



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 10:08 AM UTC

PDB ID : 4YGO / pdb_00004ygo
Title : Dodecameric structure of spermidine N-acetyltransferase from *Vibrio cholerae* in intermediate state
Authors : Filippova, E.V.; Minasov, G.; Kiryukhina, O.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2015-02-26
Resolution : 2.50 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

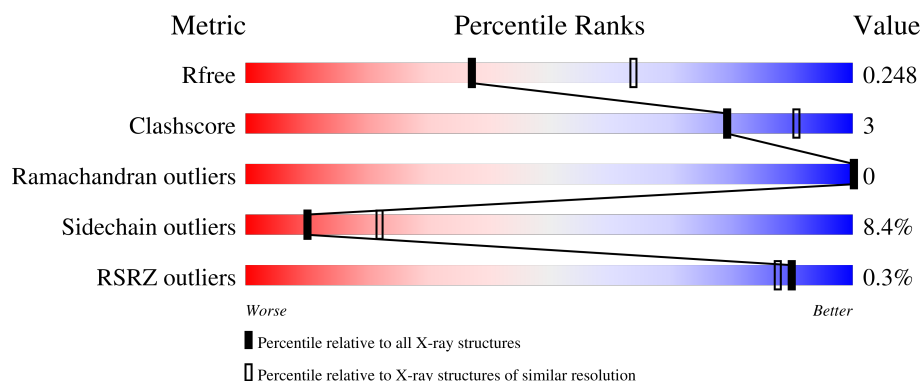
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	173	% 79% 17% ...
1	B	173	86% 10% ..
1	C	173	84% 13% ..
1	D	173	82% 16% ..
1	E	173	% 88% 8% ..

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Mol	Chain	Length	Quality of chain
1	F	173	% 77% 20% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8764 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.

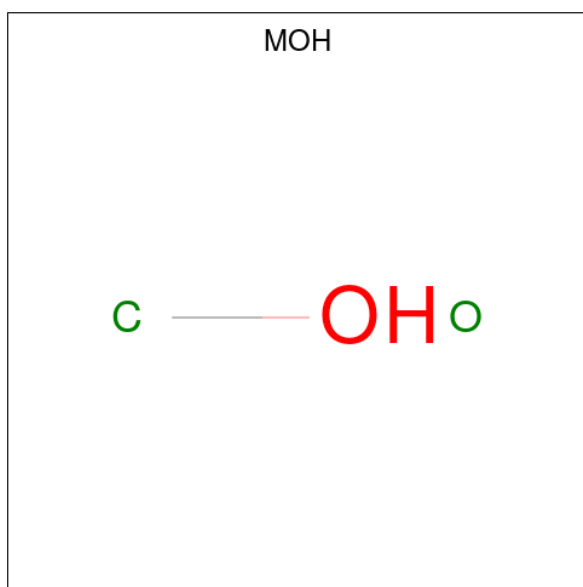
- Molecule 1 is a protein called Spermidine n1-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			
1	B	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			
1	D	172	Total	C	N	O	S	0	0	0
			1455	929	255	268	3			
1	C	170	Total	C	N	O	S	0	0	0
			1439	921	253	262	3			
1	E	167	Total	C	N	O	S	0	0	0
			1414	908	246	257	3			
1	F	171	Total	C	N	O	S	0	0	0
			1447	925	253	266	3			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 3 is METHANOL (CCD ID: MOH) (formula: CH₄O).



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

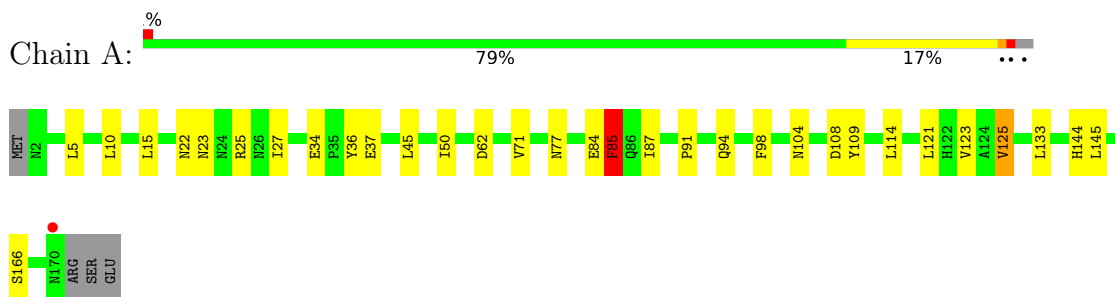
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	28	Total	O	0	1
			29	29		
4	B	17	Total	O	0	0
			17	17		
4	D	25	Total	O	0	0
			25	25		
4	C	31	Total	O	0	0
			31	31		
4	E	20	Total	O	0	0
			20	20		
4	F	23	Total	O	0	0
			23	23		

