



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 02:51 am GMT

PDB ID : 3PW3
Title : Crystal structure of a cysteine protease (BDI_2249) from Parabacteroides distasonis ATCC 8503 at 2.23 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-12-07
Resolution : 2.23 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

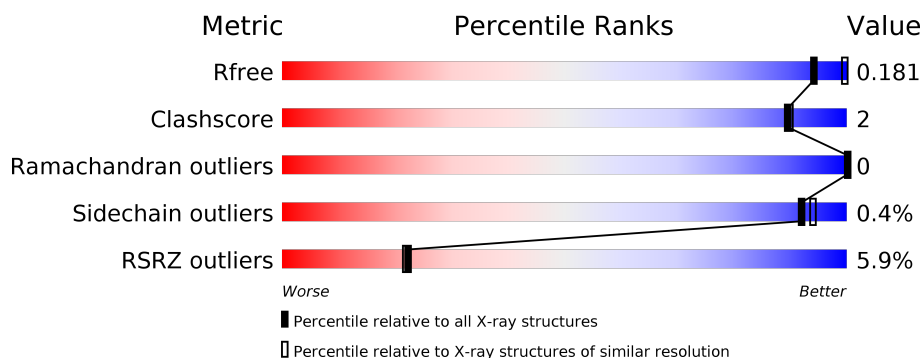
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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}	111664	2027 (2.26-2.22)
Clashscore	122126	2170 (2.26-2.22)
Ramachandran outliers	120053	2129 (2.26-2.22)
Sidechain outliers	120020	2130 (2.26-2.22)
RSRZ outliers	108989	1991 (2.26-2.22)

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	383	<div> <div>4%</div> <div>94%</div> <div>• •</div> </div>
1	B	383	<div> <div>5%</div> <div>89%</div> <div>5% 6%</div> </div>
1	C	383	<div> <div>9%</div> <div>90%</div> <div>• 6%</div> </div>
1	D	383	<div> <div>4%</div> <div>88%</div> <div>• 8%</div> </div>
1	E	383	<div> <div>5%</div> <div>89%</div> <div>• 7%</div> </div>
1	F	383	<div> <div>5%</div> <div>90%</div> <div>• 6%</div> </div>

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
5	EDO	A	431	-	-	X	-
6	ACT	F	442	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19429 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 Aminopeptidase C.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	Se	0	5	0
			2981	1897	487	579	3	15			
1	B	359	Total	C	N	O	S	Se	0	7	0
			2891	1848	471	553	3	16			
1	C	361	Total	C	N	O	S	Se	0	5	0
			2884	1843	465	557	3	16			
1	D	353	Total	C	N	O	S	Se	0	7	0
			2842	1815	460	549	3	15			
1	E	356	Total	C	N	O	S	Se	0	5	0
			2849	1820	464	547	3	15			
1	F	359	Total	C	N	O	S	Se	0	7	0
			2885	1843	468	556	3	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	leader sequence	UNP A6LE66
B	0	GLY	-	leader sequence	UNP A6LE66
C	0	GLY	-	leader sequence	UNP A6LE66
D	0	GLY	-	leader sequence	UNP A6LE66
E	0	GLY	-	leader sequence	UNP A6LE66
F	0	GLY	-	leader sequence	UNP A6LE66

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	F	1	Total 1	Zn 1	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	2	Total 2	K 2	0	0
3	E	1	Total 1	K 1	0	0
3	B	1	Total 1	K 1	0	0
3	C	2	Total 2	K 2	0	0
3	A	2	Total 2	K 2	0	0
3	F	2	Total 2	K 2	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	4	Total 5	Cl 5	0	1
4	A	1	Total 1	Cl 1	0	0
4	D	1	Total 1	Cl 1	0	0
4	F	2	Total 3	Cl 3	0	1
4	E	3	Total 4	Cl 4	0	1

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).

