wwPDB X-ray Structure Validation Summary Report (i)

Jun 25, 2024 – 08:15 AM EDT

PDB ID	:	6D01
Title	:	Crystal structure of 1210 Fab in complex with circumsporozoite protein NANP5
Authors	:	Scally, S.W.; Bosch, A.; Imkeller, K.; Wardemann, H.; Julien, J.P.
Deposited on	:	2018-04-09
Resolution	:	3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

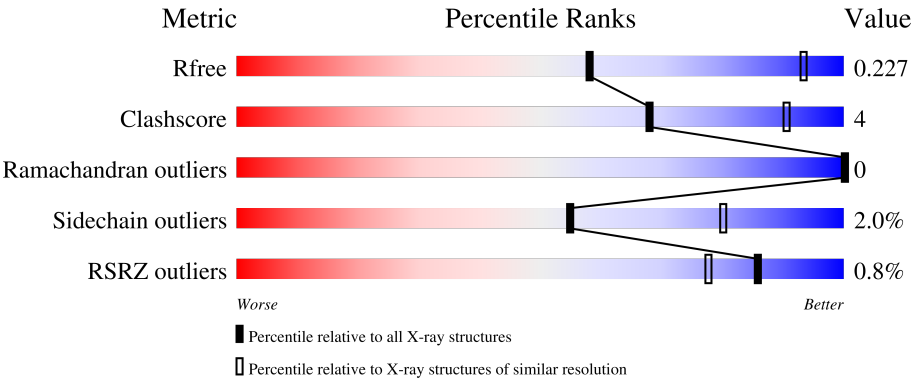
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	226	84% 13%
1	C	226	86% 11%
1	E	226	2% 85% 12%
1	G	226	% 85% 12%
2	B	213	2% 92% 7%

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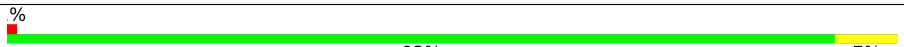
Mol	Chain	Length	Quality of chain
2	D	213	
2	F	213	
2	H	213	
3	I	20	
3	J	20	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	A	302	-	-	-	X
4	EDO	A	303	-	-	-	X
4	EDO	B	311	-	-	-	X
4	EDO	D	304	-	-	-	X
4	EDO	D	307	-	-	-	X
4	EDO	E	301	-	-	-	X
4	EDO	E	302	-	-	-	X
4	EDO	F	304	-	-	-	X
4	EDO	I	102	-	-	-	X
5	PEG	A	305	-	-	-	X
5	PEG	B	313	-	-	-	X
5	PEG	C	304	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 13609 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 1210 Antibody, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1655	1045	280	323	7			
1	C	220	Total	C	N	O	S	0	0	0
			1633	1032	274	320	7			
1	E	222	Total	C	N	O	S	0	0	0
			1652	1043	277	325	7			
1	G	219	Total	C	N	O	S	0	0	0
			1643	1037	279	320	7			

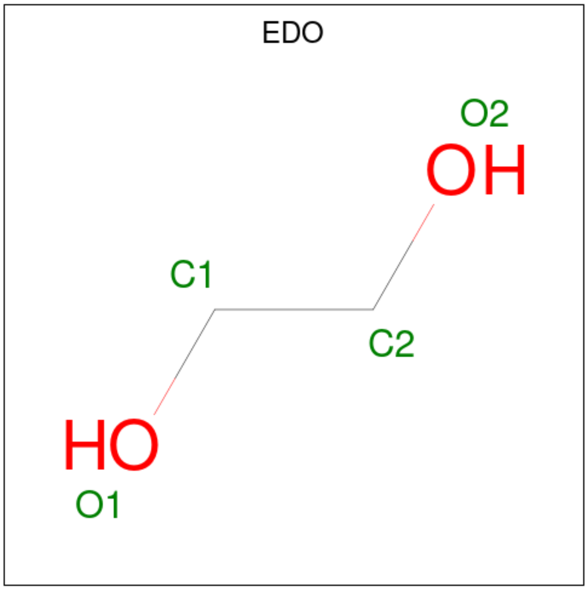
- Molecule 2 is a protein called 1210 Antibody, Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1622	1017	270	330	5			
2	D	212	Total	C	N	O	S	0	0	0
			1634	1025	272	332	5			
2	F	212	Total	C	N	O	S	0	0	0
			1630	1023	272	330	5			
2	H	213	Total	C	N	O	S	0	0	0
			1636	1025	272	333	6			

