



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:41 AM UTC

PDB ID : 2W6U / pdb_00002w6u
Title : Structures of *P. aeruginosa* FpvA bound to heterologous pyoverdines: FpvA-Pvd(G173)-Fe complex
Authors : Greenwald, J.; Nader, M.; Celia, H.; Gruffaz, C.; Meyer, J.-M.; Schalk, I.J.; Pattus, F.
Deposited on : 2008-12-19
Resolution : 3.00 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

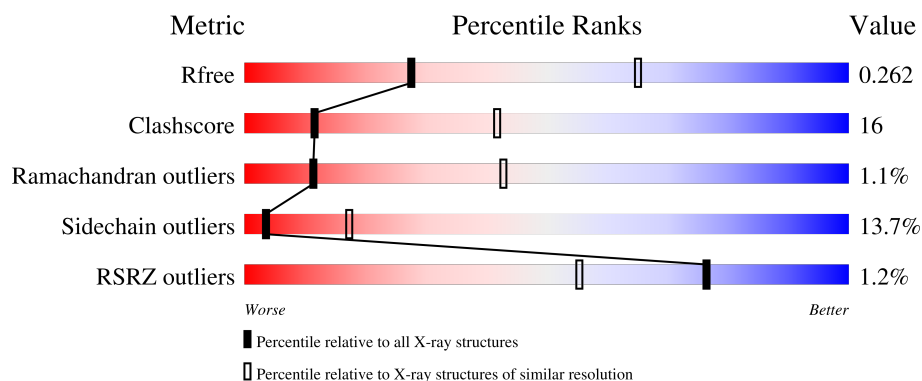
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 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	772	59% 34% 6% .
1	B	772	62% 28% 6% ..
2	C	7	29% 71%

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
2	DAS	C	7	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12314 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.

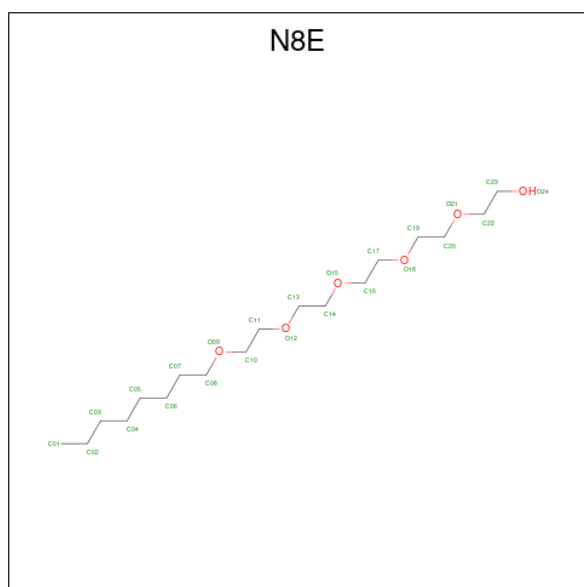
- Molecule 1 is a protein called FERRIPYOVERDINE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	772	Total	C	N	O	S	0	0	0
			6114	3845	1046	1211	12			
1	B	754	Total	C	N	O	S	0	0	0
			5994	3775	1027	1181	11			

- Molecule 2 is a protein called PYOVERDIN G173.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			57	32	10	15			

- Molecule 3 is 3,6,9,12,15-PENTAOXATRICOSAN-1-OL (CCD ID: N8E) (formula: C₁₈H₃₈O₆).



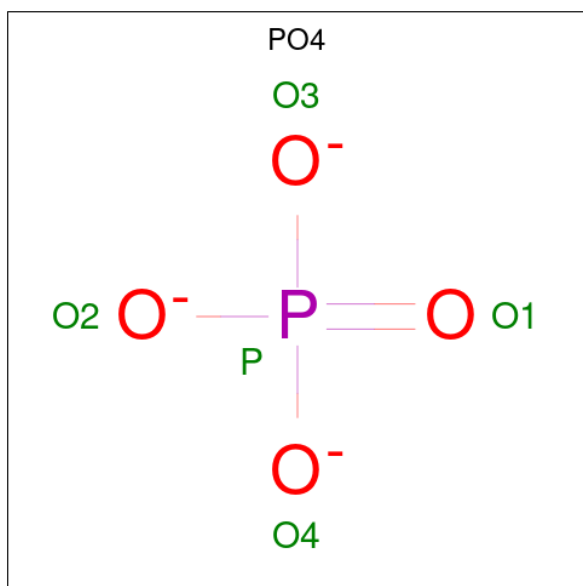
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			24	18	6		

