61
1:A:330:GLN:HE22	1:B:294:SER:N	1.86	0.61
1:A:92:HIS:CD2	2:D:164:GLY:O	2.54	0.60
2:D:277:LYS:O	2:D:281:ASP:HB2	2.01	0.60
1:B:4:ARG:HH21	2:D:230:SER:HB3	1.68	0.59
1:B:114:LYS:HB3	1:B:173:LEU:HD11	1.84	0.58
1:B:69:GLY:O	1:B:74:LYS:HD3	2.05	0.57
1:B:94:TYR:HB2	1:B:212:GLU:HG2	1.86	0.57
1:B:61:ASP:HA	1:B:254:HIS:CD2	2.40	0.56
2:C:257:GLU:HG2	2:C:259:TYR:H	1.71	0.55
1:A:52:GLU:HB3	1:A:54:ARG:HH11	1.70	0.55
1:A:270:ASN:HD22	1:A:273:ARG:NH2	2.05	0.55
1:A:27:MET:CE	1:A:33:PRO:HD2	2.38	0.54
1:B:94:TYR:HB2	1:B:212:GLU:CG	2.40	0.52
1:A:4:ARG:HH11	1:A:8:GLN:HE21	1.57	0.52
2:D:180:GLU:HG3	2:D:184:GLN:HE21	1.75	0.50
1:B:313:PRO:O	1:B:314:ARG:HB2	2.11	0.49
1:A:91:THR:N	6:A:349:SO4:O2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:HIS:NE2	2:D:164:GLY:O	2.46	0.49
1:A:108:ASN:HD22	1:A:108:ASN:H	1.59	0.49
1:A:41:ASP:HB2	1:A:45:GLN:HE22	1.77	0.49
1:A:106:GLN:HE22	1:A:237:ARG:HG3	1.79	0.47
1:B:114:LYS:HG2	1:B:156:ALA:HB3	1.96	0.47
1:A:201:ARG:HG2	1:A:228:TYR:OH	2.16	0.46
2:D:189:GLU:HA	2:D:192:LEU:HB3	1.97	0.46
1:A:108:ASN:HD22	1:A:108:ASN:N	2.13	0.45
1:A:4:ARG:HH21	2:C:230:SER:CB	2.30	0.45
1:A:229:GLU:OE2	1:A:237:ARG:HD3	2.17	0.45
1:B:41:ASP:HB2	1:B:45:GLN:NE2	2.32	0.45
1:A:114:LYS:HG2	1:A:156:ALA:HB3	1.99	0.44
2:C:182:GLU:HG3	8:C:404:HOH:O	2.17	0.44
1:B:263:GLY:O	1:B:264:LYS:HB2	2.18	0.44
1:B:41:ASP:HB2	1:B:45:GLN:HE22	1.82	0.43
2:C:262:GLU:HG2	2:C:266:LYS:HE2	2.00	0.43
1:B:230:LEU:HG	1:B:240:VAL:HA	2.01	0.43
1:B:6:SER:HB2	1:B:34:PRO:HG2	2.01	0.43
2:D:172:VAL:O	2:D:172:VAL:CG1	2.67	0.43
1:A:115:SER:OG	1:A:157:SER:HB3	2.19	0.42
1:A:117:HIS:CD2	1:A:159:VAL:HG22	2.54	0.42
1:A:192:SER:OG	1:A:193:TYR:N	2.51	0.42
1:B:119:GLY:HA2	1:B:160:PRO:HD2	2.01	0.42
2:C:180:GLU:HG3	2:C:184:GLN:HE21	1.84	0.42
1:B:130:ILE:HG22	1:B:332:LEU:HD11	2.00	0.42
1:A:142:PRO:HA	1:A:144:GLU:N	2.34	0.42
1:A:108:ASN:H	1:A:108:ASN:ND2	2.17	0.42
1:A:212:GLU:HG3	1:A:243:PHE:CE1	2.55	0.41
1:A:130:ILE:HG22	1:A:332:LEU:HD11	2.01	0.41
1:B:157:SER:C	1:B:173:LEU:HB2	2.41	0.41
1:A:62:GLY:HA2	1:A:65:ILE:HD12	2.02	0.41
1:B:106:GLN:HB2	1:B:108:ASN:ND2	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:HIS:NE2	2:C:164:GLY:N[1_556]	2.16	0.04

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	329/344 (96%)	312 (95%)	17 (5%)	0	100	100
1	B	329/344 (96%)	315 (96%)	14 (4%)	0	100	100
2	C	103/125 (82%)	100 (97%)	2 (2%)	1 (1%)	15	43
2	D	103/125 (82%)	97 (94%)	6 (6%)	0	100	100
All	All	864/938 (92%)	824 (95%)	39 (4%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	194	GLU

