



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 11:52 AM GMT

PDB ID : 4CBT
Title : Design, synthesis, and biological evaluation of potent and selective Class IIa HDAC inhibitors as a potential therapy for Huntingtons disease
Authors : Burli, R.W.; Luckhurst, C.A.; Aziz, O.; Matthews, K.L.; Yates, D.; Lyons, K.A.; Beconi, M.; McAllister, G.; Breccia, P.; Stott, A.J.; Penrose, S.D.; Wall, M.; Lamers, M.; Leonard, P.; Mueller, I.; Richardson, C.M.; Jarvis, R.; Stones, L.; Hughes, S.; Wishart, G.; Haughan, A.F.; OConnell, C.; Mead, T.; McNeil, H.; Vann, J.; Mangette, J.; Maillard, M.; Beaumont, V.; Munoz-Sanjuan, I.; Dominguez, C.
Deposited on : 2013-10-16
Resolution : 3.03 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

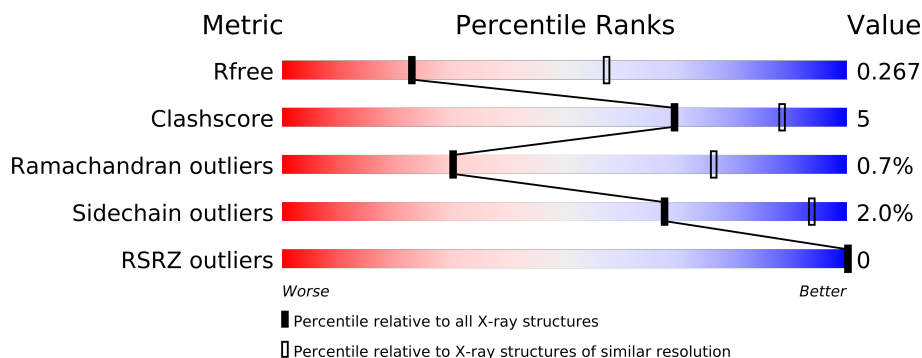
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
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) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.03 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	1460 (3.08-3.00)
Clashscore	79885	1881 (3.08-3.00)
Ramachandran outliers	78287	1814 (3.08-3.00)
Sidechain outliers	78261	1817 (3.08-3.00)
RSRZ outliers	66119	1462 (3.08-3.00)

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. 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	395	
1	B	395	
1	C	395	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7993 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 HISTONE DEACETYLASE 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2638	1660	465	494	19			
1	B	352	Total	C	N	O	S	0	0	0
			2645	1666	461	499	19			
1	C	346	Total	C	N	O	S	0	0	0
			2616	1650	462	485	19			

There are 27 discrepancies between the modelled and reference sequences:

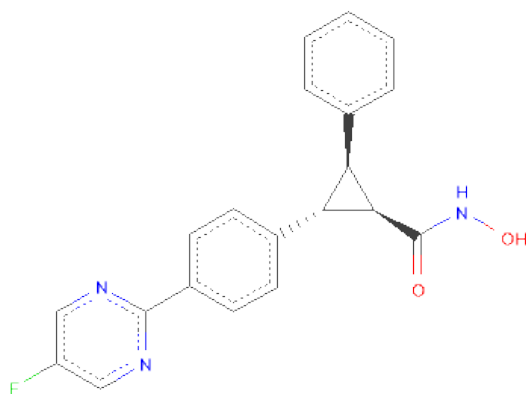
Chain	Residue	Modelled	Actual	Comment	Reference
A	645	MET	-	EXPRESSION TAG	UNP P56524
A	646	GLY	-	EXPRESSION TAG	UNP P56524
A	647	SER	-	EXPRESSION TAG	UNP P56524
A	1034	HIS	-	EXPRESSION TAG	UNP P56524
A	1035	HIS	-	EXPRESSION TAG	UNP P56524
A	1036	HIS	-	EXPRESSION TAG	UNP P56524
A	1037	HIS	-	EXPRESSION TAG	UNP P56524
A	1038	HIS	-	EXPRESSION TAG	UNP P56524
A	1039	HIS	-	EXPRESSION TAG	UNP P56524
B	645	MET	-	EXPRESSION TAG	UNP P56524
B	646	GLY	-	EXPRESSION TAG	UNP P56524
B	647	SER	-	EXPRESSION TAG	UNP P56524
B	1035	HIS	-	EXPRESSION TAG	UNP P56524
B	1036	HIS	-	EXPRESSION TAG	UNP P56524
B	1037	HIS	-	EXPRESSION TAG	UNP P56524
B	1038	HIS	-	EXPRESSION TAG	UNP P56524
B	1039	HIS	-	EXPRESSION TAG	UNP P56524
B	1040	HIS	-	EXPRESSION TAG	UNP P56524
C	645	MET	-	EXPRESSION TAG	UNP P56524
C	646	GLY	-	EXPRESSION TAG	UNP P56524
C	647	SER	-	EXPRESSION TAG	UNP P56524
C	1034	HIS	-	EXPRESSION TAG	UNP P56524
C	1035	HIS	-	EXPRESSION TAG	UNP P56524