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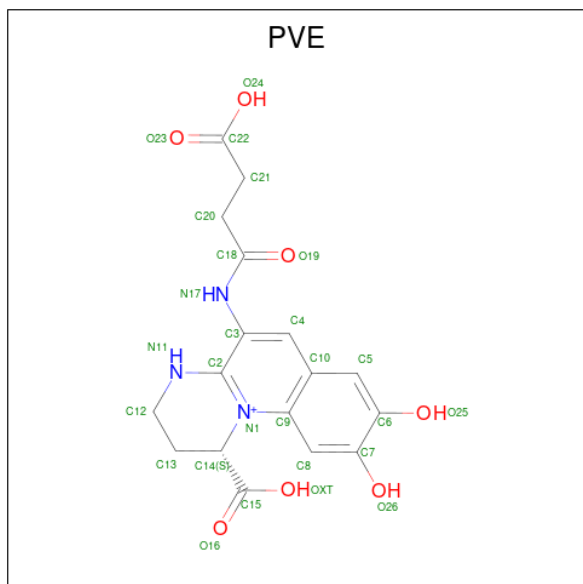
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			48	36	12		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 5 is (1S)-1-CARBOXY-5-[(3-CARBOXYPROPANOYL)AMINO]-8,9-DIHYDROXY-1,2,3,4-TETRAHYDROPYRIMIDO[1,2-A]QUINOLIN-11-IUM (CCD ID: PVE) (formula: C₁₇H₁₈N₃O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	5	0
			26	17	3	6		

