



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 16, 2017 – 11:48 PM EST

PDB ID : 4PPH
Title : Crystal structure of conglutin gamma, a unique basic 7S globulin from lupine seeds
Authors : Czubinski, J.; Barciszewski, J.; Gilski, M.; Lampart-Szczapa, E.; Jaskolski, M.
Deposited on : unknown
Resolution : 2.01 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

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

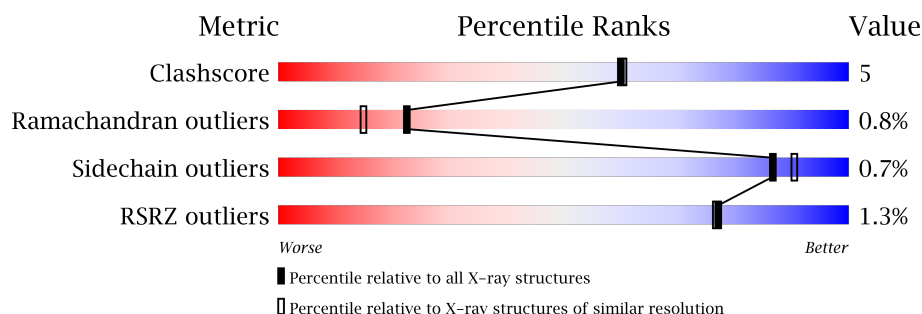
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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))
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	417	
1	B	417	
1	C	417	
1	D	417	
1	E	417	
1	F	417	

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
2	NAG	F	501	-	-	-	X
4	EDO	A	505	-	-	-	X
4	EDO	A	506	-	-	-	X
4	EDO	A	507	-	-	-	X
4	EDO	A	508	-	-	-	X
4	EDO	B	502	-	-	-	X
4	EDO	B	504	-	-	-	X
4	EDO	B	506	-	-	-	X
4	EDO	C	506	-	-	-	X
4	EDO	D	505	-	-	-	X
4	EDO	D	506	-	-	-	X
4	EDO	D	507	-	-	-	X
4	EDO	D	508	-	-	-	X
4	EDO	D	509	-	-	-	X
4	EDO	D	510	-	-	-	X
4	EDO	F	503	-	-	-	X
4	EDO	F	505	-	-	-	X
4	EDO	F	508	-	-	-	X

2 Entry composition [i](#)

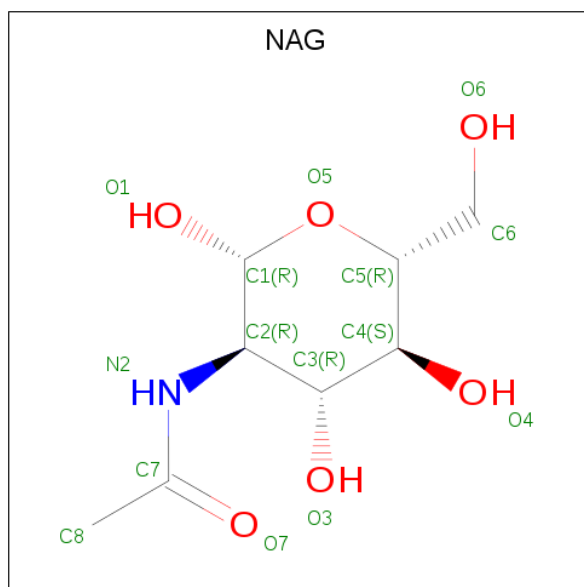
There are 5 unique types of molecules in this entry. The entry contains 19098 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Conglutin gamma.

