



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:05 AM GMT

PDB ID : 3KS7
Title : Crystal structure of Putative Peptide:N-glycosidase F (PNGase F) (YP_210507.1) from Bacteroides fragilis NCTC 9343 at 2.30 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2009-11-20
Resolution : 2.30 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

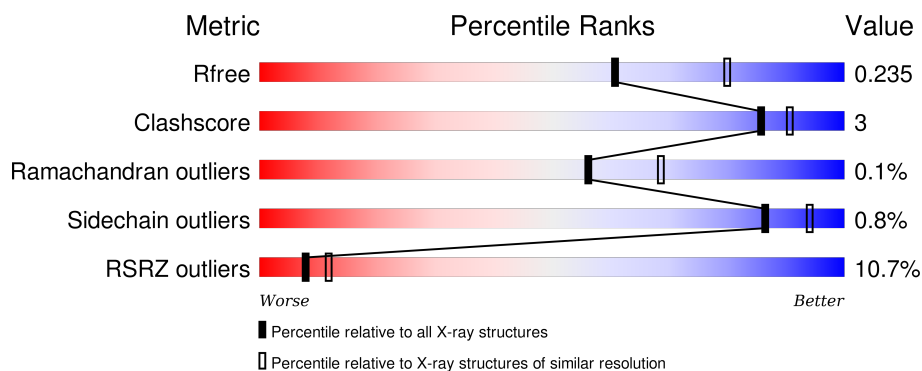
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	397	
1	B	397	
1	C	397	
1	D	397	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	A	419	-	-	-	X
4	EDO	A	420	-	-	-	X
4	EDO	A	421	-	-	-	X
4	EDO	B	416	-	-	-	X
4	EDO	B	418	-	-	-	X
4	EDO	C	417	-	-	-	X
4	EDO	C	418	-	-	-	X
4	EDO	D	18	-	-	-	X
4	EDO	D	417	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12893 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 Putative Putative PNGase F.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	Se	0	7	0
			3085	1973	520	582	4	6			
1	B	390	Total	C	N	O	S	Se	0	4	0
			3066	1956	519	581	4	6			
1	C	390	Total	C	N	O	S	Se	0	7	0
			3091	1977	522	582	4	6			
1	D	392	Total	C	N	O	S	Se	0	4	0
			3090	1975	522	583	4	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP Q5LH31
B	0	GLY	-	leader sequence	UNP Q5LH31
C	0	GLY	-	leader sequence	UNP Q5LH31
D	0	GLY	-	leader sequence	UNP Q5LH31

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	I	0	0
			2	2		
2	A	2	Total	I	0	0
			2	2		
2	D	2	Total	I	0	0
			2	2		
2	C	1	Total	I	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Cl 3 3	0	0
3	A	3	Total Cl 3 3	0	0
3	D	1	Total Cl 1 1	0	0
3	C	3	Total Cl 3 3	0	0

- 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	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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
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	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	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

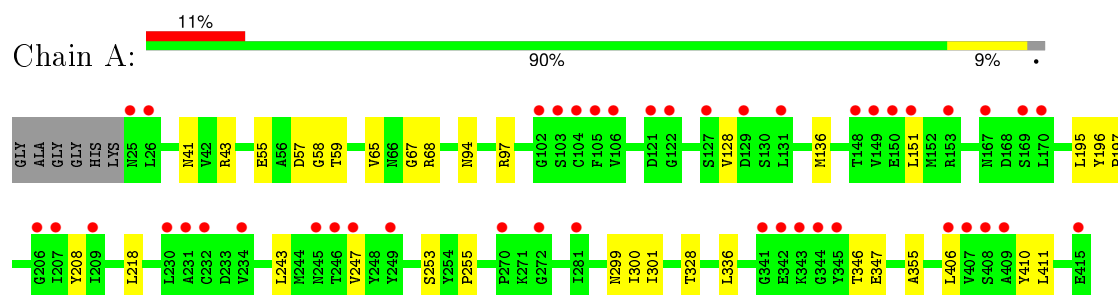
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	105	Total O 105 105	0	0
5	B	130	Total O 130 130	0	1
5	C	106	Total O 106 106	0	0
5	D	115	Total O 115 115	0	1