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	273/282 (97%)	261 (96%)	12 (4%)	28	60
1	B	273/282 (97%)	262 (96%)	11 (4%)	31	63
2	C	91/105 (87%)	85 (93%)	6 (7%)	16	42
2	D	91/105 (87%)	82 (90%)	9 (10%)	8	23
All	All	728/774 (94%)	690 (95%)	38 (5%)	23	54

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	31	ARG
1	A	86	GLU
1	A	90	ARG
1	A	108	ASN
1	A	147	GLU
1	A	157	SER
1	A	177	THR
1	A	212	GLU
1	A	248	LEU
1	A	274	GLN
1	A	314	ARG
1	B	4	ARG
1	B	31	ARG
1	B	59	THR
1	B	108	ASN
1	B	157	SER
1	B	177	THR
1	B	211	ARG
1	B	212	GLU
1	B	236	THR
1	B	248	LEU
1	B	274	GLN
2	C	172	VAL
2	C	177	LYS
2	C	182	GLU
2	C	248	LYS
2	C	261	LYS
2	C	286	VAL
2	D	165	SER
2	D	177	LYS
2	D	182	GLU
2	D	248	LYS
2	D	261	LYS
2	D	277	LYS
2	D	283	LYS
2	D	286	VAL
2	D	287	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	GLN

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Mol	Chain	Res	Type
1	A	106	GLN
1	A	108	ASN
1	A	127	ASN
1	A	235	ASN
1	A	262	ASN
1	A	270	ASN
1	A	330	GLN
1	B	45	GLN
1	B	108	ASN
1	B	127	ASN
1	B	235	ASN
1	B	262	ASN
1	B	270	ASN
2	C	287	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	B	345	1	14,14,15	0.67	0	17,19,21	1.25	2 (11%)
6	SO4	B	350	-	4,4,4	0.13	0	6,6,6	0.16	0
6	SO4	A	348	-	4,4,4	0.13	0	6,6,6	0.30	0
6	SO4	B	349	-	4,4,4	0.16	0	6,6,6	0.21	0
4	CO3	B	346	5	2,3,3	0.42	0	2,3,3	0.33	0
4	CO3	A	346	5	2,3,3	0.36	0	2,3,3	0.15	0
3	NAG	A	345	1	14,14,15	0.67	0	17,19,21	1.25	1 (5%)
6	SO4	A	349	-	4,4,4	0.14	0	6,6,6	0.21	0
6	SO4	A	350	-	4,4,4	0.12	0	6,6,6	0.15	0
6	SO4	B	348	-	4,4,4	0.14	0	6,6,6	0.31	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
3	NAG	B	345	1	-	2/6/23/26	0/1/1/1
3	NAG	A	345	1	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	345	NAG	C1-O5-C5	3.10	116.39	112.19
3	B	345	NAG	C1-O5-C5	2.76	115.93	112.19
3	B	345	NAG	C4-C3-C2	2.46	114.62	111.02

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	345	NAG	C8-C7-N2-C2
3	A	345	NAG	O7-C7-N2-C2
3	B	345	NAG	C8-C7-N2-C2
3	B	345	NAG	O7-C7-N2-C2
3	A	345	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	349	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	331/344 (96%)	-0.10	0 100 100	17, 28, 43, 51	0
1	B	331/344 (96%)	-0.07	1 (0%) 94 94	17, 28, 43, 51	0
2	C	109/125 (87%)	0.15	3 (2%) 53 50	11, 37, 55, 61	0
2	D	109/125 (87%)	0.13	2 (1%) 68 67	11, 37, 55, 61	0
All	All	880/938 (93%)	-0.03	6 (0%) 87 88	11, 30, 47, 61	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	288	GLU	3.8
1	B	143	PRO	3.7
2	D	288	GLU	3.4
2	C	164	GLY	2.3
2	C	195	ILE	2.0
2	D	164	GLY	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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	B	345	14/15	0.70	0.29	57,60,63,64	0
3	NAG	A	345	14/15	0.71	0.25	57,59,62,62	0
6	SO4	B	349	5/5	0.92	0.21	65,65,65,65	0
6	SO4	A	349	5/5	0.94	0.21	73,73,73,73	0
6	SO4	A	350	5/5	0.97	0.13	71,72,72,72	0
6	SO4	B	350	5/5	0.97	0.19	62,63,63,63	0
6	SO4	B	348	5/5	0.98	0.11	26,26,26,27	0
6	SO4	A	348	5/5	0.99	0.10	25,26,27,27	0
4	CO3	A	346	4/4	0.99	0.12	21,21,21,21	0
4	CO3	B	346	4/4	0.99	0.13	21,21,21,22	0
7	ZN	C	502	1/1	0.99	0.10	20,20,20,20	0
7	ZN	D	501	1/1	0.99	0.08	16,16,16,16	0
5	FE	A	347	1/1	1.00	0.08	18,18,18,18	0
5	FE	B	347	1/1	1.00	0.09	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.