



wwPDB X-ray Structure Validation Summary Report

May 9, 2014 – 02:25 PM EDT

PDB ID : 4C8R
Title : Human gamma-butyrobetaine dioxygenase (BBOX1) in complex with Ni(II) and N-(3-hydroxypicolinoyl)-S-(pyridin-2-ylmethyl)-L-cysteine(AR692B)
Authors : Chowdhury, R.; Rydzik, A.M.; Kochan, G.T.; McDonough, M.A.; Schofield, C.J.
Deposited on : 2013-10-01
Resolution : 2.82 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

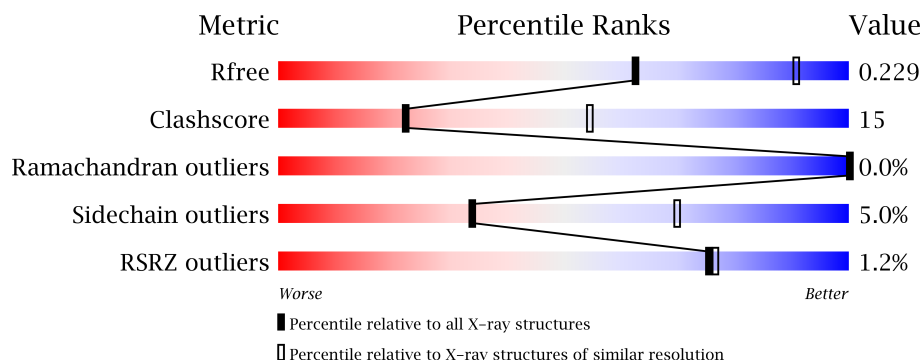
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable22978
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.82 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}	66092	1963 (2.84-2.80)
Clashscore	79885	2478 (2.84-2.80)
Ramachandran outliers	78287	2429 (2.84-2.80)
Sidechain outliers	78261	2431 (2.84-2.80)
RSRZ outliers	66119	1966 (2.84-2.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	388	
1	B	388	
1	C	388	
1	D	388	
1	E	388	
1	F	388	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	6YT	B	601	-	X
4	6YT	C	601	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	6YT	F	601	-	X
5	EDO	A	702	-	X
5	EDO	B	701	-	X
5	EDO	C	701	-	X
5	EDO	C	702	-	X
5	EDO	C	703	-	X
5	EDO	C	704	-	X
5	EDO	E	701	-	X
5	EDO	F	701	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19352 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GAMMA-BUTYROBETAINE DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	0	0
			3116	1995	533	573	15			
1	B	384	Total	C	N	O	S	0	0	0
			3130	2006	535	574	15			
1	C	384	Total	C	N	O	S	0	0	0
			3117	1997	530	576	14			
1	D	384	Total	C	N	O	S	0	0	0
			3109	1995	535	565	14			
1	E	384	Total	C	N	O	S	0	0	0
			3097	1986	532	565	14			
1	F	384	Total	C	N	O	S	0	0	0
			3109	1997	531	567	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP O75936
B	0	SER	-	EXPRESSION TAG	UNP O75936
C	0	SER	-	EXPRESSION TAG	UNP O75936
D	0	SER	-	EXPRESSION TAG	UNP O75936
E	0	SER	-	EXPRESSION TAG	UNP O75936
F	0	SER	-	EXPRESSION TAG	UNP O75936

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

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

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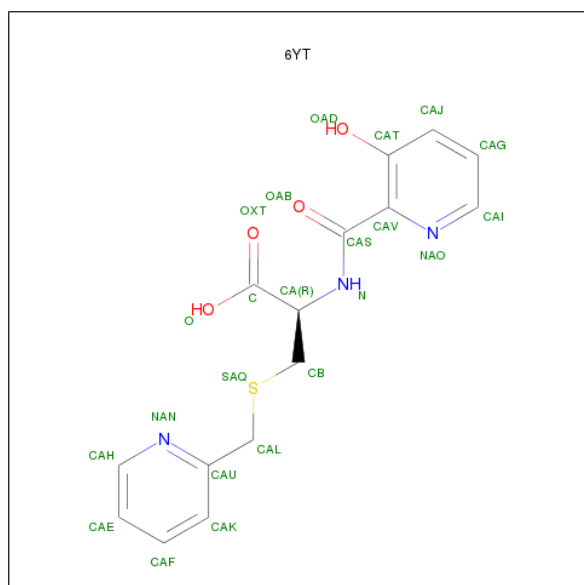
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Ni 1 1	0	0
2	A	1	Total Ni 1 1	0	0
2	F	1	Total Ni 1 1	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