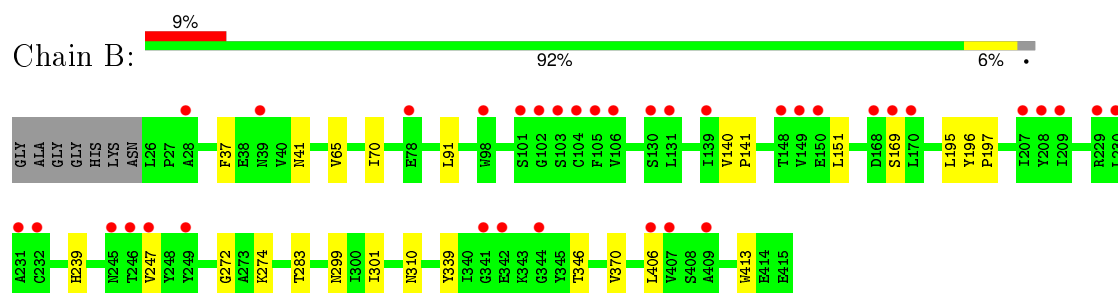
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

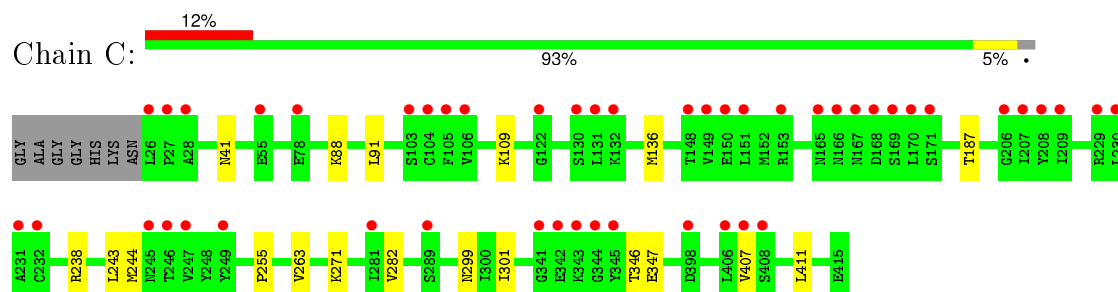
• Molecule 1: Putative Putative PNGase F



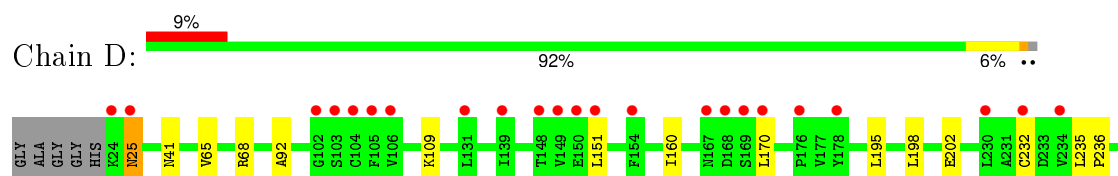
• Molecule 1: Putative Putative PNGase F

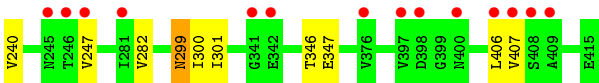


• Molecule 1: Putative Putative PNGase F



• Molecule 1: Putative Putative PNGase F





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.06Å 119.22Å 154.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 2.30 29.88 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.88-2.30) 99.8 (29.88-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.201 , 0.237 0.200 , 0.235	Depositor DCC
R_{free} test set	4374 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 87221 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12893	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.76% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: IOD, EDO, CL

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	0.62	0/3179	0.53	0/4325
1	B	0.60	0/3151	0.53	0/4286
1	C	0.59	0/3185	0.53	0/4328
1	D	0.62	1/3175 (0.0%)	0.53	0/4317
All	All	0.61	1/12690 (0.0%)	0.53	0/17256

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	232	CYS	CB-SG	6.90	1.94	1.82

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	3085	0	2991	26	0
1	B	3066	0	2967	14	0
1	C	3091	0	3010	13	0
1	D	3090	0	3003	16	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	2	0	0	0	0
3	A	3	0	0	1	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	1	0	0	0	0
4	A	24	0	36	0	0
4	B	24	0	36	0	0
4	C	20	0	30	0	0
4	D	20	0	30	0	0
5	A	105	0	0	1	0
5	B	130	0	0	1	0
5	C	106	0	0	3	0
5	D	115	0	0	0	0
All	All	12893	0	12103	69	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 3.