- Molecule 3 is a protein called NANP5.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	19	Total	C	N	O	0	0	0
			132	76	28	28			
3	J	19	Total	C	N	O	0	0	0
			132	76	28	28			

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	D	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	E	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0

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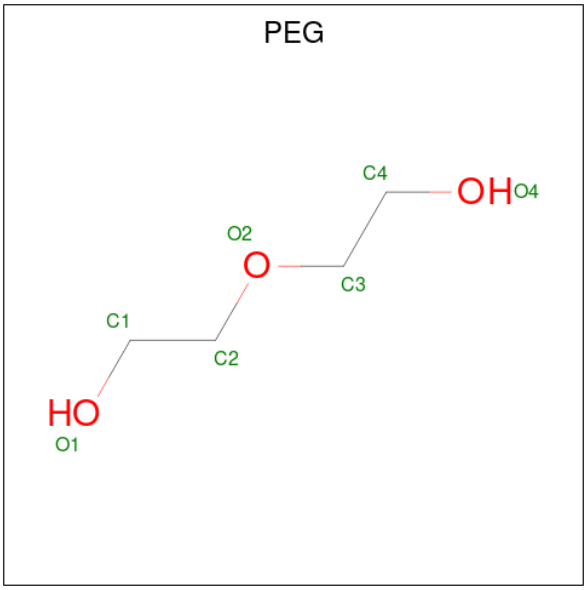
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	1	Total C O 4 2 2	0	0
4	F	1	Total C O 4 2 2	0	0
4	G	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	H	1	Total C O 4 2 2	0	0
4	I	1	Total C O 4 2 2	0	0
4	I	1	Total C O 4 2 2	0	0
4	I	1	Total C O 4 2 2	0	0
4	J	1	Total C O 4 2 2	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



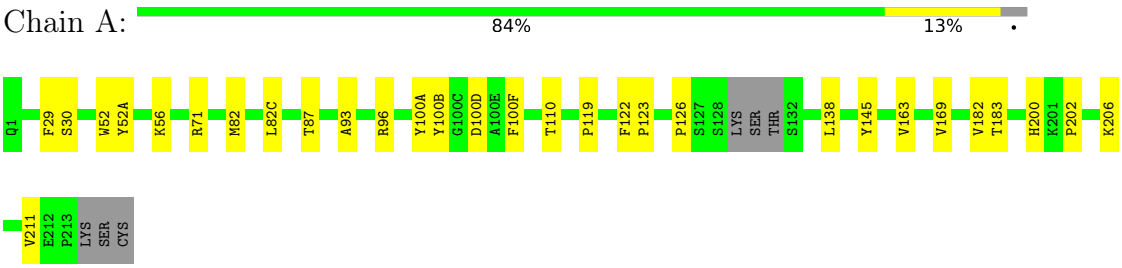
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		

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.

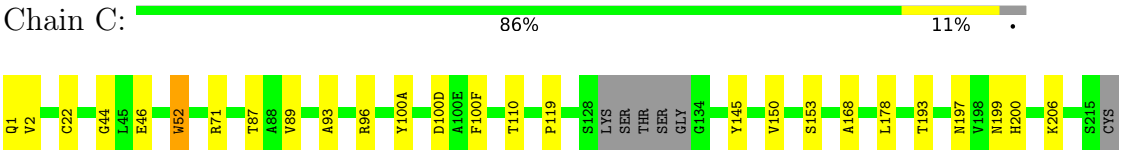
• Molecule 1: 1210 Antibody, heavy chain

Chain A:



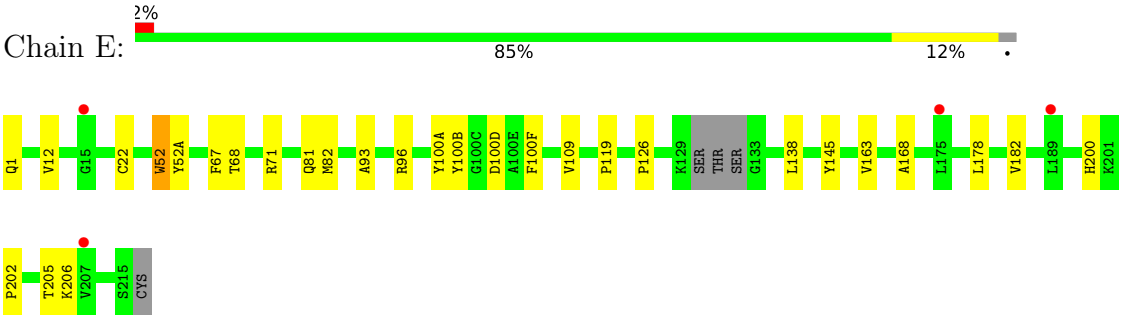
• Molecule 1: 1210 Antibody, heavy chain

Chain C:



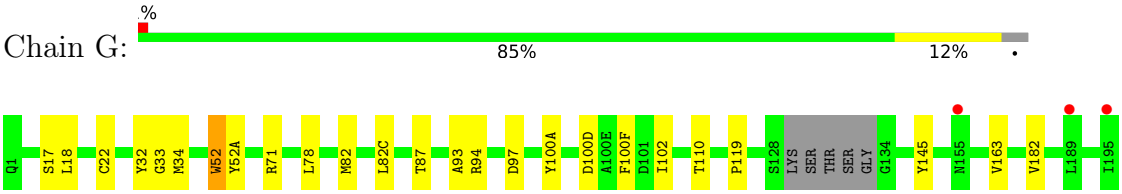
• Molecule 1: 1210 Antibody, heavy chain

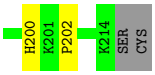
Chain E:



• Molecule 1: 1210 Antibody, heavy chain

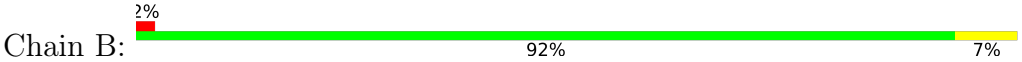
Chain G:

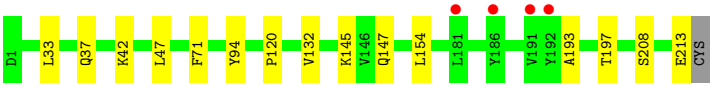




• Molecule 2: 1210 Antibody, Light chain

Chain B:



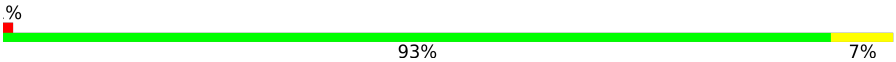


• Molecule 2: 1210 Antibody, Light chain

Chain D:

• Molecule 2: 1210 Antibody, Light chain

Chain F:

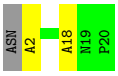


• Molecule 2: 1210 Antibody, Light chain

Chain H:

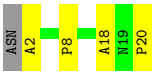
• Molecule 3: NANP5

Chain I:



• Molecule 3: NANP5

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	205.96Å 150.86Å 134.65Å 90.00° 94.81° 90.00°	Depositor
Resolution (Å)	39.87 – 3.20 39.87 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.87-3.20) 93.4 (39.87-3.20)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.49 (at 3.18Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.204 , 0.227 0.204 , 0.227	Depositor DCC
R_{free} test set	2001 reflections (2.96%)	wwPDB-VP
Wilson B-factor (Å^2)	68.3	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 50.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	13609	wwPDB-VP
Average B, all atoms (Å^2)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.87% 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: PEG, EDO

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	0.24	0/1696	0.45	0/2311
1	C	0.25	0/1674	0.45	0/2286
1	E	0.25	0/1693	0.45	0/2310
1	G	0.24	0/1684	0.45	0/2297
2	B	0.25	0/1659	0.45	0/2261
2	D	0.26	0/1671	0.46	0/2274
2	F	0.25	0/1667	0.45	0/2269
2	H	0.25	0/1673	0.47	0/2278
3	I	0.27	0/136	0.42	0/191
3	J	0.27	0/136	0.44	0/191
All	All	0.25	0/13689	0.45	0/18668