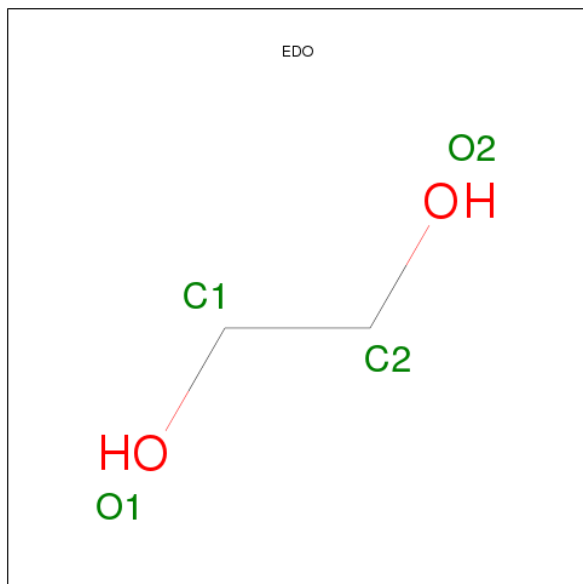
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Zn 1 1	0	0
3	E	1	Total Zn 1 1	0	0
3	B	1	Total Zn 1 1	0	0
3	C	1	Total Zn 1 1	0	0
3	A	1	Total Zn 1 1	0	0
3	F	1	Total Zn 1 1	0	0

- Molecule 4 is N-(3-HYDROXYPICOLINOYL)-S-(PYRIDIN-2-YLMETHYL)-L-CYSTEINE E (three-letter code: 6YT) (formula: C₁₅H₁₅N₃O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			23	15	3	4	1		
4	B	1	Total	C	N	O	S	0	0
			23	15	3	4	1		
4	C	1	Total	C	N	O	S	0	0
			23	15	3	4	1		
4	D	1	Total	C	N	O	S	0	0
			23	15	3	4	1		
4	E	1	Total	C	N	O	S	0	0
			23	15	3	4	1		
4	F	1	Total	C	N	O	S	0	0
			23	15	3	4	1		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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	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		

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

- Molecule 6 is water.

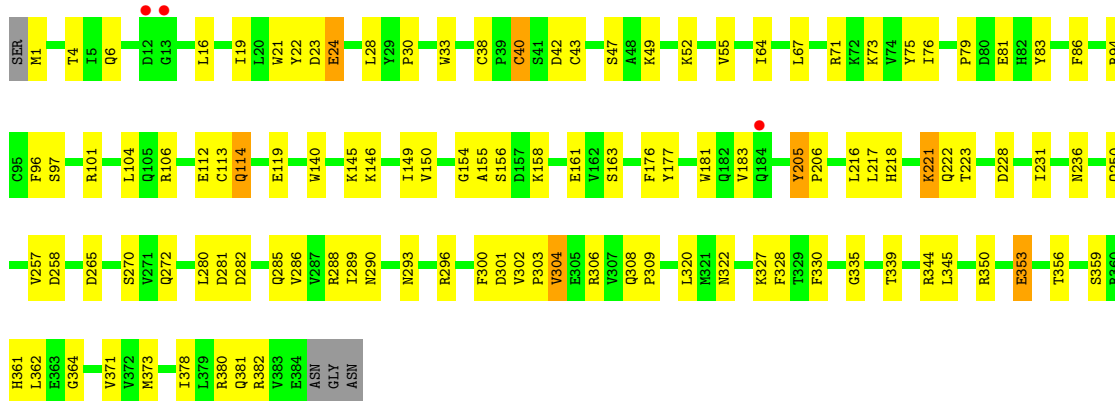
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	106	Total O 106 106	0	0
6	B	95	Total O 95 95	0	0
6	C	90	Total O 90 90	0	0
6	D	60	Total O 60 60	0	0
6	E	52	Total O 52 52	0	0
6	F	65	Total O 65 65	0	0

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 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 ($RSRZ > 2$). 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.