All (69) 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:346:THR:HG22	1:A:347:GLU:H	1.38	0.86
1:C:346:THR:HG22	1:C:347:GLU:H	1.49	0.78
1:C:136:MSE:HE1	1:C:255:PRO:HB3	1.77	0.66
1:A:301:ILE:N	1:A:301:ILE:HD12	2.12	0.65
1:C:238:ARG:HG2	5:C:432:HOH:O	1.98	0.63
1:D:109[A]:LYS:NZ	1:D:202:GLU:O	2.32	0.62
1:C:301:ILE:HD12	1:C:301:ILE:N	2.14	0.62
1:A:136:MSE:HE2	1:A:136:MSE:HA	1.80	0.62
1:A:65:VAL:HG11	1:A:68[A]:ARG:HH11	1.65	0.61
1:A:151:LEU:HD23	1:A:195:LEU:HD13	1.83	0.60
1:B:247:VAL:HA	1:B:406:LEU:HD22	1.85	0.58
1:B:301:ILE:N	1:B:301:ILE:HD12	2.17	0.58
1:C:243:LEU:HD11	1:C:411:LEU:HG	1.88	0.54
1:D:65:VAL:HG11	1:D:68[A]:ARG:HH11	1.73	0.54
1:D:346:THR:HG22	1:D:347:GLU:N	2.23	0.54
1:A:346:THR:HG22	1:A:347:GLU:N	2.18	0.53
1:B:151:LEU:HD23	1:B:195:LEU:HD13	1.92	0.51
1:A:300:ILE:N	1:A:300:ILE:HD12	2.26	0.50
1:A:57[B]:ASP:OD1	1:A:59:THR:OG1	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:LEU:O	1:D:170:LEU:HD12	2.12	0.49
1:A:243:LEU:HD11	1:A:411:LEU:HG	1.94	0.48
1:A:128:VAL:HG22	5:A:496:HOH:O	2.13	0.48
1:D:300:ILE:N	1:D:300:ILE:HD12	2.29	0.48
1:D:151:LEU:HD23	1:D:195:LEU:HD13	1.94	0.48
1:A:94:ASN:HB2	1:A:218[A]:LEU:HG	1.95	0.47
1:C:244:MSE:HE2	1:C:263:VAL:HG12	1.96	0.46
1:A:195:LEU:HD21	1:A:410:TYR:CZ	2.50	0.46
1:A:328:THR:HG21	1:A:355:ALA:HB1	1.97	0.46
1:D:282:VAL:HG23	1:D:407:VAL:HG22	1.98	0.46
1:D:346:THR:HG22	1:D:347:GLU:H	1.80	0.46
1:D:299:ASN:HD22	1:D:299:ASN:N	2.13	0.46
1:C:109:LYS:N	5:C:478:HOH:O	2.47	0.46
1:A:65:VAL:HG11	1:A:68[A]:ARG:NH1	2.29	0.46
1:C:136:MSE:HE1	1:C:255:PRO:CB	2.44	0.46
1:A:346:THR:CG2	1:A:347:GLU:H	2.18	0.45
1:B:339:TYR:CE1	1:B:346:THR:HG23	2.51	0.45
1:D:247:VAL:HA	1:D:406:LEU:HD22	1.99	0.45
1:A:196:TYR:N	1:A:197:PRO:CD	2.79	0.45