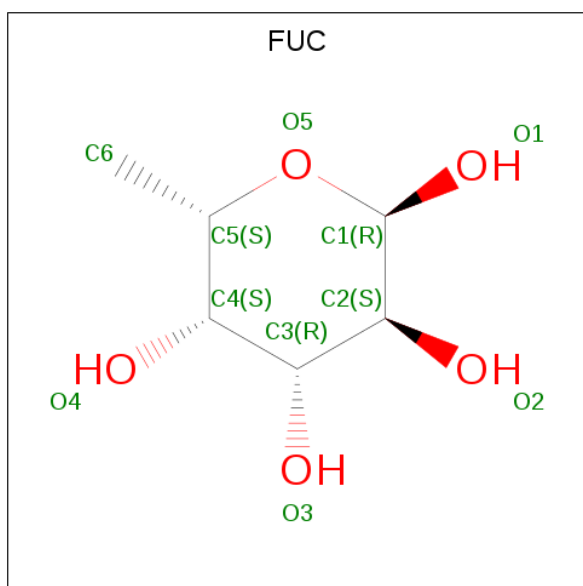
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	25	2	0
			2996	1887	529	563	17			
1	B	391	Total	C	N	O	S	26	7	0
			3020	1905	533	565	17			
1	C	392	Total	C	N	O	S	33	3	0
			3017	1900	534	566	17			
1	D	392	Total	C	N	O	S	30	2	0
			3017	1900	534	567	16			
1	E	391	Total	C	N	O	S	47	4	0
			3007	1895	530	565	17			
1	F	392	Total	C	N	O	S	46	3	0
			3011	1897	532	565	17			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	143	Total	O	0	0
			143	143		

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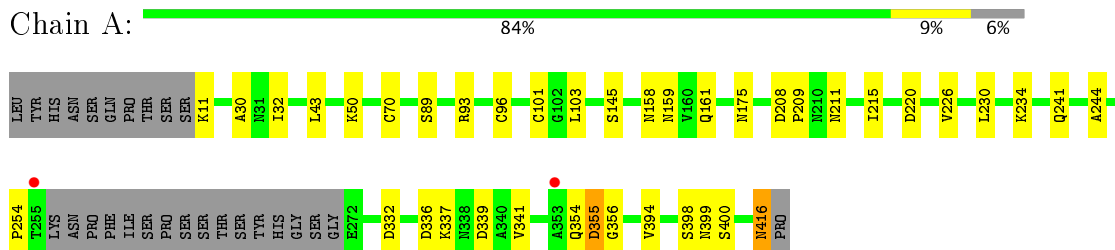
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	146	Total 146	O 146	0	0
5	C	128	Total 128	O 128	0	0
5	D	124	Total 124	O 124	0	0
5	E	102	Total 102	O 102	0	0
5	F	151	Total 151	O 151	0	0

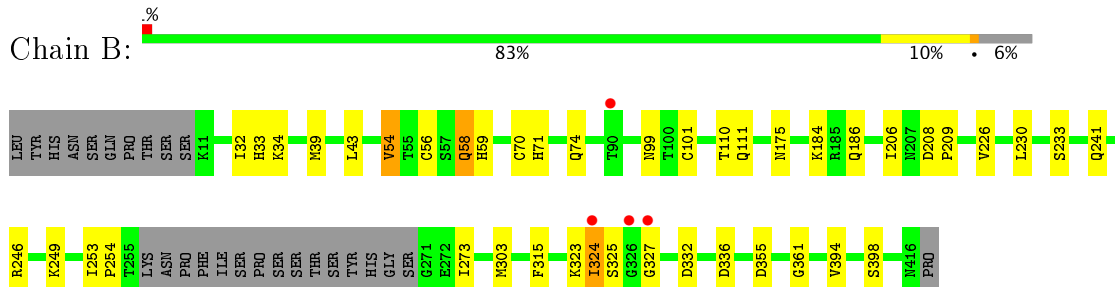
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). 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.