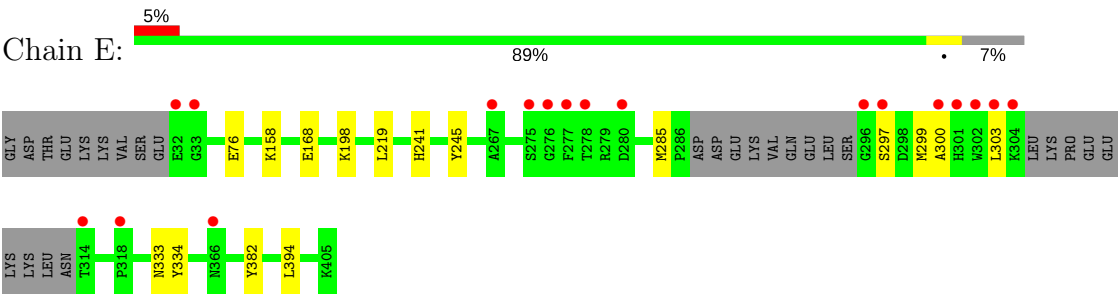


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	F	1	Total	C	O	0	0
			4	2	2		

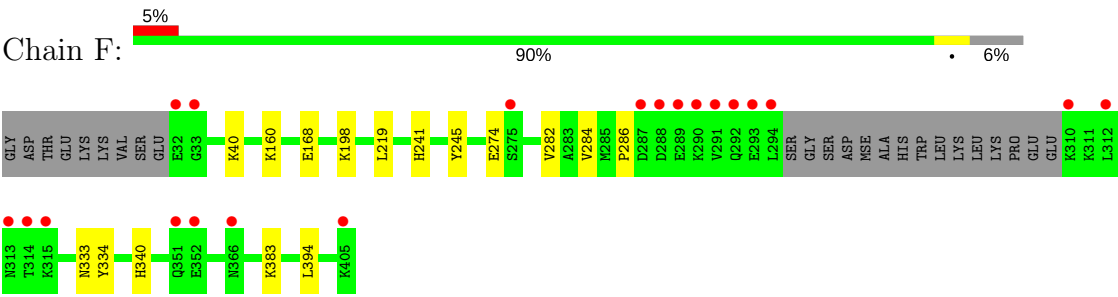
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	459	Total	O	0	1
			460	460		
7	B	382	Total	O	0	1
			382	382		
7	C	218	Total	O	0	1
			218	218		
7	D	282	Total	O	0	2
			284	284		
7	E	328	Total	O	0	0
			328	328		
7	F	334	Total	O	0	1
			335	335		

● Molecule 1: Aminopeptidase C



● Molecule 1: Aminopeptidase C



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.59Å 137.81Å 223.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.97 – 2.23 29.97 – 2.23	Depositor EDS
% Data completeness (in resolution range)	98.4 (29.97-2.23) 98.4 (29.97-2.23)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.6.0093	Depositor
R, R_{free}	0.159 , 0.181 0.159 , 0.181	Depositor DCC
R_{free} test set	7771 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19429	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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, ACT, EDO, K, 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	0.68	0/3049	0.67	0/4109
1	B	0.61	0/2973	0.63	0/3998
1	C	0.54	0/2961	0.60	0/3988
1	D	0.57	0/2924	0.61	0/3941
1	E	0.60	0/2925	0.62	0/3936
1	F	0.59	1/2968 (0.0%)	0.62	0/3996
All	All	0.60	1/17800 (0.0%)	0.62	0/23968

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	168	GLU	CG-CD	6.00	1.60	1.51