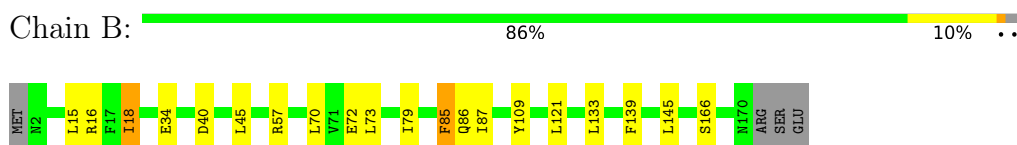
3 Residue-property plots

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

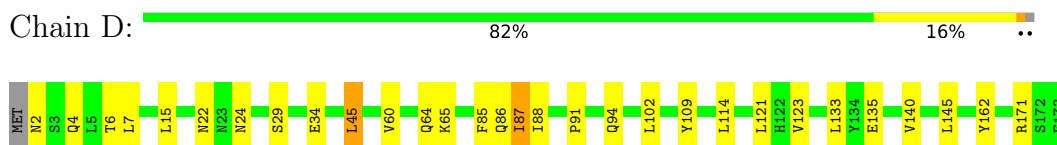
- Molecule 1: Spermidine n1-acetyltransferase



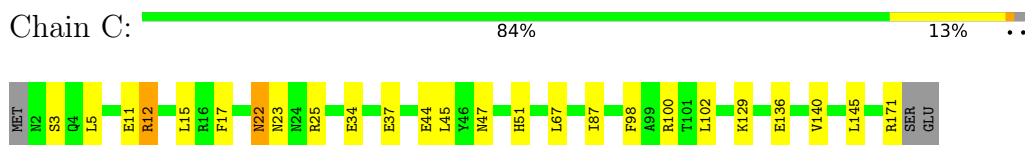
- Molecule 1: Spermidine n1-acetyltransferase



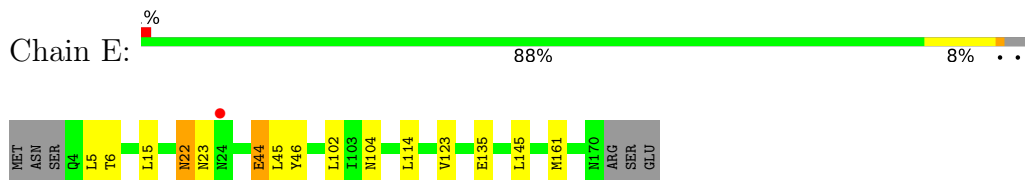
- Molecule 1: Spermidine n1-acetyltransferase



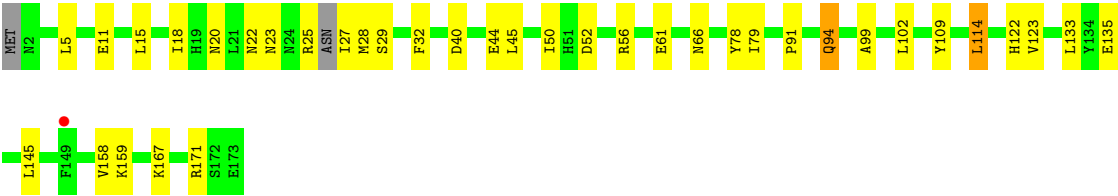
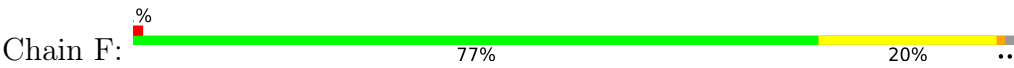
- Molecule 1: Spermidine n1-acetyltransferase