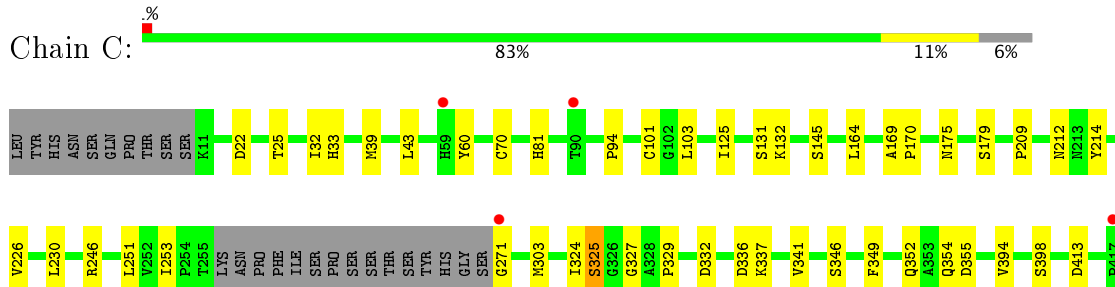
- Molecule 1: Conglutin gamma



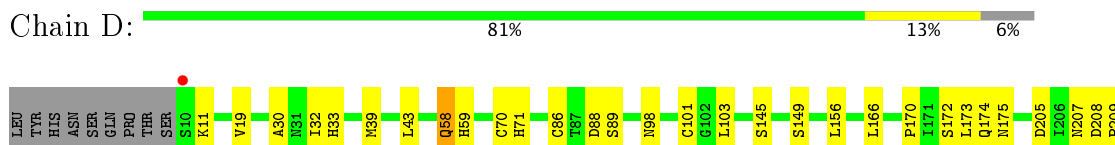
- Molecule 1: Conglutin gamma

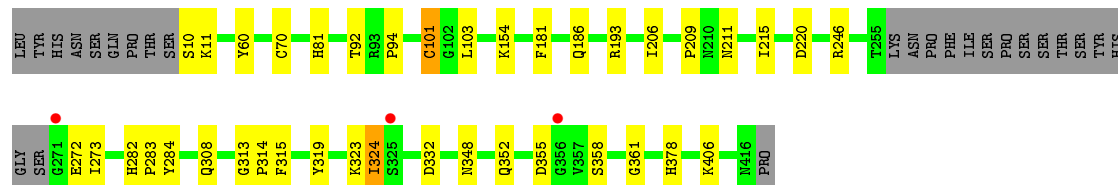


- Molecule 1: Conglutin gamma



- Molecule 1: Conglutin gamma





4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	121.99Å 121.99Å 188.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.76 – 2.01 43.76 – 2.01	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.76-2.01) 99.5 (43.76-2.01)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.3_1479)	Depositor
R, R_{free}	0.145 , 0.174 0.145 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.098 for -h,-k,l 0.107 for h,-h-k,-l 0.248 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	19098	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: FUC, EDO, NAG

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	0.52	0/3073	0.67	0/4180
1	B	0.54	1/3117 (0.0%)	0.67	0/4239
1	C	0.52	0/3096	0.68	0/4212
1	D	0.52	0/3092	0.70	0/4207
1	E	0.54	0/3092	0.72	0/4205
1	F	0.53	0/3093	0.68	0/4207
All	All	0.53	1/18563 (0.0%)	0.69	0/25250

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	56	CYS	CB-SG	-5.09	1.73	1.81

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	2996	0	2921	31	0
1	B	3020	0	2953	30	0
1	C	3017	0	2937	40	0
1	D	3017	0	2939	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3007	0	2936	37	0
1	F	3011	0	2935	24	0
2	A	28	0	24	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
2	D	14	0	13	0	0
2	F	28	0	25	1	0
3	A	10	0	10	0	0
4	A	24	0	36	5	0
4	B	20	0	30	0	0
4	C	20	0	30	3	0
4	D	36	0	54	7	0
4	E	4	0	6	1	0
4	F	24	0	36	3	0
5	A	143	0	0	1	0
5	B	146	0	0	2	0
5	C	128	0	0	6	0
5	D	124	0	0	1	0
5	E	102	0	0	3	0
5	F	151	0	0	2	0
All	All	19098	0	17911	189	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 5.

The worst 5 of 189 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:416:ASN:H	1:A:416:ASN:HD22	1.20	0.84
1:E:50:LYS:H	4:E:501:EDO:H11	1.43	0.84
1:E:175[A]:ASN:OD1	5:E:694:HOH:O	1.97	0.82
1:E:60:TYR:HB3	1:E:94:PRO:HG2	1.66	0.77
1:C:125:ILE:HA	4:C:506:EDO:H22	1.67	0.76

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	388/417 (93%)	374 (96%)	13 (3%)	1 (0%)	44	40
1	B	394/417 (94%)	378 (96%)	13 (3%)	3 (1%)	22	15
1	C	391/417 (94%)	378 (97%)	12 (3%)	1 (0%)	44	40
1	D	390/417 (94%)	373 (96%)	13 (3%)	4 (1%)	18	10
1	E	391/417 (94%)	374 (96%)	11 (3%)	6 (2%)	12	5
1	F	391/417 (94%)	372 (95%)	16 (4%)	3 (1%)	22	15
All	All	2345/2502 (94%)	2249 (96%)	78 (3%)	18 (1%)	22	15