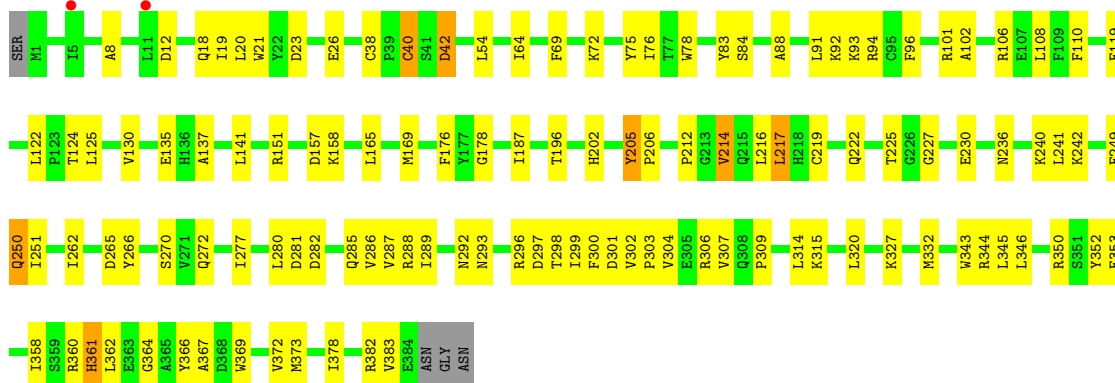
• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

Chain A: 



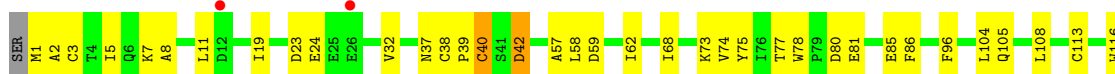
• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

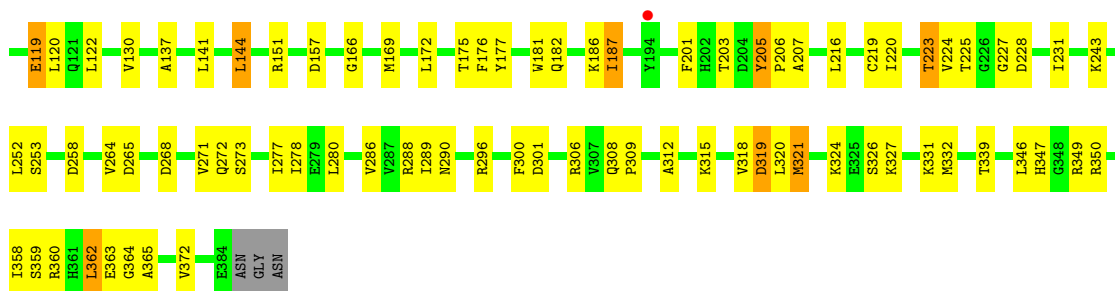
Chain B: 



• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

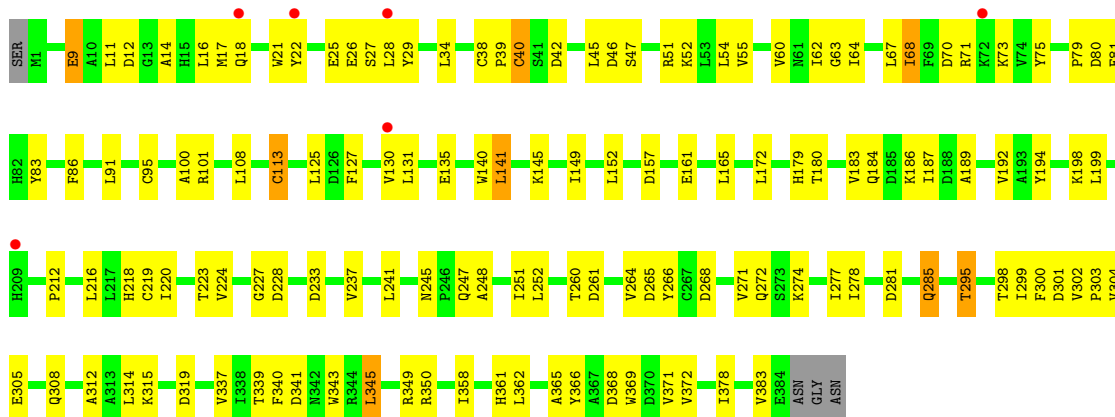
Chain C: 





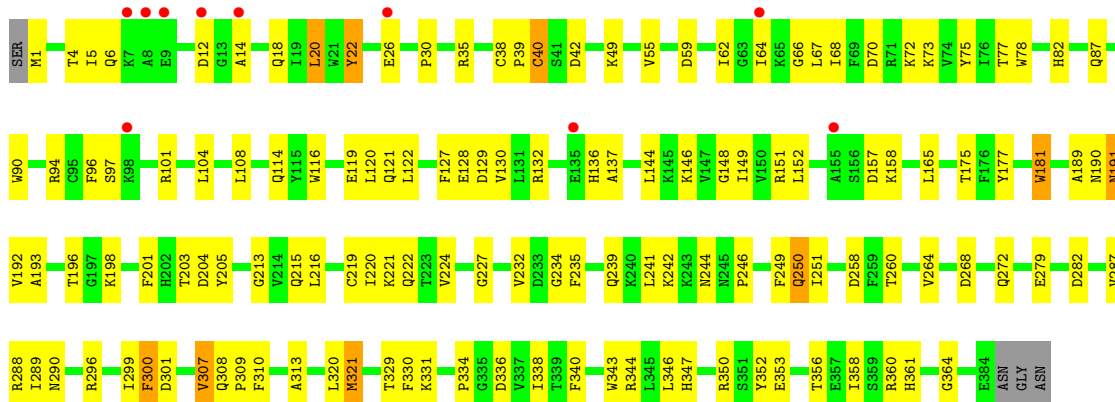
• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

Chain D:



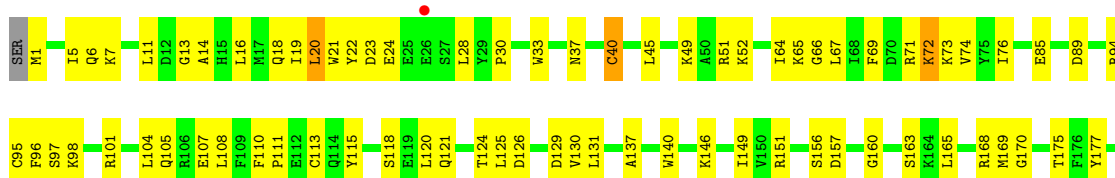
• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

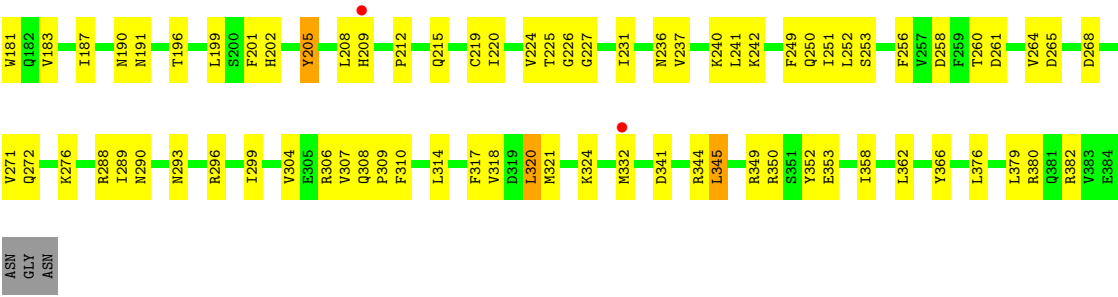
Chain E:



• Molecule 1: GAMMA-BUTYROBETAINE DIOXYGENASE

Chain F:





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	195.74Å 91.66Å 167.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.42 – 2.82 48.94 – 2.82	Depositor EDS
% Data completeness (in resolution range)	97.8 (48.42-2.82) 96.9 (48.94-2.82)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.81Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.215 , 0.244 0.226 , 0.229	Depositor DCC
R_{free} test set	3576 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	58.8	Xtriage
Anisotropy	0.233	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 70966 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19352	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.22 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.2781e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NI, ZN, EDO, 6YT

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	0.47	0/3193	0.65	1/4323 (0.0%)
1	B	0.48	0/3208	0.65	0/4341
1	C	0.45	0/3195	0.62	0/4327
1	D	0.44	0/3187	0.61	0/4315
1	E	0.43	0/3175	0.59	0/4302
1	F	0.43	0/3187	0.60	0/4315
All	All	0.45	0/19145	0.62	1/25923 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	GLU	CB-CA-C	-6.00	98.40	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3116	0	3043	79	0
1	B	3130	0	3070	89	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3117	0	3031	91	0
1	D	3109	0	3042	104	0
1	E	3097	0	3012	110	0
1	F	3109	0	3042	120	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	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	23	0	0	2	0
4	B	23	0	0	3	0
4	C	23	0	0	0	0
4	D	23	0	0	1	0
4	E	23	0	0	0	0
4	F	23	0	0	1	0
5	A	12	0	18	0	0
5	B	8	0	12	0	0
5	C	16	0	24	1	0
5	E	12	0	18	2	0
5	F	8	0	12	0	0
6	A	106	0	0	5	0
6	B	95	0	0	2	0
6	C	90	0	0	5	0
6	D	60	0	0	4	0
6	E	52	0	0	2	0
6	F	65	0	0	5	0
All	All	19352	0	18324	556	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

The worst 5 of 556 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:199:LEU:HD21	1:F:349:ARG:HB3	1.34	1.09
1:B:93:LYS:HE2	1:B:94:ARG:HH12	1.32	0.91

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:224:VAL:HG12	1:F:358:ILE:HA	1.56	0.85
1:B:93:LYS:HE2	1:B:94:ARG:NH1	1.92	0.85
1:C:219:CYS:HB2	1:C:332:MET:HE2	1.59	0.84

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	382/388 (98%)	353 (92%)	29 (8%)	0	100	100
1	B	382/388 (98%)	349 (91%)	33 (9%)	0	100	100
1	C	382/388 (98%)	341 (89%)	41 (11%)	0	100	100
1	D	382/388 (98%)	356 (93%)	26 (7%)	0	100	100
1	E	382/388 (98%)	349 (91%)	33 (9%)	0	100	100
1	F	382/388 (98%)	355 (93%)	26 (7%)	1 (0%)	50	83
All	All	2292/2328 (98%)	2103 (92%)	188 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	170	GLY

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	336/343 (98%)	316 (94%)	20 (6%)	27	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	339/343 (99%)	326 (96%)	13 (4%)	44	80
1	C	335/343 (98%)	315 (94%)	20 (6%)	27	61
1	D	333/343 (97%)	314 (94%)	19 (6%)	29	63
1	E	330/343 (96%)	313 (95%)	17 (5%)	32	68
1	F	333/343 (97%)	322 (97%)	11 (3%)	50	84
All	All	2006/2058 (98%)	1906 (95%)	100 (5%)	34	70