1:D:301:ILE:N	1:D:301:ILE:HD12	2.32	0.44
1:D:235:LEU:HD12	1:D:236:PRO:HD2	1.98	0.44
1:C:91:LEU:C	1:C:91:LEU:HD23	2.38	0.44
1:B:339:TYR:CZ	1:B:346:THR:HG23	2.53	0.43
1:A:97:ARG:HG2	3:A:12:CL:CL	2.55	0.43
1:B:37:PHE:CD1	1:B:70:ILE:HD12	2.52	0.43
1:D:25:ASN:ND2	1:D:25:ASN:O	2.52	0.43
1:B:140:VAL:HB	1:B:141:PRO:HD2	2.00	0.43
1:A:136:MSE:SE	1:A:255:PRO:HA	2.69	0.43
1:B:65:VAL:HG11	5:B:462[B]:HOH:O	2.18	0.43
1:A:195:LEU:HD21	1:A:410:TYR:CE1	2.54	0.42
1:B:140:VAL:HB	1:B:141:PRO:CD	2.49	0.42
1:B:239:HIS:CD2	1:B:413:TRP:CZ2	3.08	0.42
1:A:43:ARG:O	1:A:67:GLY:C	2.58	0.42
1:D:109[A]:LYS:HA	1:D:109[A]:LYS:HD3	1.72	0.42
1:B:272:GLY:O	1:B:274:LYS:HG3	2.20	0.42
1:D:198:LEU:HD11	1:D:240:VAL:HG11	2.01	0.41
1:B:91:LEU:C	1:B:91:LEU:HD23	2.40	0.41
1:B:196:TYR:N	1:B:197:PRO:CD	2.84	0.41
1:C:282:VAL:HG23	1:C:407:VAL:HG22	2.02	0.41
1:C:88:LYS:NZ	1:C:187:THR:HG21	2.34	0.41
1:A:68[A]:ARG:NH2	1:A:208:TYR:OH	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:346:THR:HG22	1:C:347:GLU:N	2.28	0.41
1:D:92:ALA:HA	1:D:160:ILE:HG23	2.02	0.41
1:A:57[A]:ASP:CG	1:A:58:GLY:H	2.24	0.41
1:B:283:THR:CG2	1:B:370:VAL:HG21	2.51	0.41
1:A:136:MSE:HE1	1:A:253:SER:OG	2.21	0.40
1:A:336:LEU:HD11	1:A:347:GLU:HG2	2.04	0.40
1:C:271[A]:LYS:HD3	5:C:439:HOH:O	2.20	0.40
1:A:299:ASN:HB3	1:A:301:ILE:HD11	2.04	0.40
1:A:247:VAL:HA	1:A:406:LEU:HD22	2.03	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	396/397 (100%)	378 (96%)	18 (4%)	0	100	100
1	B	392/397 (99%)	377 (96%)	14 (4%)	1 (0%)	46	57
1	C	395/397 (100%)	383 (97%)	12 (3%)	0	100	100
1	D	394/397 (99%)	375 (95%)	19 (5%)	0	100	100
All	All	1577/1588 (99%)	1513 (96%)	63 (4%)	1 (0%)	56	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	169	SER