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	1655	0	1590	17	0
1	C	1633	0	1544	14	0
1	E	1652	0	1569	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1643	0	1565	14	0
2	B	1622	0	1539	9	0
2	D	1634	0	1565	13	0
2	F	1630	0	1561	6	0
2	H	1636	0	1559	7	0
3	I	132	0	113	2	0
3	J	132	0	113	3	0
4	A	16	0	24	3	0
4	B	44	0	66	3	0
4	C	12	0	18	1	0
4	D	32	0	48	2	0
4	E	16	0	24	1	0
4	F	28	0	42	0	0
4	G	4	0	6	0	0
4	H	16	0	24	2	0
4	I	12	0	18	0	0
4	J	4	0	6	1	0
5	A	7	0	10	1	0
5	B	14	0	20	1	0
5	C	7	0	10	3	0
5	D	7	0	10	2	0
5	E	7	0	10	0	0
5	F	14	0	20	1	0
All	All	13609	0	13074	100	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.

The worst 5 of 100 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)
2:F:39:LYS:NZ	2:F:81:ASP:OD1	2.24	0.71
1:E:100(A):TYR:HH	3:J:2:ALA:N	1.91	0.68
1:G:52:TRP:O	1:G:71:ARG:NH1	2.25	0.68
1:E:93:ALA:HB1	1:E:100(F):PHE:HB3	1.76	0.67
1:G:82:MET:HE2	1:G:82(C):LEU:HD21	1.77	0.67

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	216/226 (96%)	209 (97%)	7 (3%)	0	100	100
1	C	216/226 (96%)	209 (97%)	7 (3%)	0	100	100
1	E	218/226 (96%)	210 (96%)	8 (4%)	0	100	100
1	G	215/226 (95%)	207 (96%)	8 (4%)	0	100	100
2	B	210/213 (99%)	204 (97%)	6 (3%)	0	100	100
2	D	210/213 (99%)	203 (97%)	7 (3%)	0	100	100
2	F	210/213 (99%)	202 (96%)	8 (4%)	0	100	100
2	H	211/213 (99%)	200 (95%)	11 (5%)	0	100	100
3	I	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
3	J	17/20 (85%)	16 (94%)	1 (6%)	0	100	100
All	All	1740/1796 (97%)	1676 (96%)	64 (4%)	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	181/190 (95%)	177 (98%)	4 (2%)	52	79
1	C	176/190 (93%)	170 (97%)	6 (3%)	37	70
1	E	179/190 (94%)	175 (98%)	4 (2%)	52	79
1	G	178/190 (94%)	173 (97%)	5 (3%)	43	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	181/188 (96%)	180 (99%)	1 (1%)	86 94
2	D	184/188 (98%)	181 (98%)	3 (2%)	62 84
2	F	183/188 (97%)	181 (99%)	2 (1%)	73 88
2	H	184/188 (98%)	179 (97%)	5 (3%)	44 75
3	I	14/15 (93%)	14 (100%)	0	100 100
3	J	14/15 (93%)	14 (100%)	0	100 100
All	All	1474/1542 (96%)	1444 (98%)	30 (2%)	55 80

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1	GLN
2	H	7	SER
1	E	52	TRP
2	H	213	GLU
1	G	100(D)	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	199	ASN
2	D	124	GLN

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)