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	2981	0	2803	14	0
1	B	2891	0	2761	13	0
1	C	2884	0	2711	11	0
1	D	2842	0	2691	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2849	0	2698	12	0
1	F	2885	0	2732	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	2	0	0	0	0
4	A	1	0	0	0	0
4	B	5	0	0	2	0
4	D	1	0	0	0	0
4	E	4	0	0	1	0
4	F	3	0	0	1	0
5	A	24	0	36	5	0
5	B	8	0	12	1	0
5	C	8	0	12	0	0
5	D	4	0	6	0	0
5	F	8	0	12	0	0
6	B	4	0	3	0	0
6	F	4	0	3	2	0
7	A	460	0	0	4	0
7	B	382	0	0	1	0
7	C	218	0	0	2	0
7	D	284	0	0	1	0
7	E	328	0	0	2	0
7	F	335	0	0	3	0
All	All	19429	0	16480	67	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (67) 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:B:285:MSE:HE1	1:B:382:TYR:CD2	2.16	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ARG:NH1	7:A:2308:HOH:O	2.25	0.69
1:A:284:VAL:HG11	5:A:431:EDO:H21	1.74	0.69
1:B:110:SER:HA	5:B:433:EDO:H22	1.79	0.63
1:B:285:MSE:HE1	1:B:382:TYR:CG	2.34	0.62
6:F:442:ACT:H3	7:F:2353:HOH:O	1.99	0.62
7:A:1630:HOH:O	1:C:299:MSE:HE2	2.00	0.61
1:B:241:HIS:CE1	1:C:241:HIS:CE1	2.90	0.59
1:C:340:HIS:HB2	4:E:419:CL:CL	2.41	0.57
1:D:282[B]:VAL:HG12	1:D:284:VAL:HG13	1.86	0.57
1:D:241:HIS:CE1	1:E:241:HIS:CE1	2.93	0.56
1:C:337:THR:HG22	7:C:1047:HOH:O	2.06	0.55
1:E:158[B]:LYS:NZ	7:E:2087:HOH:O	2.38	0.54
1:C:333:ASN:O	1:C:334:TYR:HB2	2.08	0.54
1:A:284:VAL:HG11	5:A:431:EDO:C2	2.37	0.54
1:A:241:HIS:CE1	1:F:241:HIS:CE1	2.96	0.54
1:E:285:MSE:HE1	1:E:382:TYR:CG	2.44	0.53
1:E:297:SER:HB3	1:E:300:ALA:HB3	1.91	0.53
1:A:337[A]:THR:HG22	7:A:527:HOH:O	2.08	0.53
1:D:333:ASN:O	1:D:334:TYR:HB2	2.08	0.53
1:F:333:ASN:O	1:F:334:TYR:HB2	2.08	0.53
1:B:333:ASN:O	1:B:334:TYR:HB2	2.08	0.52
1:E:333:ASN:O	1:E:334:TYR:HB2	2.09	0.52
1:A:333:ASN:O	1:A:334:TYR:HB2	2.10	0.51
1:B:297:SER:HB3	1:B:300:ALA:HB3	1.92	0.51
1:C:297:SER:HB3	1:C:300:ALA:HB3	1.92	0.51
1:A:219:LEU:HD11	1:A:394:LEU:HD21	1.93	0.51
1:E:219:LEU:HD11	1:E:394:LEU:HD21	1.92	0.50
1:F:282:VAL:HG12	1:F:284:VAL:HG13	1.93	0.50
1:C:106:SER:OG	7:C:1499:HOH:O	2.20	0.49
1:F:219:LEU:HD11	1:F:394:LEU:HD21	1.93	0.49
6:F:442:ACT:CH3	7:F:2340:HOH:O	2.62	0.48
1:B:274:GLU:OE2	1:B:383:LYS:NZ	2.36	0.47
1:A:317:GLN:N	5:A:431:EDO:H12	2.29	0.47
1:B:340[B]:HIS:HB2	4:B:417[B]:CL:CL	2.52	0.46
1:D:74:LYS:NZ	7:D:2391:HOH:O	2.41	0.46
1:C:279:ARG:CB	1:E:303:LEU:HD13	2.46	0.46
1:D:219:LEU:HD11	1:D:394:LEU:HD21	1.96	0.46
1:B:168:GLU:H	1:B:168:GLU:CD	2.19	0.46
1:C:235:ILE:HD12	1:C:339[B]:ASP:OD1	2.15	0.46
1:E:168[A]:GLU:CD	1:E:168[A]:GLU:H	2.18	0.46
1:B:219:LEU:HD23	1:B:245:TYR:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:VAL:HG12	1:B:284:VAL:HG13	1.98	0.46
1:E:285:MSE:HE1	1:E:382:TYR:HB2	1.98	0.46
1:F:40:LYS:NZ	7:F:1974:HOH:O	2.48	0.45
1:A:219:LEU:HD23	1:A:245:TYR:HB2	1.99	0.45
1:F:284:VAL:HG23	1:F:286:PRO:HD3	1.99	0.45
1:A:253:MSE:HE2	7:A:1524:HOH:O	2.15	0.45
1:D:168[A]:GLU:CD	1:D:168[A]:GLU:H	2.19	0.45
4:B:422:CL:CL	1:D:340:HIS:HB2	2.54	0.44
1:C:268:TRP:CE3	1:C:342:MSE:HE3	2.53	0.44
1:F:219:LEU:HD23	1:F:245:TYR:HB2	1.99	0.44
1:D:219:LEU:HD23	1:D:245:TYR:HB2	2.00	0.44
1:E:76:GLU:OE2	7:E:1491:HOH:O	2.21	0.44
1:E:219:LEU:HD23	1:E:245:TYR:HB2	2.01	0.43
1:B:212:LYS:NZ	7:B:2198:HOH:O	2.39	0.42
1:B:219:LEU:HD11	1:B:394:LEU:HD21	2.01	0.42
1:F:274:GLU:OE2	1:F:383:LYS:NZ	2.44	0.42
1:C:282:VAL:HG12	1:C:284:VAL:HG13	2.02	0.42
1:A:62:TYR:HH	1:A:84:THR:HG1	1.63	0.41
1:A:317:GLN:H	5:A:431:EDO:H12	1.85	0.41
1:E:285:MSE:HE1	1:E:382:TYR:CB	2.51	0.41
1:A:284:VAL:CG1	5:A:431:EDO:C2	2.98	0.41
1:D:274:GLU:OE2	1:D:383:LYS:NZ	2.48	0.41
1:A:235:ILE:HD12	1:A:338[B]:ASP:CG	2.42	0.40
1:F:340[A]:HIS:HB2	4:F:418[A]:CL:CL	2.58	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	377/383 (98%)	371 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	360/383 (94%)	353 (98%)	7 (2%)	0	100	100
1	C	360/383 (94%)	352 (98%)	8 (2%)	0	100	100
1	D	356/383 (93%)	349 (98%)	7 (2%)	0	100	100
1	E	355/383 (93%)	348 (98%)	7 (2%)	0	100	100
1	F	362/383 (94%)	355 (98%)	7 (2%)	0	100	100
All	All	2170/2298 (94%)	2128 (98%)	42 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	311/313 (99%)	309 (99%)	2 (1%)	87	91
1	B	307/313 (98%)	306 (100%)	1 (0%)	93	95
1	C	302/313 (96%)	301 (100%)	1 (0%)	93	95
1	D	301/313 (96%)	300 (100%)	1 (0%)	93	95
1	E	300/313 (96%)	298 (99%)	2 (1%)	85	89
1	F	304/313 (97%)	302 (99%)	2 (1%)	85	89
All	All	1825/1878 (97%)	1816 (100%)	9 (0%)	92	92