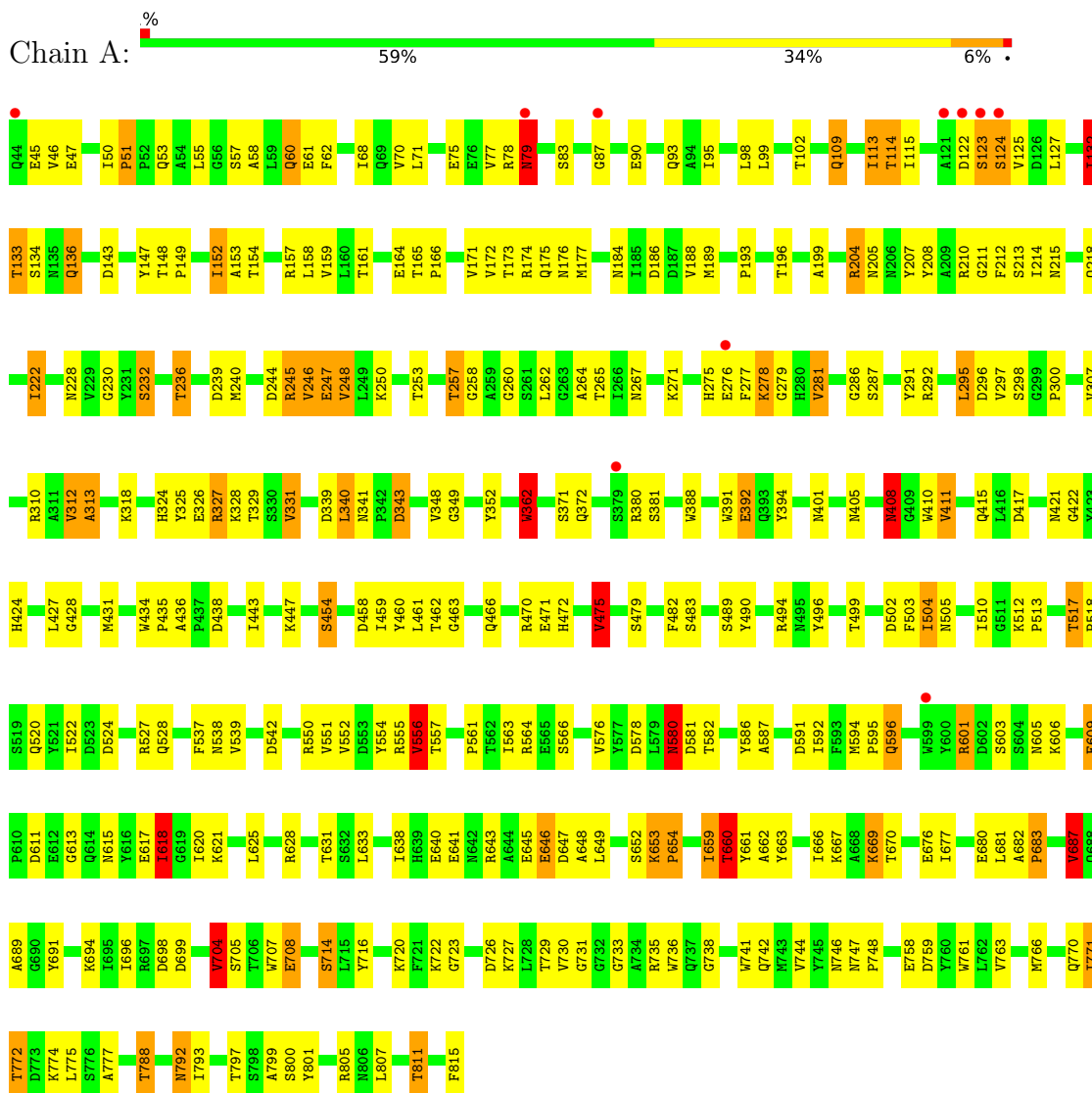
- Molecule 6 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	1	Total	Fe	0	0
			1	1		

3 Residue-property plots

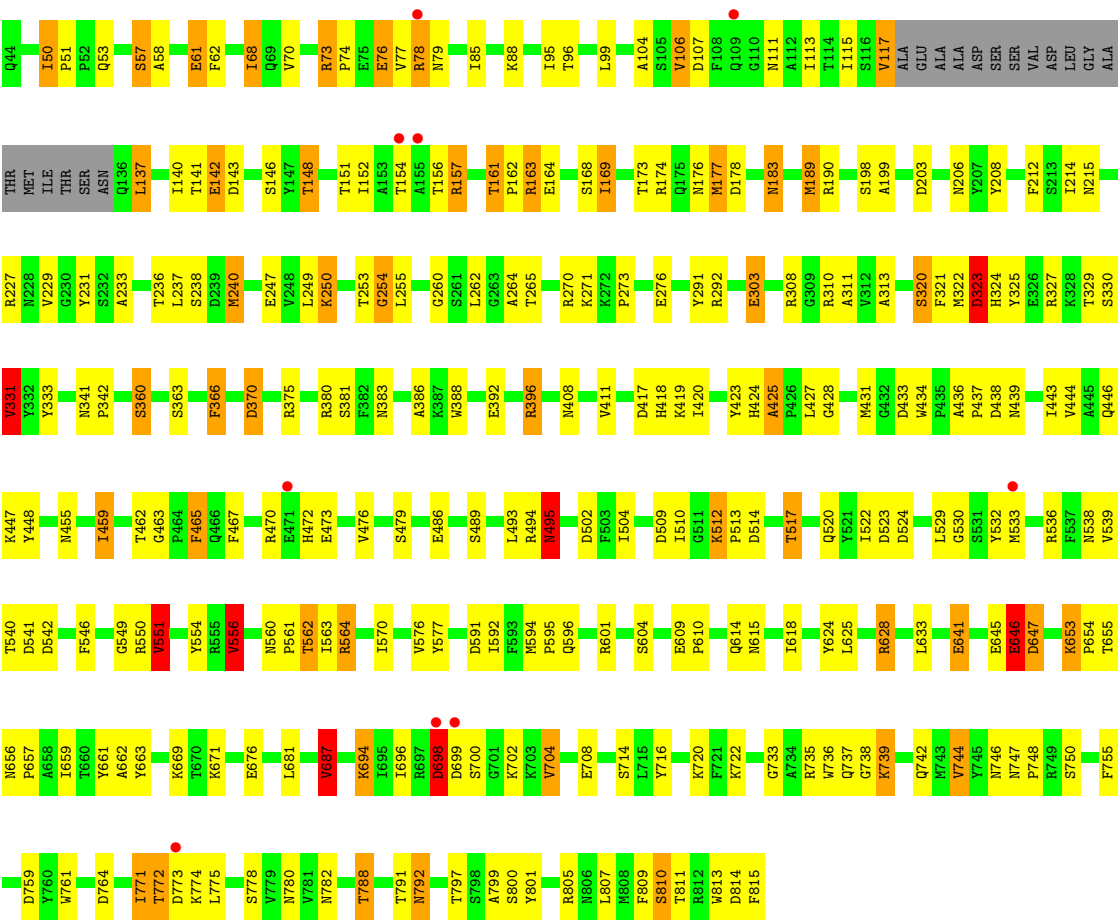
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: FERRIPYOVERDINE RECEPTOR