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	334/339 (98%)	332 (99%)	2 (1%)	90	96
1	B	333/339 (98%)	330 (99%)	3 (1%)	84	93
1	C	335/339 (99%)	333 (99%)	2 (1%)	90	96
1	D	335/339 (99%)	332 (99%)	3 (1%)	84	93
All	All	1337/1356 (99%)	1327 (99%)	10 (1%)	86	95

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	55	GLU
1	B	41	ASN
1	B	299	ASN
1	B	310	ASN
1	C	41	ASN
1	C	299	ASN
1	D	25	ASN
1	D	41	ASN
1	D	299	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	41	ASN

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 ⓘ

Of 39 ligands modelled in this entry, 17 are monoatomic - leaving 22 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	$\# Z > 2$
4	EDO	A	416	-	3,3,3	0.50	0	2,2,2	0.39	0
4	EDO	A	417	-	3,3,3	0.46	0	2,2,2	0.40	0
4	EDO	A	418	-	3,3,3	0.61	0	2,2,2	0.30	0
4	EDO	A	419	-	3,3,3	0.52	0	2,2,2	0.38	0
4	EDO	A	420	-	3,3,3	0.56	0	2,2,2	0.33	0
4	EDO	A	421	-	3,3,3	0.56	0	2,2,2	0.33	0
4	EDO	B	416	-	3,3,3	0.58	0	2,2,2	0.27	0
4	EDO	B	417	-	3,3,3	0.50	0	2,2,2	0.46	0
4	EDO	B	418	-	3,3,3	0.64	0	2,2,2	0.22	0
4	EDO	B	419	-	3,3,3	0.53	0	2,2,2	0.36	0
4	EDO	B	420	-	3,3,3	0.50	0	2,2,2	0.41	0
4	EDO	B	421	-	3,3,3	0.48	0	2,2,2	0.43	0
4	EDO	C	416	-	3,3,3	0.43	0	2,2,2	0.43	0
4	EDO	C	417	-	3,3,3	0.42	0	2,2,2	0.46	0
4	EDO	C	418	-	3,3,3	0.41	0	2,2,2	0.46	0
4	EDO	C	419	-	3,3,3	0.59	0	2,2,2	0.31	0
4	EDO	C	420	-	3,3,3	0.68	0	2,2,2	0.26	0
4	EDO	D	18	-	3,3,3	0.52	0	2,2,2	0.35	0
4	EDO	D	416	-	3,3,3	0.58	0	2,2,2	0.34	0
4	EDO	D	417	-	3,3,3	0.58	0	2,2,2	0.29	0
4	EDO	D	418	-	3,3,3	0.53	0	2,2,2	0.37	0
4	EDO	D	419	-	3,3,3	0.54	0	2,2,2	0.33	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	A	416	-	-	0/1/1/1	0/0/0/0
4	EDO	A	417	-	-	0/1/1/1	0/0/0/0
4	EDO	A	418	-	-	0/1/1/1	0/0/0/0
4	EDO	A	419	-	-	0/1/1/1	0/0/0/0
4	EDO	A	420	-	-	0/1/1/1	0/0/0/0
4	EDO	A	421	-	-	0/1/1/1	0/0/0/0
4	EDO	B	416	-	-	0/1/1/1	0/0/0/0
4	EDO	B	417	-	-	0/1/1/1	0/0/0/0
4	EDO	B	418	-	-	0/1/1/1	0/0/0/0
4	EDO	B	419	-	-	0/1/1/1	0/0/0/0
4	EDO	B	420	-	-	0/1/1/1	0/0/0/0
4	EDO	B	421	-	-	0/1/1/1	0/0/0/0
4	EDO	C	416	-	-	0/1/1/1	0/0/0/0
4	EDO	C	417	-	-	0/1/1/1	0/0/0/0
4	EDO	C	418	-	-	0/1/1/1	0/0/0/0
4	EDO	C	419	-	-	0/1/1/1	0/0/0/0
4	EDO	C	420	-	-	0/1/1/1	0/0/0/0
4	EDO	D	18	-	-	0/1/1/1	0/0/0/0
4	EDO	D	416	-	-	0/1/1/1	0/0/0/0
4	EDO	D	417	-	-	0/1/1/1	0/0/0/0
4	EDO	D	418	-	-	0/1/1/1	0/0/0/0
4	EDO	D	419	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	385/397 (96%)	0.41	44 (11%) 7 10	18, 25, 36, 46	0
1	B	384/397 (96%)	0.39	36 (9%) 11 16	18, 25, 35, 46	0