- Molecule 1: Spermidine n1-acetyltransferase



● Molecule 1: Spermidine n1-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	155.12Å 135.79Å 72.85Å 90.00° 117.13° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 30.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.3 (30.00-2.50) 99.9 (30.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.180 , 0.253 0.182 , 0.248	Depositor DCC
R_{free} test set	2408 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	54.8	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 24.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.004 for k+l,h+l,-l 0.003 for -k+l,-h-l,-l 0.043 for -h-2*l,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8764	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.18% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MOH, CA

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	1.07	2/1461 (0.1%)	1.08	4/1973 (0.2%)
1	B	1.06	0/1461	1.07	0/1973
1	C	1.10	2/1472 (0.1%)	1.11	4/1987 (0.2%)
1	D	1.08	1/1488 (0.1%)	1.13	1/2007 (0.0%)
1	E	1.00	1/1447 (0.1%)	1.06	1/1954 (0.1%)
1	F	1.00	0/1479	1.06	3/1993 (0.2%)
All	All	1.05	6/8808 (0.1%)	1.09	13/11887 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	140	VAL	C-O	-5.89	1.18	1.24
1	C	87	ILE	C-O	-5.86	1.18	1.24
1	A	77	ASN	N-CA	-5.85	1.39	1.46
1	A	108	ASP	N-CA	-5.70	1.39	1.46
1	E	22	ASN	N-CA	5.49	1.53	1.46
1	D	140	VAL	C-O	-5.20	1.18	1.24