54 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	EDO	I	101	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	F	305	-	3,3,3	0.46	0	2,2,2	0.31	0
4	EDO	I	103	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	D	306	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	H	304	-	3,3,3	0.49	0	2,2,2	0.34	0
4	EDO	B	310	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	D	302	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	D	305	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	A	302	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	C	303	-	3,3,3	0.45	0	2,2,2	0.34	0
4	EDO	E	301	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	E	304	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	E	302	-	3,3,3	0.47	0	2,2,2	0.33	0
4	EDO	C	302	-	3,3,3	0.47	0	2,2,2	0.32	0
4	EDO	C	301	-	3,3,3	0.45	0	2,2,2	0.34	0
4	EDO	B	301	-	3,3,3	0.47	0	2,2,2	0.29	0
4	EDO	H	301	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	B	304	-	3,3,3	0.45	0	2,2,2	0.34	0
4	EDO	B	302	-	3,3,3	0.46	0	2,2,2	0.35	0
4	EDO	F	304	-	3,3,3	0.47	0	2,2,2	0.26	0
4	EDO	F	302	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	H	302	-	3,3,3	0.46	0	2,2,2	0.42	0
4	EDO	A	304	-	3,3,3	0.45	0	2,2,2	0.32	0
4	EDO	D	304	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	B	307	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	D	301	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	B	305	-	3,3,3	0.46	0	2,2,2	0.35	0
4	EDO	A	301	-	3,3,3	0.45	0	2,2,2	0.34	0
4	EDO	I	102	-	3,3,3	0.46	0	2,2,2	0.31	0
5	PEG	B	313	-	6,6,6	0.49	0	5,5,5	0.28	0
4	EDO	F	301	-	3,3,3	0.42	0	2,2,2	0.41	0
4	EDO	F	307	-	3,3,3	0.40	0	2,2,2	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	EDO	B	306	-	3,3,3	0.46	0	2,2,2	0.34	0
5	PEG	D	309	-	6,6,6	0.49	0	5,5,5	0.45	0
4	EDO	D	303	-	3,3,3	0.46	0	2,2,2	0.30	0
4	EDO	D	307	-	3,3,3	0.45	0	2,2,2	0.34	0
4	EDO	A	303	-	3,3,3	0.46	0	2,2,2	0.35	0
5	PEG	E	305	-	6,6,6	0.49	0	5,5,5	0.28	0
4	EDO	F	306	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	F	303	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	G	301	-	3,3,3	0.47	0	2,2,2	0.33	0
5	PEG	B	312	-	6,6,6	0.49	0	5,5,5	0.28	0
4	EDO	D	308	-	3,3,3	0.46	0	2,2,2	0.04	0
4	EDO	B	309	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	B	303	-	3,3,3	0.46	0	2,2,2	0.33	0
5	PEG	A	305	-	6,6,6	0.49	0	5,5,5	0.26	0
4	EDO	H	303	-	3,3,3	0.45	0	2,2,2	0.33	0
5	PEG	F	308	-	6,6,6	0.48	0	5,5,5	0.30	0
5	PEG	C	304	-	6,6,6	0.48	0	5,5,5	0.34	0
4	EDO	B	308	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	E	303	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	J	101	-	3,3,3	0.46	0	2,2,2	0.31	0
5	PEG	F	309	-	6,6,6	0.50	0	5,5,5	0.28	0
4	EDO	B	311	-	3,3,3	0.45	0	2,2,2	0.32	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
4	EDO	I	101	-	-	0/1/1/1	-
4	EDO	F	305	-	-	0/1/1/1	-
4	EDO	I	103	-	-	0/1/1/1	-
4	EDO	D	306	-	-	0/1/1/1	-
4	EDO	H	304	-	-	0/1/1/1	-
4	EDO	B	310	-	-	0/1/1/1	-
4	EDO	D	302	-	-	0/1/1/1	-
4	EDO	D	305	-	-	0/1/1/1	-
4	EDO	A	302	-	-	0/1/1/1	-
4	EDO	C	303	-	-	0/1/1/1	-
4	EDO	E	301	-	-	0/1/1/1	-
4	EDO	E	304	-	-	0/1/1/1	-
4	EDO	E	302	-	-	0/1/1/1	-
4	EDO	C	302	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	301	-	-	0/1/1/1	-
4	EDO	B	301	-	-	1/1/1/1	-
4	EDO	H	301	-	-	0/1/1/1	-
4	EDO	B	304	-	-	0/1/1/1	-
4	EDO	B	302	-	-	0/1/1/1	-
4	EDO	F	304	-	-	0/1/1/1	-
4	EDO	F	302	-	-	0/1/1/1	-
4	EDO	H	302	-	-	0/1/1/1	-
4	EDO	A	304	-	-	0/1/1/1	-
4	EDO	D	304	-	-	0/1/1/1	-
4	EDO	B	307	-	-	0/1/1/1	-
4	EDO	D	301	-	-	1/1/1/1	-
4	EDO	B	305	-	-	0/1/1/1	-
4	EDO	A	301	-	-	0/1/1/1	-
4	EDO	I	102	-	-	0/1/1/1	-
5	PEG	B	313	-	-	3/4/4/4	-
4	EDO	F	301	-	-	0/1/1/1	-
4	EDO	F	307	-	-	0/1/1/1	-
4	EDO	B	306	-	-	0/1/1/1	-
5	PEG	D	309	-	-	2/4/4/4	-
4	EDO	D	303	-	-	0/1/1/1	-
4	EDO	D	307	-	-	0/1/1/1	-
4	EDO	A	303	-	-	0/1/1/1	-
5	PEG	E	305	-	-	0/4/4/4	-
4	EDO	F	306	-	-	0/1/1/1	-
4	EDO	F	303	-	-	0/1/1/1	-
4	EDO	G	301	-	-	0/1/1/1	-
5	PEG	B	312	-	-	0/4/4/4	-
4	EDO	D	308	-	-	0/1/1/1	-
4	EDO	B	309	-	-	0/1/1/1	-
4	EDO	B	303	-	-	0/1/1/1	-
5	PEG	A	305	-	-	4/4/4/4	-
4	EDO	H	303	-	-	0/1/1/1	-
5	PEG	F	308	-	-	3/4/4/4	-
5	PEG	C	304	-	-	3/4/4/4	-
4	EDO	B	308	-	-	0/1/1/1	-
4	EDO	E	303	-	-	0/1/1/1	-
4	EDO	J	101	-	-	0/1/1/1	-
5	PEG	F	309	-	-	4/4/4/4	-
4	EDO	B	311	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	304	PEG	C1-C2-O2-C3
5	B	313	PEG	O2-C3-C4-O4
5	F	309	PEG	O1-C1-C2-O2
5	C	304	PEG	O1-C1-C2-O2
5	A	305	PEG	O2-C3-C4-O4