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1036	HIS	-	EXPRESSION TAG	UNP P56524
C	1037	HIS	-	EXPRESSION TAG	UNP P56524
C	1038	HIS	-	EXPRESSION TAG	UNP P56524
C	1039	HIS	-	EXPRESSION TAG	UNP P56524

- Molecule 2 is (1R,2R,3R)-2-[4-(5-FLUORANYLPYRIMIDIN-2-YL)PHENYL]-N-OXIDANYL-3-PHENYL-CYCLOPROPANE-1-CARBOXAMIDE (three-letter code: 9F4) (formula: $C_{20}H_{16}FN_3O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			26	20	1	3	2		
2	B	1	Total	C	F	N	O	0	0
			26	20	1	3	2		
2	C	1	Total	C	F	N	O	0	0
			26	20	1	3	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		
3	A	2	Total	Zn	0	0
			2	2		
3	C	2	Total	Zn	0	0
			2	2		

- Molecule 4 is water.

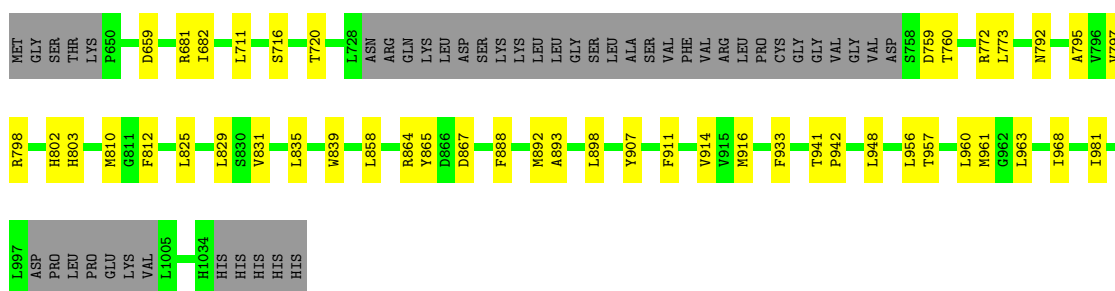
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	O 5	0	0
4	B	4	Total 4	O 4	0	0
4	C	1	Total 1	O 1	0	0

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.

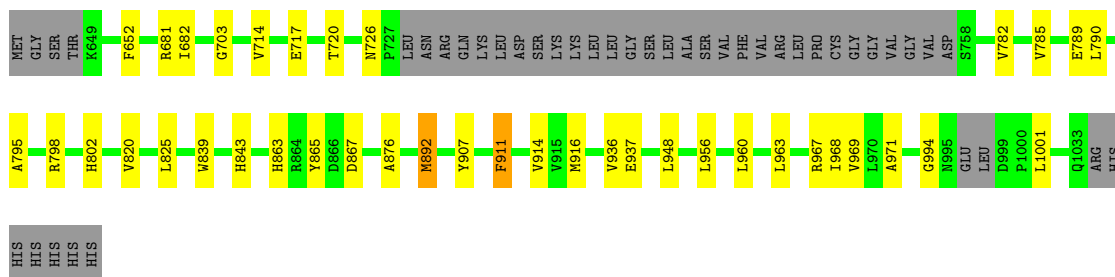
• Molecule 1: HISTONE DEACETYLASE 4

Chain A:



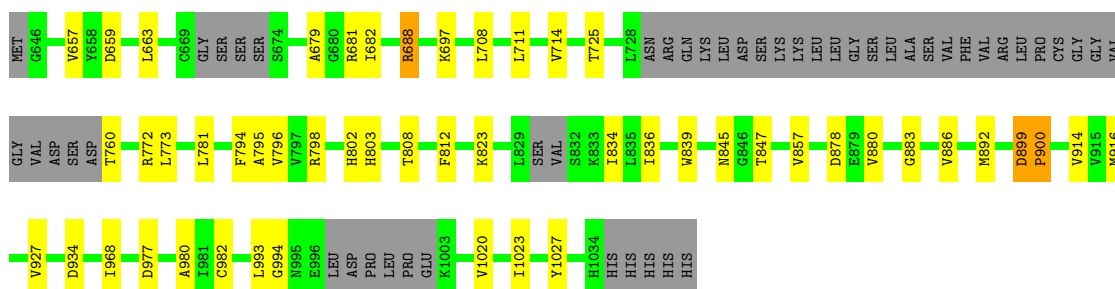
• Molecule 1: HISTONE DEACETYLASE 4

Chain B:



• Molecule 1: HISTONE DEACETYLASE 4

Chain C:



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	104.41Å 104.41Å 88.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	90.42 – 3.03 90.42 – 3.03	Depositor EDS
% Data completeness (in resolution range)	100.0 (90.42-3.03) 99.8 (90.42-3.03)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.211 , 0.273 0.211 , 0.267	Depositor DCC
R_{free} test set	1070 reflections (5.41%)	DCC
Wilson B-factor (Å ²)	47.8	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , -6.8	EDS
Estimated twinning fraction	0.011 for -h,-k,l 0.049 for h,-h-k,-l 0.032 for -k,-h,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 20863 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7993	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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 22.14 % 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 6.0533e-03. 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: 9F4, ZN

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	0.48	0/2699	0.53	1/3661 (0.0%)
1	B	0.43	0/2707	0.53	2/3679 (0.1%)
1	C	0.52	0/2675	0.54	2/3628 (0.1%)
All	All	0.48	0/8081	0.53	5/10968 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	681	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	C	681	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	A	681	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	B	681	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	C	681	ARG	NE-CZ-NH2	-5.30	117.65	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	899	ASP	Peptide

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	2638	0	2554	25	0
1	B	2645	0	2550	22	0
1	C	2616	0	2537	26	0
2	A	26	0	12	0	0
2	B	26	0	13	0	0
2	C	26	0	12	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	5	0	0	0	0
4	B	4	0	0	0	0
4	C	1	0	0	0	0
All	All	7993	0	7678	73	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 5.