1	C	384/397 (96%)	0.47	48 (12%) 5 8	18, 25, 36, 46	0
1	D	386/397 (97%)	0.33	37 (9%) 10 15	18, 25, 35, 46	0
All	All	1539/1588 (96%)	0.40	165 (10%) 8 12	18, 25, 36, 46	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	170	LEU	8.3
1	C	167	ASN	6.6
1	B	231	ALA	6.4
1	B	131	LEU	6.0
1	C	131	LEU	6.0
1	B	232	CYS	5.7
1	A	131	LEU	5.4
1	B	247	VAL	5.1
1	C	168	ASP	4.9
1	C	169	SER	4.9
1	D	131	LEU	4.8
1	C	247	VAL	4.8
1	B	149	VAL	4.6
1	A	407	VAL	4.4
1	C	171	SER	4.3
1	A	247	VAL	4.3
1	D	247	VAL	4.3
1	C	105	PHE	4.2
1	A	167	ASN	4.2
1	C	343	LYS	4.2
1	B	105	PHE	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	103	SER	4.1
1	C	406	LEU	4.1
1	D	167	ASN	4.0
1	A	169	SER	4.0
1	A	170	LEU	4.0
1	B	246	THR	3.8
1	C	408	SER	3.8
1	A	406	LEU	3.8
1	A	26	LEU	3.7
1	C	245	ASN	3.7
1	C	341	GLY	3.7
1	C	106	VAL	3.6
1	C	104	CYS	3.6
1	D	104	CYS	3.5
1	C	407	VAL	3.5
1	A	105	PHE	3.5
1	D	103	SER	3.5
1	D	149	VAL	3.5
1	A	341	GLY	3.5
1	D	106	VAL	3.5
1	C	344	GLY	3.5
1	C	149	VAL	3.4
1	C	229	ARG	3.4
1	B	106	VAL	3.4
1	C	103	SER	3.4
1	D	407	VAL	3.3
1	A	408	SER	3.3
1	C	398	ASP	3.3
1	C	148	THR	3.2
1	B	130	SER	3.1
1	B	148	THR	3.1
1	D	105	PHE	3.1
1	D	409	ALA	3.1
1	B	28	ALA	3.1
1	A	249	TYR	3.1
1	D	230	LEU	3.0
1	A	342	GLU	3.0
1	D	281	ILE	3.0
1	B	249	TYR	3.0
1	D	342	GLU	3.0
1	B	169	SER	3.0
1	A	272	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	207	ILE	3.0
1	B	245	ASN	3.0
1	C	249	TYR	3.0
1	A	25	ASN	3.0
1	B	103	SER	3.0
1	B	406	LEU	3.0
1	D	406	LEU	3.0
1	D	408	SER	2.9
1	B	102	GLY	2.9
1	D	178	TYR	2.9
1	A	234	VAL	2.8
1	B	168	ASP	2.8
1	A	102	GLY	2.8
1	A	344	GLY	2.8
1	A	409	ALA	2.8
1	C	78	GLU	2.8
1	C	26	LEU	2.8
1	B	342	GLU	2.8
1	C	246	THR	2.8
1	B	341	GLY	2.8
1	C	231	ALA	2.8
1	D	245	ASN	2.8
1	A	245	ASN	2.8
1	C	130	SER	2.7
1	B	407	VAL	2.7
1	D	341	GLY	2.7
1	A	207	ILE	2.7
1	D	246	THR	2.7
1	D	25	ASN	2.7
1	A	281	ILE	2.7
1	C	345	TYR	2.7
1	A	415	GLU	2.7
1	A	127	SER	2.6
1	D	102	GLY	2.6
1	A	345	TYR	2.6
1	C	281	ILE	2.6
1	C	206	GLY	2.6
1	C	342	GLU	2.6
1	C	151	LEU	2.6
1	B	229	ARG	2.6
1	C	209	ILE	2.6
1	B	78	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	151	LEU	2.5
1	B	230	LEU	2.5
1	A	149	VAL	2.5
1	C	207	ILE	2.5
1	B	409	ALA	2.5
1	A	106	VAL	2.5
1	A	122	GLY	2.5
1	A	246	THR	2.5
1	D	151	LEU	2.5
1	D	24	LYS	2.5
1	D	148	THR	2.4
1	A	153	ARG	2.4
1	C	27	PRO	2.4
1	A	230	LEU	2.4
1	D	170	LEU	2.4
1	D	376	VAL	2.4
1	A	206	GLY	2.4
1	C	28	ALA	2.4
1	A	209	ILE	2.4
1	B	344	GLY	2.4
1	D	398	ASP	2.4
1	B	101	SER	2.4
1	D	234	VAL	2.4
1	D	169	SER	2.3
1	A	270	PRO	2.3
1	C	232	CYS	2.3
1	B	170	LEU	2.3