There are no ring outliers.

17 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	304	EDO	1	0
4	D	305	EDO	1	0
4	C	303	EDO	1	0
4	H	301	EDO	1	0
4	A	304	EDO	2	0
4	B	307	EDO	1	0
4	A	301	EDO	1	0
5	B	313	PEG	1	0
5	D	309	PEG	2	0
4	D	303	EDO	1	0
4	B	303	EDO	1	0
5	A	305	PEG	1	0
5	C	304	PEG	3	0
4	B	308	EDO	1	0
4	E	303	EDO	1	0
4	J	101	EDO	1	0
5	F	309	PEG	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	220/226 (97%)	-0.14	0 100 100	41, 72, 124, 153	0
1	C	220/226 (97%)	-0.12	0 100 100	44, 75, 118, 168	0
1	E	222/226 (98%)	0.24	4 (1%) 68 55	70, 105, 129, 203	0
1	G	219/226 (96%)	0.11	3 (1%) 75 63	63, 96, 135, 156	0
2	B	212/213 (99%)	-0.07	4 (1%) 66 53	39, 64, 135, 147	0
2	D	212/213 (99%)	-0.20	0 100 100	37, 63, 88, 107	0
2	F	212/213 (99%)	-0.13	2 (0%) 84 75	39, 68, 129, 140	0
2	H	213/213 (100%)	-0.02	1 (0%) 91 86	54, 80, 103, 119	0
3	I	19/20 (95%)	0.02	0 100 100	48, 57, 119, 135	0
3	J	19/20 (95%)	0.08	0 100 100	71, 88, 153, 160	0
All	All	1768/1796 (98%)	-0.04	14 (0%) 86 78	37, 79, 127, 203	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	192	TYR	3.5
2	F	192	TYR	3.0
2	F	181	LEU	2.8
1	G	189	LEU	2.7
1	E	175	LEU	2.6