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	338[A]	ASP
1	A	338[B]	ASP
1	B	160	LYS
1	C	299	MSE
1	D	352	GLU
1	E	198	LYS
1	E	299	MSE
1	F	160	LYS

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Mol	Chain	Res	Type
1	F	198	LYS

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

Mol	Chain	Res	Type
1	E	241	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 45 ligands modelled in this entry, 30 are monoatomic - leaving 15 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	$\# Z > 2$
5	EDO	A	428	-	3,3,3	0.72	0	2,2,2	0.18	0
5	EDO	A	431	-	3,3,3	0.91	0	2,2,2	0.85	0
5	EDO	A	434	-	3,3,3	0.50	0	2,2,2	0.52	0
5	EDO	A	435	-	3,3,3	0.37	0	2,2,2	0.08	0
5	EDO	A	436	-	3,3,3	0.58	0	2,2,2	0.36	0
5	EDO	A	438	-	3,3,3	0.70	0	2,2,2	0.08	0
5	EDO	B	433	-	3,3,3	0.59	0	2,2,2	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	B	439	-	3,3,3	0.61	0	2,2,2	0.29	0
6	ACT	B	441	2	1,3,3	2.39	1 (100%)	0,3,3	0.00	-
5	EDO	C	432	-	3,3,3	0.64	0	2,2,2	0.14	0
5	EDO	C	440	-	3,3,3	0.52	0	2,2,2	0.20	0
5	EDO	D	437	-	3,3,3	0.44	0	2,2,2	0.30	0
5	EDO	F	429	-	3,3,3	0.75	0	2,2,2	0.08	0
5	EDO	F	430	-	3,3,3	0.54	0	2,2,2	0.20	0
6	ACT	F	442	2	1,3,3	1.60	0	0,3,3	0.00	-