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	ASN	N-CA-C	8.30	121.90	111.69
1	F	79	ILE	N-CA-C	-6.94	105.08	111.67
1	F	123	VAL	CB-CA-C	-6.50	100.49	110.50
1	C	12	ARG	NE-CZ-NH2	5.70	124.33	119.20
1	F	99	ALA	N-CA-C	5.66	117.45	111.28
1	C	22	ASN	CA-C-N	5.46	127.55	120.44
1	C	22	ASN	C-N-CA	5.46	127.55	120.44
1	C	23	ASN	CB-CA-C	-5.45	102.32	110.88
1	E	23	ASN	N-CA-C	5.41	118.10	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	GLU	CA-C-N	-5.27	114.31	122.59
1	A	84	GLU	C-N-CA	-5.27	114.31	122.59
1	A	85	PHE	N-CA-C	5.06	117.36	109.52
1	D	123	VAL	CB-CA-C	-5.02	103.01	110.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1428	0	1384	13	0
1	B	1428	0	1384	6	0
1	C	1439	0	1397	7	0
1	D	1455	0	1408	10	0
1	E	1414	0	1373	4	0
1	F	1447	0	1401	11	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	D	2	0	0	0	0
2	E	1	0	0	0	0
3	A	2	0	0	0	0
4	A	29	0	0	0	0
4	B	17	0	0	0	0
4	C	31	0	0	0	0
4	D	25	0	0	0	0
4	E	20	0	0	0	0
4	F	23	0	0	0	0
All	All	8764	0	8347	45	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 (45) 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:D:22:ASN:OD1	1:D:29:SER:HB3	1.75	0.86
1:C:12:ARG:NH1	1:C:47:ASN:OD1	2.21	0.73
1:C:5:LEU:HD13	1:C:102:LEU:HD21	1.76	0.66
1:A:85:PHE:HE2	1:A:87:ILE:HD11	1.61	0.65
1:A:22:ASN:ND2	1:A:36:TYR:OH	2.32	0.62
1:D:121:LEU:HD12	1:D:121:LEU:C	2.25	0.61
1:B:18:ILE:HD11	1:B:70:LEU:HD13	1.89	0.55
1:A:5:LEU:HD11	1:A:98:PHE:CD1	2.42	0.54
1:E:5:LEU:HD13	1:E:102:LEU:HD21	1.90	0.54
1:F:109:TYR:CE2	1:F:114:LEU:HD22	2.43	0.53
1:D:22:ASN:OD1	1:D:29:SER:CB	2.53	0.53
1:B:57:ARG:HG2	1:B:72:GLU:HG3	1.93	0.51
1:D:60:VAL:HG21	1:D:102:LEU:HD13	1.93	0.51
1:F:20:ASN:O	1:F:23:ASN:HB3	2.11	0.50
1:A:85:PHE:CE2	1:A:87:ILE:HD11	2.43	0.50
1:A:50:ILE:HG21	1:E:44:GLU:OE2	2.11	0.49
1:B:109:TYR:OH	1:C:37:GLU:OE1	2.27	0.49
1:D:24:ASN:ND2	1:D:91:PRO:HG3	2.26	0.49
1:D:86:GLN:HE22	1:D:88:ILE:HD11	1.78	0.48
1:F:5:LEU:HD13	1:F:102:LEU:HD21	1.96	0.47
1:A:125:VAL:HG21	1:A:144:HIS:CE1	2.50	0.46
1:E:46:TYR:OH	1:F:40:ASP:OD2	2.32	0.46
1:F:61:GLU:HA	1:F:66:ASN:O	2.16	0.45
1:C:100:ARG:NH2	1:C:136:GLU:OE1	2.50	0.45
1:B:73:LEU:HD23	1:B:85:PHE:HB2	1.99	0.45
1:E:135:GLU:HG3	1:E:161:MET:HE1	1.99	0.45
1:A:91:PRO:HA	1:A:94:GLN:HG3	1.99	0.44
1:F:32:PHE:CE2	1:F:52:ASP:HB3	2.53	0.44
1:A:62:ASP:OD1	1:A:62:ASP:C	2.60	0.44
1:D:45:LEU:HD13	1:C:51:HIS:CE1	2.53	0.44
1:A:121:LEU:CD1	1:A:123:VAL:HG23	2.48	0.44
1:B:121:LEU:CD2	1:B:139:PHE:CE2	3.01	0.43
1:F:167:LYS:O	1:F:171:ARG:HB2	2.18	0.43
1:A:109:TYR:CE2	1:A:114:LEU:HD22	2.54	0.43
1:A:71:VAL:HG22	1:A:87:ILE:HD13	2.00	0.43
1:D:162:TYR:CD2	1:D:162:TYR:C	2.94	0.42
1:A:37:GLU:OE1	1:D:109:TYR:OH	2.23	0.42
1:B:40:ASP:HB3	1:F:50:ILE:HD11	2.01	0.41
1:F:91:PRO:HA	1:F:94:GLN:CG	2.50	0.41
1:F:122:HIS:HA	1:F:159:LYS:O	2.20	0.41
1:C:5:LEU:HD11	1:C:98:PHE:CD1	2.55	0.41
1:C:17:PHE:CZ	1:C:67:LEU:HB3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:56:ARG:NH2	1:F:78:TYR:OH	2.49	0.41
1:A:85:PHE:HE1	1:A:121:LEU:HD23	1.86	0.40
1:D:87:ILE:HD11	1:D:102:LEU:HD12	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	167/173 (96%)	162 (97%)	5 (3%)	0	100	100
1	B	167/173 (96%)	163 (98%)	4 (2%)	0	100	100
1	C	168/173 (97%)	166 (99%)	2 (1%)	0	100	100
1	D	170/173 (98%)	165 (97%)	5 (3%)	0	100	100
1	E	165/173 (95%)	158 (96%)	7 (4%)	0	100	100
1	F	167/173 (96%)	162 (97%)	5 (3%)	0	100	100
All	All	1004/1038 (97%)	976 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	153/157 (98%)	141 (92%)	12 (8%)	11	24
1	B	153/157 (98%)	141 (92%)	12 (8%)	11	24
1	C	154/157 (98%)	143 (93%)	11 (7%)	13	29
1	D	156/157 (99%)	139 (89%)	17 (11%)	6	13
1	E	151/157 (96%)	142 (94%)	9 (6%)	17	36
1	F	155/157 (99%)	139 (90%)	16 (10%)	7	14
All	All	922/942 (98%)	845 (92%)	77 (8%)	10	22