6.2 Non-standard residues in protein, DNA, RNA chains

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, 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
4	EDO	E	302	4/4	0.56	0.42	95,95,104,106	0
4	EDO	A	302	4/4	0.60	0.42	85,88,91,91	0
4	EDO	D	307	4/4	0.65	0.42	98,106,107,109	0
4	EDO	B	308	4/4	0.65	0.31	103,103,103,105	0
4	EDO	F	306	4/4	0.65	0.21	91,98,98,99	0
4	EDO	D	306	4/4	0.70	0.35	72,72,79,90	0
4	EDO	J	101	4/4	0.70	0.36	86,88,92,93	0
4	EDO	I	102	4/4	0.71	0.43	69,81,88,95	0
4	EDO	I	103	4/4	0.71	0.24	87,94,96,101	0
4	EDO	E	301	4/4	0.71	0.51	85,89,91,94	0
4	EDO	D	304	4/4	0.72	0.55	70,84,96,99	0
4	EDO	B	310	4/4	0.73	0.39	98,100,105,111	0
5	PEG	D	309	7/7	0.73	0.26	97,109,116,123	0
5	PEG	E	305	7/7	0.74	0.27	75,89,97,97	0
5	PEG	C	304	7/7	0.75	0.67	71,91,99,100	0
4	EDO	H	304	4/4	0.76	0.30	94,119,119,129	0
4	EDO	B	307	4/4	0.77	0.33	79,85,85,86	0
4	EDO	A	303	4/4	0.77	0.46	88,99,107,116	0
4	EDO	F	304	4/4	0.78	0.84	90,95,96,100	0
4	EDO	D	301	4/4	0.78	0.28	80,84,92,94	0
5	PEG	A	305	7/7	0.78	0.55	60,91,107,108	0
4	EDO	E	303	4/4	0.79	0.38	91,94,97,98	0
4	EDO	B	311	4/4	0.79	0.47	104,105,107,108	0
5	PEG	B	313	7/7	0.79	0.48	94,107,109,140	0
4	EDO	B	305	4/4	0.80	0.36	84,86,96,102	0
4	EDO	D	302	4/4	0.81	0.33	83,84,87,90	0
4	EDO	F	302	4/4	0.81	0.28	82,83,87,91	0
4	EDO	C	303	4/4	0.81	0.40	100,102,102,103	0
5	PEG	B	312	7/7	0.81	0.22	73,99,106,107	0
4	EDO	F	301	4/4	0.82	0.30	80,96,99,102	0
4	EDO	G	301	4/4	0.82	0.38	88,92,96,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PEG	F	308	7/7	0.82	0.23	66,81,83,84	0
4	EDO	B	306	4/4	0.83	0.43	67,85,102,107	0
4	EDO	I	101	4/4	0.83	0.34	76,78,83,83	0
4	EDO	B	303	4/4	0.84	0.32	72,86,87,95	0
5	PEG	F	309	7/7	0.84	0.33	100,103,123,123	0
4	EDO	H	303	4/4	0.85	0.31	89,96,106,108	0
4	EDO	C	301	4/4	0.85	0.40	83,90,91,93	0
4	EDO	H	301	4/4	0.86	0.30	92,93,98,99	0
4	EDO	C	302	4/4	0.86	0.32	66,87,89,98	0
4	EDO	D	305	4/4	0.86	0.38	53,74,86,91	0
4	EDO	F	303	4/4	0.87	0.38	65,76,76,84	0
4	EDO	F	307	4/4	0.87	0.30	91,97,98,104	0
4	EDO	D	303	4/4	0.87	0.35	73,86,89,97	0
4	EDO	D	308	4/4	0.88	0.37	90,97,98,104	0
4	EDO	F	305	4/4	0.88	0.23	72,76,80,81	0
4	EDO	H	302	4/4	0.90	0.34	73,76,80,85	0
4	EDO	A	301	4/4	0.90	0.23	67,74,89,89	0
4	EDO	B	301	4/4	0.90	0.30	65,66,68,76	0
4	EDO	B	304	4/4	0.91	0.32	73,78,79,85	0
4	EDO	E	304	4/4	0.91	0.36	85,90,94,95	0
4	EDO	A	304	4/4	0.92	0.29	86,86,91,94	0
4	EDO	B	309	4/4	0.93	0.44	67,70,78,92	0
4	EDO	B	302	4/4	0.94	0.18	81,87,92,96	0

6.5 Other polymers (i)

There are no such residues in this entry.