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
5	EDO	A	428	-	-	0/1/1/1	0/0/0/0
5	EDO	A	431	-	-	0/1/1/1	0/0/0/0
5	EDO	A	434	-	-	0/1/1/1	0/0/0/0
5	EDO	A	435	-	-	0/1/1/1	0/0/0/0
5	EDO	A	436	-	-	0/1/1/1	0/0/0/0
5	EDO	A	438	-	-	0/1/1/1	0/0/0/0
5	EDO	B	433	-	-	0/1/1/1	0/0/0/0
5	EDO	B	439	-	-	0/1/1/1	0/0/0/0
6	ACT	B	441	2	-	0/0/0/0	0/0/0/0
5	EDO	C	432	-	-	0/1/1/1	0/0/0/0
5	EDO	C	440	-	-	0/1/1/1	0/0/0/0
5	EDO	D	437	-	-	0/1/1/1	0/0/0/0
5	EDO	F	429	-	-	0/1/1/1	0/0/0/0
5	EDO	F	430	-	-	0/1/1/1	0/0/0/0
6	ACT	F	442	2	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	441	ACT	CH3-C	2.39	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	431	EDO	5	0
5	B	433	EDO	1	0
6	F	442	ACT	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	359/383 (93%)	-0.29	14 (3%)	39 39	16, 24, 77, 129	0
1	B	344/383 (89%)	-0.09	21 (6%)	21 21	19, 28, 88, 186	0
1	C	346/383 (90%)	0.25	36 (10%)	6 5	24, 47, 88, 127	0
1	D	339/383 (88%)	-0.13	14 (4%)	37 37	22, 41, 74, 118	0
1	E	341/383 (89%)	-0.00	18 (5%)	26 26	19, 33, 92, 155	0
1	F	345/383 (90%)	-0.05	20 (5%)	23 22	16, 35, 84, 127	0
All	All	2074/2298 (90%)	-0.06	123 (5%)	22 22	16, 34, 85, 186	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	310	LYS	13.2
1	B	312	LEU	13.0
1	E	300	ALA	11.0
1	E	275	SER	10.5
1	B	311	LYS	8.7
1	A	296	GLY	7.5
1	E	276	GLY	7.4
1	B	275	SER	7.0
1	E	32	GLU	6.9
1	C	312	LEU	6.9
1	F	289	GLU	6.7
1	B	313	ASN	6.1
1	F	291	VAL	5.8
1	A	300	ALA	5.8
1	E	314	THR	5.7
1	A	304	LYS	5.4
1	F	294	LEU	5.4
1	F	314	THR	5.1
1	C	314	THR	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	314	THR	4.8
1	C	366	ASN	4.7
1	A	295	SER	4.7
1	F	292	GLN	4.6
1	E	303	LEU	4.4
1	E	280	ASP	4.4
1	E	301	HIS	4.3
1	F	290	LYS	4.3
1	F	312	LEU	4.2
1	D	310	LYS	4.1
1	D	287	ASP	4.1
1	A	305	LEU	4.1
1	E	302	TRP	4.1
1	E	297	SER	4.0
1	F	275	SER	4.0
1	C	310	LYS	4.0
1	C	268	TRP	4.0
1	A	302	TRP	4.0
1	C	313	ASN	4.0
1	C	287	ASP	3.9
1	F	288	ASP	3.9
1	F	293	GLU	3.8
1	B	32	GLU	3.7
1	B	280	ASP	3.7
1	C	267	ALA	3.7
1	D	312	LEU	3.6
1	F	405	LYS	3.6
1	C	365	THR	3.6
1	E	304	LYS	3.6
1	F	32	GLU	3.5
1	C	317	GLN	3.5
1	D	311	LYS	3.5
1	B	300	ALA	3.4
1	E	277	PHE	3.4
1	E	278	THR	3.4
1	B	302	TRP	3.4
1	B	276	GLY	3.4
1	C	275	SER	3.3
1	B	297	SER	3.3
1	C	288	ASP	3.2
1	D	318	PRO	3.2
1	C	405	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	288	ASP	3.2
1	D	275	SER	3.2
1	A	309	GLU	3.1
1	F	287	ASP	3.0
1	B	286	PRO	3.0
1	D	366	ASN	3.0
1	C	387	ILE	2.9
1	D	387	ILE	2.9
1	C	286	PRO	2.9
1	C	318	PRO	2.9
1	C	301	HIS	2.9
1	E	296	GLY	2.9
1	F	366	ASN	2.8
1	C	300	ALA	2.8
1	C	384	THR	2.8
1	B	277	PHE	2.8
1	B	303	LEU	2.8
1	C	280	ASP	2.8
1	C	266	ILE	2.8
1	C	351	GLN	2.8
1	A	303	LEU	2.7
1	C	37	THR	2.7
1	E	366	ASN	2.7