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	355	ASP
1	B	58	GLN
1	D	58	GLN
1	D	338	ASN
1	E	88	ASP

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	339/362 (94%)	337 (99%)	2 (1%)	89	92
1	B	344/362 (95%)	342 (99%)	2 (1%)	89	92
1	C	341/362 (94%)	341 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	341/362 (94%)	340 (100%)	1 (0%)	94	96
1	E	341/362 (94%)	337 (99%)	4 (1%)	75	80
1	F	341/362 (94%)	334 (98%)	7 (2%)	59	62
All	All	2047/2172 (94%)	2031 (99%)	16 (1%)	87	88

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	351	VAL
1	E	416	ASN
1	F	154	LYS
1	E	324	ILE
1	F	193	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	98	ASN
1	F	352	GLN
1	E	213	ASN
1	D	416	ASN
1	E	153	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

40 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	NAG	A	501	1,3,2	14,14,15	0.88	1 (7%)	15,19,21	0.64	0
2	NAG	A	502	2	14,14,15	0.49	0	15,19,21	0.58	0
3	FUC	A	503	2	9,10,11	1.38	1 (11%)	13,14,16	1.15	1 (7%)
4	EDO	A	504	-	3,3,3	0.54	0	2,2,2	0.11	0
4	EDO	A	505	-	3,3,3	0.56	0	2,2,2	0.09	0
4	EDO	A	506	-	3,3,3	0.29	0	2,2,2	0.39	0
4	EDO	A	507	-	3,3,3	0.38	0	2,2,2	0.54	0
4	EDO	A	508	-	3,3,3	0.38	0	2,2,2	0.67	0
4	EDO	A	509	-	3,3,3	0.52	0	2,2,2	0.11	0
2	NAG	B	501	1	14,14,15	0.43	0	15,19,21	0.58	0
4	EDO	B	502	-	3,3,3	0.42	0	2,2,2	0.37	0
4	EDO	B	503	-	3,3,3	0.38	0	2,2,2	0.31	0
4	EDO	B	504	-	3,3,3	0.50	0	2,2,2	0.25	0
4	EDO	B	505	-	3,3,3	0.44	0	2,2,2	0.23	0
4	EDO	B	506	-	3,3,3	0.46	0	2,2,2	0.44	0
2	NAG	C	501	1	14,14,15	0.44	0	15,19,21	0.46	0
4	EDO	C	502	-	3,3,3	0.45	0	2,2,2	0.20	0
4	EDO	C	503	-	3,3,3	0.46	0	2,2,2	0.17	0
4	EDO	C	504	-	3,3,3	0.48	0	2,2,2	0.36	0
4	EDO	C	505	-	3,3,3	0.36	0	2,2,2	0.66	0
4	EDO	C	506	-	3,3,3	0.59	0	2,2,2	0.12	0
2	NAG	D	501	1	14,14,15	0.80	1 (7%)	15,19,21	0.68	0
4	EDO	D	502	-	3,3,3	0.35	0	2,2,2	0.73	0
4	EDO	D	503	-	3,3,3	0.49	0	2,2,2	0.27	0
4	EDO	D	504	-	3,3,3	0.40	0	2,2,2	0.22	0
4	EDO	D	505	-	3,3,3	0.50	0	2,2,2	0.23	0
4	EDO	D	506	-	3,3,3	0.46	0	2,2,2	0.08	0
4	EDO	D	507	-	3,3,3	0.56	0	2,2,2	0.27	0
4	EDO	D	508	-	3,3,3	0.64	0	2,2,2	0.05	0
4	EDO	D	509	-	3,3,3	0.54	0	2,2,2	0.13	0
4	EDO	D	510	-	3,3,3	0.45	0	2,2,2	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	E	501	-	3,3,3	0.53	0	2,2,2	0.47	0
2	NAG	F	501	1,2	14,14,15	0.93	1 (7%)	15,19,21	0.67	0
2	NAG	F	502	2	14,14,15	0.64	0	15,19,21	0.38	0
4	EDO	F	503	-	3,3,3	0.42	0	2,2,2	0.83	0
4	EDO	F	504	-	3,3,3	0.49	0	2,2,2	0.29	0