1	A	129	ASP	2.3
1	C	208	TYR	2.3
1	D	397	VAL	2.3
1	D	176	PRO	2.3
1	B	139	ILE	2.3
1	D	400	ASN	2.2
1	B	104	CYS	2.2
1	D	154	PHE	2.2
1	C	165	ASN	2.2
1	D	139	ILE	2.2
1	C	55	GLU	2.2
1	C	150	GLU	2.2
1	D	150	GLU	2.2
1	A	148	THR	2.2
1	B	208	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	104	CYS	2.2
1	C	122	GLY	2.1
1	C	166	ASN	2.1
1	C	230	LEU	2.1
1	A	231	ALA	2.1
1	D	232	CYS	2.1
1	B	209	ILE	2.1
1	C	132	LYS	2.1
1	A	150	GLU	2.1
1	C	289	SER	2.1
1	A	343	LYS	2.1
1	C	153	ARG	2.1
1	B	150	GLU	2.0
1	B	98	TRP	2.0
1	B	39	ASN	2.0
1	A	121	ASP	2.0
1	D	168	ASP	2.0
1	A	232	CYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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	A	420	4/4	0.73	0.24	5.74	61,63,64,64	0
4	EDO	C	418	4/4	0.83	0.23	3.51	52,52,52,53	0
4	EDO	A	421	4/4	0.81	0.17	3.32	61,61,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	EDO	D	417	4/4	0.81	0.19	3.17	52,52,53,53	0
4	EDO	C	417	4/4	0.93	0.19	2.96	62,62,62,63	0
4	EDO	A	419	4/4	0.88	0.18	2.87	49,49,49,50	0
4	EDO	B	418	4/4	0.80	0.19	2.44	56,56,56,56	0
4	EDO	B	416	4/4	0.85	0.22	2.26	50,52,53,55	0
4	EDO	D	18	4/4	0.85	0.26	2.21	66,67,67,67	0
4	EDO	D	419	4/4	0.57	0.23	1.46	88,89,89,89	0
4	EDO	C	420	4/4	0.71	0.21	0.77	58,59,59,60	0
4	EDO	B	420	4/4	0.91	0.15	0.15	58,59,59,60	0
4	EDO	C	419	4/4	0.80	0.15	0.02	56,57,57,57	0
2	IOD	D	3	1/1	0.99	0.14	-0.12	33,33,33,33	1
3	CL	B	8	1/1	0.97	0.13	-0.18	36,36,36,36	0
4	EDO	B	419	4/4	0.95	0.11	-0.24	61,63,64,64	0
4	EDO	A	417	4/4	0.90	0.12	-0.45	54,55,55,55	0
2	IOD	C	2	1/1	0.99	0.13	-0.55	35,35,35,35	1
3	CL	B	16	1/1	0.96	0.10	-0.64	48,48,48,48	0
2	IOD	B	1	1/1	1.00	0.10	-0.77	36,36,36,36	1
2	IOD	A	4	1/1	0.98	0.11	-0.98	36,36,36,36	1
4	EDO	D	418	4/4	0.91	0.11	-1.65	65,66,66,66	0
3	CL	D	17	1/1	0.97	0.05	-3.81	49,49,49,49	0
4	EDO	B	417	4/4	0.88	0.17	-	54,55,55,55	0
3	CL	A	12	1/1	0.99	0.08	-	42,42,42,42	0
4	EDO	D	416	4/4	0.79	0.21	-	58,58,58,58	0
2	IOD	A	6	1/1	0.97	0.11	-	45,45,45,45	1
3	CL	C	13	1/1	0.96	0.14	-	41,41,41,41	0
4	EDO	A	416	4/4	0.72	0.24	-	67,67,68,69	0
4	EDO	C	416	4/4	0.86	0.23	-	51,52,53,54	0
3	CL	B	14	1/1	0.96	0.09	-	48,48,48,48	0
2	IOD	B	5	1/1	0.98	0.24	-	45,45,45,45	1
3	CL	A	11	1/1	0.98	0.24	-	40,40,40,40	0
3	CL	C	10	1/1	0.98	0.10	-	35,35,35,35	0
3	CL	C	15	1/1	0.90	0.22	-	49,49,49,49	0
4	EDO	A	418	4/4	0.81	0.21	-	63,63,64,64	0
4	EDO	B	421	4/4	0.80	0.16	-	67,68,69,69	0
2	IOD	D	7	1/1	0.98	0.21	-	44,44,44,44	1
3	CL	A	9	1/1	0.87	0.16	-	58,58,58,58	0

6.5 Other polymers ⓘ

There are no such residues in this entry.