1	C	311	LYS	2.7
1	E	33	GLY	2.7
1	C	339[A]	ASP	2.7
1	C	320	LYS	2.7
1	C	303	LEU	2.7
1	B	315[A]	LYS	2.6
1	B	33	GLY	2.6
1	B	301	HIS	2.6
1	C	35	VAL	2.6
1	B	339[A]	ASP	2.5
1	D	32	GLU	2.5
1	C	344	ILE	2.4
1	A	291	VAL	2.4
1	F	315	LYS	2.4
1	A	294	LEU	2.4
1	A	293	GLU	2.4
1	A	301	HIS	2.3
1	D	268	TRP	2.3
1	F	310	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	304	LYS	2.3
1	C	269	GLY	2.3
1	B	318	PRO	2.3
1	A	297	SER	2.3
1	F	351	GLN	2.3
1	C	370	ASN	2.2
1	D	267	ALA	2.2
1	A	32	GLU	2.2
1	E	318	PRO	2.2
1	C	73	GLY	2.2
1	C	388	VAL	2.1
1	C	296	GLY	2.1
1	F	313	ASN	2.1
1	B	267	ALA	2.1
1	E	267	ALA	2.1
1	F	352	GLU	2.1
1	C	276	GLY	2.1
1	D	353	GLY	2.1
1	D	266	ILE	2.1
1	F	33	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 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CL	A	421	1/1	0.71	0.37	70,70,70,70	0
3	K	F	413	1/1	0.72	0.24	90,90,90,90	0
3	K	C	412	1/1	0.72	0.09	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	A	436	4/4	0.82	0.24	47,55,56,62	0
4	CL	B	427	1/1	0.82	0.09	60,60,60,60	0
5	EDO	B	439	4/4	0.84	0.27	56,63,63,65	0
5	EDO	A	434	4/4	0.85	0.52	55,59,61,65	0
5	EDO	D	437	4/4	0.86	0.58	66,71,76,80	0
5	EDO	C	432	4/4	0.86	0.67	61,62,64,65	0
5	EDO	A	435	4/4	0.86	0.21	42,45,52,60	0
4	CL	E	419	1/1	0.87	0.15	86,86,86,86	0
5	EDO	F	430	4/4	0.89	0.46	56,60,61,63	0
4	CL	F	425	1/1	0.90	0.09	56,56,56,56	0
5	EDO	F	429	4/4	0.90	0.28	52,55,57,60	0
4	CL	B	423	1/1	0.90	0.09	67,67,67,67	0
5	EDO	B	433	4/4	0.90	0.68	60,63,64,64	0
5	EDO	A	431	4/4	0.90	0.25	49,52,60,61	0
5	EDO	C	440	4/4	0.91	0.16	53,69,75,83	0
5	EDO	A	438	4/4	0.91	0.14	47,50,53,56	0
5	EDO	A	428	4/4	0.92	0.24	40,45,49,53	0
3	K	C	414	1/1	0.93	0.05	52,52,52,52	0
3	K	D	411	1/1	0.93	0.14	70,70,70,70	0
4	CL	D	426	1/1	0.94	0.07	58,58,58,58	0
4	CL	E	424	1/1	0.94	0.06	68,68,68,68	0
4	CL	B	417[B]	1/1	0.96	0.21	70,70,70,70	1
4	CL	F	418[B]	1/1	0.96	0.11	68,68,68,68	1
6	ACT	B	441	4/4	0.96	0.22	35,49,60,71	0
4	CL	B	417[A]	1/1	0.96	0.21	60,60,60,60	1
4	CL	F	418[A]	1/1	0.96	0.11	65,65,65,65	1
4	CL	E	420[A]	1/1	0.97	0.15	65,65,65,65	1
6	ACT	F	442	4/4	0.97	0.19	46,59,69,72	0
4	CL	E	420[B]	1/1	0.97	0.15	68,68,68,68	1
3	K	B	410	1/1	0.98	0.06	29,29,29,29	0
3	K	D	409	1/1	0.98	0.05	42,42,42,42	0
4	CL	B	422	1/1	0.98	0.12	72,72,72,72	0
3	K	F	416	1/1	0.98	0.05	40,40,40,40	0
2	ZN	B	406	1/1	0.99	0.04	33,33,33,33	0
3	K	E	415	1/1	0.99	0.04	39,39,39,39	0
3	K	A	408	1/1	0.99	0.10	31,31,31,31	0
2	ZN	A	406	1/1	1.00	0.05	28,28,28,28	0
2	ZN	C	406	1/1	1.00	0.04	45,45,45,45	0
2	ZN	E	406	1/1	1.00	0.03	39,39,39,39	0
2	ZN	D	406	1/1	1.00	0.04	37,37,37,37	0
2	ZN	F	406	1/1	1.00	0.02	37,37,37,37	0
3	K	A	407	1/1	1.00	0.03	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.