4	EDO	F	505	-	3,3,3	0.37	0	2,2,2	0.68	0
4	EDO	F	506	-	3,3,3	0.37	0	2,2,2	0.25	0
4	EDO	F	507	-	3,3,3	0.51	0	2,2,2	0.08	0
4	EDO	F	508	-	3,3,3	0.42	0	2,2,2	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	501	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	A	502	2	-	0/6/23/26	0/1/1/1
3	FUC	A	503	2	-	0/0/17/20	0/1/1/1
4	EDO	A	504	-	-	0/1/1/1	0/0/0/0
4	EDO	A	505	-	-	0/1/1/1	0/0/0/0
4	EDO	A	506	-	-	0/1/1/1	0/0/0/0
4	EDO	A	507	-	-	0/1/1/1	0/0/0/0
4	EDO	A	508	-	-	0/1/1/1	0/0/0/0
4	EDO	A	509	-	-	0/1/1/1	0/0/0/0
2	NAG	B	501	1	-	0/6/23/26	0/1/1/1
4	EDO	B	502	-	-	0/1/1/1	0/0/0/0
4	EDO	B	503	-	-	0/1/1/1	0/0/0/0
4	EDO	B	504	-	-	0/1/1/1	0/0/0/0
4	EDO	B	505	-	-	0/1/1/1	0/0/0/0
4	EDO	B	506	-	-	0/1/1/1	0/0/0/0
2	NAG	C	501	1	-	0/6/23/26	0/1/1/1
4	EDO	C	502	-	-	0/1/1/1	0/0/0/0
4	EDO	C	503	-	-	0/1/1/1	0/0/0/0
4	EDO	C	504	-	-	0/1/1/1	0/0/0/0
4	EDO	C	505	-	-	0/1/1/1	0/0/0/0
4	EDO	C	506	-	-	0/1/1/1	0/0/0/0
2	NAG	D	501	1	-	0/6/23/26	0/1/1/1
4	EDO	D	502	-	-	0/1/1/1	0/0/0/0
4	EDO	D	503	-	-	0/1/1/1	0/0/0/0
4	EDO	D	504	-	-	0/1/1/1	0/0/0/0
4	EDO	D	505	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	D	506	-	-	0/1/1/1	0/0/0/0
4	EDO	D	507	-	-	0/1/1/1	0/0/0/0
4	EDO	D	508	-	-	0/1/1/1	0/0/0/0
4	EDO	D	509	-	-	0/1/1/1	0/0/0/0
4	EDO	D	510	-	-	0/1/1/1	0/0/0/0
4	EDO	E	501	-	-	0/1/1/1	0/0/0/0
2	NAG	F	501	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	502	2	-	0/6/23/26	0/1/1/1
4	EDO	F	503	-	-	0/1/1/1	0/0/0/0
4	EDO	F	504	-	-	0/1/1/1	0/0/0/0
4	EDO	F	505	-	-	0/1/1/1	0/0/0/0
4	EDO	F	506	-	-	0/1/1/1	0/0/0/0
4	EDO	F	507	-	-	0/1/1/1	0/0/0/0
4	EDO	F	508	-	-	0/1/1/1	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	501	NAG	O5-C1	-2.94	1.38	1.43
2	D	501	NAG	O5-C1	2.71	1.48	1.43
3	A	503	FUC	C4-C5	2.81	1.58	1.53
2	A	501	NAG	O5-C1	2.94	1.48	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FUC	O5-C1-C2	2.35	114.47	110.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	506	EDO	3	0
4	A	507	EDO	1	0
4	A	509	EDO	1	0
4	C	502	EDO	1	0
4	C	504	EDO	1	0
4	C	506	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	502	EDO	1	0
4	D	505	EDO	1	0
4	D	506	EDO	1	0
4	D	508	EDO	3	0
4	D	509	EDO	1	0
4	E	501	EDO	1	0
2	F	501	NAG	1	0
4	F	504	EDO	3	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	390/417 (93%)	-0.51	2 (0%) 90 90	23, 41, 76, 99	5 (1%)
1	B	391/417 (93%)	-0.53	4 (1%) 82 82	20, 36, 73, 96	5 (1%)
1	C	392/417 (94%)	-0.47	4 (1%) 82 82	24, 41, 79, 96	7 (1%)