All (73) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:785:VAL:HG21	1:B:969:VAL:HG23	1.51	0.91
1:B:785:VAL:HG21	1:B:969:VAL:CG2	2.02	0.88
1:A:825:LEU:HD22	1:A:831:VAL:HG21	1.68	0.73
1:B:916:MET:HE1	1:B:960:LEU:HD23	1.74	0.69
1:B:682:ILE:HD13	1:B:798:ARG:HG2	1.76	0.66
1:C:682:ILE:HD13	1:C:798:ARG:HG2	1.79	0.63
1:C:927:VAL:HB	1:C:968:ILE:HG22	1.80	0.63
1:C:657:VAL:HG12	1:C:795:ALA:HA	1.82	0.60
1:B:717:GLU:O	1:B:720:THR:HG22	2.02	0.59
1:A:892:MET:HE3	1:A:914:VAL:HG11	1.84	0.59
1:A:892:MET:CE	1:A:914:VAL:HG11	2.36	0.56
1:B:785:VAL:HG21	1:B:969:VAL:HG21	1.86	0.56
1:C:836:ILE:HG21	1:C:847:THR:HG21	1.86	0.56
1:B:782:VAL:CG1	1:B:825:LEU:HD11	2.36	0.55
1:C:886:VAL:HG12	1:C:1027:TYR:CE1	2.41	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:864:ARG:CZ	1:A:898:LEU:HD11	2.36	0.55
1:C:688:ARG:HD2	1:C:982:CYS:HB3	1.89	0.53
1:B:892:MET:HE1	1:B:914:VAL:HG21	1.89	0.53
1:B:865:TYR:OH	1:B:876:ALA:HB2	2.09	0.52
1:A:858:LEU:HD12	1:A:888:PHE:O	2.10	0.52
1:C:711:LEU:HD11	1:C:772:ARG:HG2	1.91	0.52
1:A:682:ILE:HD13	1:A:798:ARG:HG2	1.93	0.51
1:A:711:LEU:HD11	1:A:772:ARG:HG2	1.92	0.51
1:A:916:MET:HE1	1:A:963:LEU:HD11	1.93	0.51
1:C:892:MET:HE2	1:C:1020:VAL:HG11	1.93	0.50
1:B:967:ARG:C	1:B:968:ILE:HD12	2.31	0.50
1:B:789:GLU:O	1:B:790:LEU:HD23	2.11	0.50
1:C:803:HIS:HD2	1:C:845:ASN:OD1	1.95	0.49
1:C:916:MET:HE2	1:C:916:MET:HA	1.94	0.49
1:B:916:MET:CE	1:B:963:LEU:HD11	2.43	0.48
1:C:708:LEU:HD21	1:C:725:THR:HG23	1.95	0.48
1:A:865:TYR:CB	1:A:893:ALA:HB1	2.43	0.48
1:B:907:TYR:CG	1:B:948:LEU:HD21	2.50	0.47
1:C:883:GLY:O	1:C:886:VAL:HG23	2.16	0.46
1:C:878:ASP:O	1:C:880:VAL:HG13	2.14	0.46
1:B:714:VAL:HG23	1:B:820:VAL:HG22	1.98	0.46
1:B:936:VAL:HG12	1:B:937:GLU:N	2.30	0.46
1:C:682:ILE:HB	1:C:796:VAL:HG12	1.98	0.45
1:C:834:ILE:HB	1:C:857:VAL:HG22	1.99	0.45
1:A:803:HIS:HB3	1:A:810:MET:HG3	1.97	0.45
1:C:697:LYS:HD2	1:C:993:LEU:HD13	1.99	0.45
1:A:795:ALA:HB1	1:A:797:VAL:HG13	1.98	0.45
1:C:714:VAL:HG22	1:C:823:LYS:HG3	1.99	0.44
1:A:911:PHE:CD1	1:A:956:LEU:HD22	2.52	0.44
1:A:659:ASP:HB3	1:A:773:LEU:HD21	2.00	0.44
1:B:916:MET:HE2	1:B:963:LEU:HD11	2.00	0.44
1:A:933:PHE:HB2	1:A:981:ILE:HG22	1.99	0.44
1:C:892:MET:HE3	1:C:914:VAL:HG11	2.00	0.43
1:A:911:PHE:CE1	1:A:956:LEU:HD22	2.53	0.43
1:A:760:THR:HG22	1:A:812:PHE:CD1	2.54	0.43
1:C:892:MET:CE	1:C:914:VAL:HG11	2.49	0.43
1:B:682:ILE:HG23	1:B:798:ARG:HD2	2.01	0.43
1:A:957:THR:O	1:A:961:MET:HE2	2.19	0.42
1:A:835:LEU:HD13	1:A:858:LEU:HD23	2.00	0.42
1:A:716:SER:O	1:A:720:THR:HG23	2.19	0.42
1:C:781:LEU:HD21	1:C:794:PHE:N	2.34	0.42
1:A:907:TYR:CD1	1:A:948:LEU:HD11	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:892:MET:HE1	1:B:914:VAL:CG2	2.50	0.42
1:C:878:ASP:HA	1:C:1023:ILE:HD13	2.02	0.42
1:A:898:LEU:N	1:A:898:LEU:CD1	2.83	0.41
1:C:899:ASP:CB	1:C:900:PRO:CD	2.98	0.41
1:B:843:HIS:HB2	1:B:863:HIS:CD2	2.55	0.41
1:A:960:LEU:HB3	1:A:968:ILE:HD12	2.02	0.41
1:B:911:PHE:CD1	1:B:956:LEU:HD22	2.56	0.41
1:C:663:LEU:HD22	1:C:679:ALA:HB1	2.03	0.41
1:C:659:ASP:CG	1:C:773:LEU:HD21	2.41	0.41
1:B:795:ALA:HB3	1:B:971:ALA:HA	2.01	0.41
1:A:659:ASP:CB	1:A:773:LEU:HD21	2.51	0.41
1:A:898:LEU:N	1:A:898:LEU:HD12	2.36	0.40
1:A:892:MET:CE	1:A:914:VAL:HG21	2.52	0.40
1:C:760:THR:HG22	1:C:812:PHE:HD1	1.85	0.40
1:C:977:ASP:HB3	1:C:980:ALA:HB3	2.03	0.40
1:B:1001:LEU:HD12	1:B:1001:LEU:H	1.87	0.40