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	300	PHE
1	D	42	ASP
1	F	89	ASP
1	C	319	ASP
1	C	349	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	182	GLN
1	D	322	ASN
1	F	222	GLN
1	D	285	GLN
1	E	18	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 32 ligands modelled in this entry, 12 are monoatomic - leaving 20 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	6YT	A	601	2	24,24,24	2.23	4 (16%)	31,31,31	1.38	5 (16%)
5	EDO	A	701	-	3,3,3	0.67	0	2,2,2	0.28	0
5	EDO	A	702	-	3,3,3	0.59	0	2,2,2	0.32	0
5	EDO	A	703	-	3,3,3	0.57	0	2,2,2	0.34	0
4	6YT	B	601	2	24,24,24	2.23	4 (16%)	31,31,31	1.38	5 (16%)
5	EDO	B	701	-	3,3,3	0.56	0	2,2,2	0.36	0
5	EDO	B	702	-	3,3,3	0.52	0	2,2,2	0.41	0
4	6YT	C	601	2	24,24,24	2.11	4 (16%)	31,31,31	1.21	2 (6%)
5	EDO	C	701	-	3,3,3	0.57	0	2,2,2	0.38	0
5	EDO	C	702	-	3,3,3	0.59	0	2,2,2	0.31	0
5	EDO	C	703	-	3,3,3	0.58	0	2,2,2	0.35	0
5	EDO	C	704	-	3,3,3	0.52	0	2,2,2	0.43	0
4	6YT	D	601	2	24,24,24	2.11	4 (16%)	31,31,31	1.29	4 (12%)
4	6YT	E	601	2	24,24,24	2.08	4 (16%)	31,31,31	1.38	7 (22%)
5	EDO	E	701	-	3,3,3	0.55	0	2,2,2	0.35	0
5	EDO	E	702	-	3,3,3	0.62	0	2,2,2	0.33	0
5	EDO	E	703	-	3,3,3	0.56	0	2,2,2	0.32	0
4	6YT	F	601	2	24,24,24	2.13	4 (16%)	31,31,31	1.50	7 (22%)
5	EDO	F	701	-	3,3,3	0.54	0	2,2,2	0.38	0
5	EDO	F	702	-	3,3,3	0.58	0	2,2,2	0.37	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	6YT	A	601	2	-	0/18/18/18	0/2/2/2
5	EDO	A	701	-	-	0/1/1/1	0/0/0/0
5	EDO	A	702	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	703	-	-	0/1/1/1	0/0/0/0
4	6YT	B	601	2	-	0/18/18/18	0/2/2/2
5	EDO	B	701	-	-	0/1/1/1	0/0/0/0
5	EDO	B	702	-	-	0/1/1/1	0/0/0/0
4	6YT	C	601	2	-	0/18/18/18	0/2/2/2
5	EDO	C	701	-	-	0/1/1/1	0/0/0/0
5	EDO	C	702	-	-	0/1/1/1	0/0/0/0
5	EDO	C	703	-	-	0/1/1/1	0/0/0/0
5	EDO	C	704	-	-	0/1/1/1	0/0/0/0
4	6YT	D	601	2	-	2/18/18/18	0/2/2/2
4	6YT	E	601	2	-	0/18/18/18	0/2/2/2
5	EDO	E	701	-	-	0/1/1/1	0/0/0/0
5	EDO	E	702	-	-	0/1/1/1	0/0/0/0
5	EDO	E	703	-	-	0/1/1/1	0/0/0/0
4	6YT	F	601	2	-	0/18/18/18	0/2/2/2
5	EDO	F	701	-	-	0/1/1/1	0/0/0/0
5	EDO	F	702	-	-	0/1/1/1	0/0/0/0

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	601	6YT	CAV-CAS	-6.99	1.38	1.50
4	A	601	6YT	CAV-CAS	-6.98	1.38	1.50
4	F	601	6YT	CAV-CAS	-6.75	1.39	1.50
4	E	601	6YT	OAB-CAS	6.39	1.35	1.23
4	C	601	6YT	OAB-CAS	6.26	1.35	1.23

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	601	6YT	CAV-CAS-N	4.08	120.01	115.92
4	E	601	6YT	CAJ-CAT-CAV	3.23	120.24	118.11
4	C	601	6YT	CAJ-CAT-CAV	3.02	120.10	118.11
4	B	601	6YT	CAS-CAV-NAO	2.92	120.03	115.81
4	A	601	6YT	CAS-CAV-NAO	2.91	120.02	115.81

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	601	6YT	CAT-CAV-CAS-N

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Mol	Chain	Res	Type	Atoms
4	D	601	6YT	NAO-CAV-CAS-N

There are no ring outliers.