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	15	LEU
1	A	25	ARG
1	A	27	ILE
1	A	34	GLU
1	A	45	LEU
1	A	85	PHE
1	A	104	ASN
1	A	125	VAL
1	A	133	LEU
1	A	145	LEU
1	A	166	SER
1	B	15	LEU
1	B	16	ARG
1	B	18	ILE
1	B	34	GLU
1	B	45	LEU
1	B	79	ILE
1	B	85	PHE
1	B	86	GLN
1	B	87	ILE
1	B	133	LEU
1	B	145	LEU
1	B	166	SER
1	D	2	ASN
1	D	4	GLN
1	D	6	THR
1	D	7	LEU
1	D	15	LEU
1	D	34	GLU

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Mol	Chain	Res	Type
1	D	45	LEU
1	D	64	GLN
1	D	65	LYS
1	D	85	PHE
1	D	87	ILE
1	D	94	GLN
1	D	114	LEU
1	D	133	LEU
1	D	135	GLU
1	D	145	LEU
1	D	171	ARG
1	C	3	SER
1	C	11	GLU
1	C	15	LEU
1	C	22	ASN
1	C	25	ARG
1	C	34	GLU
1	C	44	GLU
1	C	45	LEU
1	C	129	LYS
1	C	145	LEU
1	C	171	ARG
1	E	6	THR
1	E	15	LEU
1	E	22	ASN
1	E	44	GLU
1	E	45	LEU
1	E	104	ASN
1	E	114	LEU
1	E	123	VAL
1	E	145	LEU
1	F	11	GLU
1	F	15	LEU
1	F	18	ILE
1	F	22	ASN
1	F	25	ARG
1	F	27	ILE
1	F	28	MET
1	F	29	SER
1	F	44	GLU
1	F	45	LEU
1	F	94	GLN

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Mol	Chain	Res	Type
1	F	114	LEU
1	F	133	LEU
1	F	135	GLU
1	F	145	LEU
1	F	158	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	94	GLN
1	B	49	HIS
1	B	51	HIS
1	B	93	HIS
1	B	152	ASN
1	D	4	GLN
1	D	23	ASN
1	D	24	ASN
1	D	51	HIS
1	D	86	GLN
1	D	93	HIS
1	D	104	ASN
1	D	117	HIS
1	D	152	ASN
1	D	170	ASN
1	C	2	ASN
1	C	4	GLN
1	C	23	ASN
1	C	51	HIS
1	C	117	HIS
1	E	24	ASN
1	E	64	GLN
1	E	117	HIS
1	E	152	ASN
1	F	4	GLN
1	F	23	ASN
1	F	24	ASN
1	F	93	HIS
1	F	94	GLN
1	F	170	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 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	$\# Z > 2$
3	MOH	A	203	-	1,1,1	0.02	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 [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	169/173 (97%)	-0.41	1 (0%) 85 83	40, 55, 84, 124	0
1	B	169/173 (97%)	-0.38	0 100 100	42, 59, 88, 121	0
1	C	170/173 (98%)	-0.45	0 100 100	40, 55, 82, 115	0
1	D	172/173 (99%)	-0.42	0 100 100	41, 55, 86, 111	0
1	E	167/173 (96%)	-0.44	1 (0%) 85 83	45, 59, 81, 112	0
1	F	171/173 (98%)	-0.22	1 (0%) 85 83	44, 66, 104, 135	0
All	All	1018/1038 (98%)	-0.39	3 (0%) 90 87	40, 58, 93, 135	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	149	PHE	2.9
1	E	24	ASN	2.5
1	A	170	ASN	2.1

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 oligosaccharides 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
3	MOH	A	203	2/2	0.83	0.25	63,63,63,67	0
2	CA	B	201	1/1	0.90	0.07	62,62,62,62	1
2	CA	D	202	1/1	0.91	0.06	51,51,51,51	1
2	CA	A	202	1/1	0.94	0.06	57,57,57,57	1
2	CA	A	201	1/1	0.98	0.03	69,69,69,69	0
2	CA	E	201	1/1	0.98	0.03	70,70,70,70	0
2	CA	D	201	1/1	0.98	0.04	87,87,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.