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	343/395 (87%)	318 (93%)	23 (7%)	2 (1%)	33	79
1	B	346/395 (88%)	325 (94%)	18 (5%)	3 (1%)	25	71
1	C	336/395 (85%)	306 (91%)	28 (8%)	2 (1%)	33	79
All	All	1025/1185 (86%)	949 (93%)	69 (7%)	7 (1%)	30	76

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	652	PHE
1	C	900	PRO
1	A	942	PRO

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Mol	Chain	Res	Type
1	B	994	GLY
1	A	941	THR
1	C	994	GLY
1	B	703	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	279/322 (87%)	273 (98%)	6 (2%)	64	93
1	B	280/322 (87%)	274 (98%)	6 (2%)	66	93
1	C	275/322 (85%)	270 (98%)	5 (2%)	71	94
All	All	834/966 (86%)	817 (98%)	17 (2%)	68	94

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	759	ASP
1	A	792	ASN
1	A	802	HIS
1	A	829	LEU
1	A	839	TRP
1	A	867	ASP
1	B	726	ASN
1	B	802	HIS
1	B	839	TRP
1	B	867	ASP
1	B	892	MET
1	B	911	PHE
1	C	688	ARG
1	C	802	HIS
1	C	808	THR
1	C	839	TRP
1	C	934	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	678	HIS
1	A	792	ASN
1	A	995	ASN
1	B	683	GLN
1	B	712	GLN
1	B	843	HIS
1	B	869	ASN
1	B	947	ASN
1	B	995	ASN
1	C	803	HIS
1	C	843	HIS
1	C	863	HIS
1	C	1006	GLN
1	C	1032	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 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\# Z > 2$
2	9F4	A	2035	3	29,29,29	0.90	2 (6%)	41,41,41	0.90	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	9F4	B	2034	3	29,29,29	0.84	1 (3%)	41,41,41	0.98	1 (2%)
2	9F4	C	2035	3	29,29,29	0.86	2 (6%)	41,41,41	0.87	2 (4%)

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	9F4	A	2035	3	-	0/18/27/27	0/3/4/4
2	9F4	B	2034	3	-	0/18/27/27	0/3/4/4
2	9F4	C	2035	3	-	0/18/27/27	0/3/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2035	9F4	C16-N18	2.47	1.37	1.33
2	C	2035	9F4	C16-N18	2.24	1.36	1.33
2	B	2034	9F4	C16-N18	2.17	1.36	1.33
2	C	2035	9F4	C15-C16	-2.15	1.47	1.51
2	A	2035	9F4	C15-C16	-2.09	1.47	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2034	9F4	O19-N18-C16	-4.38	113.92	119.80
2	A	2035	9F4	C6-C7-C8	-3.02	114.14	121.63
2	C	2035	9F4	O19-N18-C16	-2.72	116.15	119.80
2	C	2035	9F4	C6-C7-C8	-2.31	115.90	121.63

There are no chirality outliers.

There are no torsion outliers.

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	349/395 (88%)	-0.26	0 100 100	23, 36, 50, 62	0
1	B	352/395 (89%)	-0.32	0 100 100	24, 34, 46, 48	0
1	C	346/395 (87%)	-0.20	0 100 100	30, 43, 61, 70	0
All	All	1047/1185 (88%)	-0.26	0 100 100	23, 38, 54, 70	0

There are no RSRZ outliers to report.

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
2	9F4	A	2035	26/26	0.26	0.71	30,31,33,34	0
2	9F4	C	2035	26/26	0.23	0.42	33,35,38,38	0
2	9F4	B	2034	26/26	0.20	0.27	27,28,33,34	0
3	ZN	C	2036	1/1	0.11	-1.59	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	ZN	B	2036	1/1	0.10	-2.22	38,38,38,38	0
3	ZN	C	2037	1/1	0.07	-2.42	45,45,45,45	0
3	ZN	B	2035	1/1	0.11	-2.84	25,25,25,25	0
3	ZN	A	2037	1/1	0.07	-3.27	40,40,40,40	0
3	ZN	A	2036	1/1	0.06	-3.60	28,28,28,28	0

6.5 Other polymers ⓘ

There are no such residues in this entry.