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	384/388 (98%)	-0.23	3 (0%) 83 84	36, 55, 80, 95	0
1	B	384/388 (98%)	-0.18	2 (0%) 88 90	34, 53, 76, 91	0
1	C	384/388 (98%)	-0.12	3 (0%) 83 84	27, 61, 82, 109	0
1	D	384/388 (98%)	-0.01	6 (1%) 68 69	37, 65, 98, 113	1 (0%)
1	E	384/388 (98%)	0.02	10 (2%) 53 54	43, 72, 103, 113	0
1	F	384/388 (98%)	-0.09	3 (0%) 83 84	41, 64, 85, 98	1 (0%)
All	All	2304/2328 (98%)	-0.10	27 (1%) 75 76	27, 61, 90, 113	2 (0%)

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	72	LYS	3.9
1	A	12	ASP	3.6
1	E	64	ILE	3.5
1	E	98	LYS	3.2
1	E	8	ALA	3.1

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 ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	EDO	C	704	4/4	0.33	12.16	62,63,64,65	0
5	EDO	E	701	4/4	0.37	7.01	72,72,73,73	0
5	EDO	B	701	4/4	0.23	5.90	62,63,63,63	0
5	EDO	C	702	4/4	0.29	3.95	82,83,84,84	0
5	EDO	C	703	4/4	0.24	3.70	71,72,72,73	0
4	6YT	F	601	23/23	0.39	3.63	94,97,100,101	0
4	6YT	C	601	23/23	0.26	3.55	98,100,100,101	0
4	6YT	B	601	23/23	0.30	3.15	98,100,100,101	0
5	EDO	A	702	4/4	0.30	3.00	68,68,69,70	0
5	EDO	C	701	4/4	0.28	2.55	73,73,73,74	0
5	EDO	F	701	4/4	0.26	2.13	78,79,79,80	0
4	6YT	A	601	23/23	0.23	1.27	98,100,100,101	0
4	6YT	E	601	23/23	0.25	1.05	94,97,101,101	0
3	ZN	B	502	1/1	0.17	0.85	55,55,55,55	0
5	EDO	A	701	4/4	0.21	0.83	61,63,64,65	0
3	ZN	F	502	1/1	0.15	0.80	63,63,63,63	0
5	EDO	E	702	4/4	0.23	0.73	72,76,77,79	0
3	ZN	C	502	1/1	0.16	0.58	63,63,63,63	0
3	ZN	E	502	1/1	0.17	0.35	95,95,95,95	0
4	6YT	D	601	23/23	0.23	0.32	80,84,91,91	0
5	EDO	B	702	4/4	0.17	-0.03	62,64,64,65	0
2	NI	A	501	1/1	0.15	-0.53	76,76,76,76	0
2	NI	F	501	1/1	0.14	-0.68	49,49,49,49	0
2	NI	C	501	1/1	0.15	-0.69	67,67,67,67	0
2	NI	D	501	1/1	0.14	-0.73	54,54,54,54	0
3	ZN	A	502	1/1	0.14	-0.74	52,52,52,52	0
3	ZN	D	502	1/1	0.12	-0.79	67,67,67,67	0
5	EDO	E	703	4/4	0.16	-0.94	54,58,59,60	0
5	EDO	A	703	4/4	0.15	-1.12	60,62,62,63	0
5	EDO	F	702	4/4	0.14	-1.55	63,65,65,65	0
2	NI	B	501	1/1	0.15	-1.60	70,70,70,70	0
2	NI	E	501	1/1	0.09	-1.82	81,81,81,81	0

6.5 Other polymers ⓘ

There are no such residues in this entry.