1	D	392/417 (94%)	-0.45	2 (0%) 90 90	25, 45, 79, 101	6 (1%)
1	E	389/417 (93%)	-0.34	16 (4%) 38 38	25, 45, 95, 134	7 (1%)
1	F	389/417 (93%)	-0.52	3 (0%) 86 85	23, 40, 77, 111	5 (1%)
All	All	2343/2502 (93%)	-0.47	31 (1%) 77 77	20, 42, 80, 134	35 (1%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	327	GLY	8.4
1	E	326	GLY	7.7
1	C	271	GLY	6.5
1	E	321	SER	5.0
1	D	10	SER	5.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	EDO	D	510	4/4	0.82	0.30	26.83	53,54,55,58	0
4	EDO	A	508	4/4	0.89	0.21	13.65	51,55,56,56	0
4	EDO	F	505	4/4	0.86	0.27	12.72	58,60,60,60	0
4	EDO	D	507	4/4	0.82	0.29	11.95	57,58,58,59	0
4	EDO	A	505	4/4	0.91	0.25	9.44	47,50,52,52	0
4	EDO	C	506	4/4	0.86	0.17	8.85	44,50,55,56	0
4	EDO	B	506	4/4	0.93	0.13	6.26	36,37,37,39	0
4	EDO	B	502	4/4	0.94	0.14	5.69	52,52,53,55	0
4	EDO	B	504	4/4	0.90	0.15	4.54	49,49,51,56	0
4	EDO	D	506	4/4	0.93	0.26	4.29	53,54,54,55	0
4	EDO	D	505	4/4	0.89	0.15	3.48	47,47,50,54	0
4	EDO	A	506	4/4	0.98	0.12	3.33	37,37,40,40	0
4	EDO	D	508	4/4	0.95	0.15	3.26	51,51,52,52	0
2	NAG	F	501	14/15	0.86	0.17	3.22	55,65,75,85	0
4	EDO	D	509	4/4	0.93	0.26	2.95	54,57,60,61	0
4	EDO	A	507	4/4	0.97	0.12	2.62	41,41,44,47	0
4	EDO	F	503	4/4	0.91	0.14	2.25	44,45,49,53	0
4	EDO	F	508	4/4	0.93	0.17	2.10	46,47,50,52	0
2	NAG	C	501	14/15	0.65	0.27	1.95	69,78,83,83	0
4	EDO	C	502	4/4	0.90	0.11	1.95	57,57,57,58	0
2	NAG	A	501	14/15	0.88	0.13	1.93	57,67,74,80	0
4	EDO	B	503	4/4	0.97	0.10	1.88	32,32,33,34	0
4	EDO	D	503	4/4	0.88	0.10	1.23	49,49,52,55	0
4	EDO	D	502	4/4	0.96	0.11	1.09	46,47,48,48	0
4	EDO	A	509	4/4	0.95	0.09	0.84	40,41,41,41	0
4	EDO	F	507	4/4	0.91	0.10	0.70	53,53,55,55	0
4	EDO	D	504	4/4	0.96	0.10	0.59	34,35,36,36	0
4	EDO	E	501	4/4	0.95	0.09	0.59	32,35,39,41	0
2	NAG	B	501	14/15	0.78	0.15	0.56	61,69,74,74	0
4	EDO	C	505	4/4	0.97	0.09	0.15	36,38,38,40	0
2	NAG	D	501	14/15	0.91	0.12	-0.11	61,69,71,74	0
4	EDO	F	506	4/4	0.98	0.08	-0.68	28,29,30,31	0
4	EDO	A	504	4/4	0.94	0.07	-1.34	33,34,36,39	0
4	EDO	B	505	4/4	0.98	0.08	-1.69	27,31,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	EDO	C	503	4/4	0.97	0.06	-2.19	27,28,30,32	0
2	NAG	F	502	14/15	0.83	0.22	-	91,94,98,99	0
4	EDO	C	504	4/4	0.84	0.20	-	48,51,54,58	0
2	NAG	A	502	14/15	0.72	0.28	-	86,92,93,94	0
3	FUC	A	503	10/11	0.86	0.15	-	64,71,82,83	0
4	EDO	F	504	4/4	0.78	0.16	-	44,45,45,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.