• Molecule 1: FERRIPYOVERDINE RECEPTOR





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	194.77Å 129.93Å 141.56Å 90.00° 130.36° 90.00°	Depositor
Resolution (Å)	97.59 – 3.00 97.59 – 3.00	Depositor EDS
% Data completeness (in resolution range)	89.4 (97.59-3.00) 89.4 (97.59-3.00)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.266 0.210 , 0.262	Depositor DCC
R_{free} test set	2449 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	44.0	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12314	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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: DAS, DSN, PO4, ORN, N8E, AHO, FE, PVE

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	1.24	10/6266 (0.2%)	1.36	52/8514 (0.6%)
1	B	1.11	2/6145 (0.0%)	1.25	35/8347 (0.4%)
2	C	1.31	0/9	1.92	1/9 (11.1%)
All	All	1.17	12/12420 (0.1%)	1.30	88/16870 (0.5%)

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	A	0	1
1	B	0	2
2	C	0	2
All	All	0	5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	504	ILE	CA-CB	7.29	1.63	1.54
1	B	551	VAL	CA-CB	6.66	1.62	1.54
1	A	172	VAL	CA-CB	-6.04	1.47	1.54
1	A	763	VAL	CA-CB	5.92	1.61	1.54
1	A	166	PRO	CA-CB	-5.80	1.50	1.53
1	A	153	ALA	CA-CB	-5.73	1.44	1.53
1	A	248	VAL	CA-C	5.67	1.59	1.52
1	A	113	ILE	CA-CB	5.60	1.62	1.54
1	A	556	VAL	CA-CB	5.60	1.61	1.53
1	A	618	ILE	CA-CB	5.52	1.63	1.55
1	A	247	GLU	N-CA	-5.43	1.39	1.46
1	B	517	THR	CA-CB	5.01	1.61	1.53

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	517	THR	CA-C-N	-9.88	109.58	119.76
1	A	517	THR	C-N-CA	-9.88	109.58	119.76
1	A	687	VAL	CB-CA-C	-9.46	96.17	110.55
1	A	556	VAL	CB-CA-C	8.13	121.56	110.99
1	A	281	VAL	N-CA-C	-7.88	96.79	108.45
1	B	653	LYS	CA-C-N	7.76	127.81	119.89
1	B	653	LYS	C-N-CA	7.76	127.81	119.89
1	B	514	ASP	N-CA-C	-7.75	97.44	109.76
1	A	122	ASP	N-CA-C	7.61	120.53	111.02
1	B	646	GLU	N-CA-C	7.55	119.30	111.14
1	A	109	GLN	N-CA-C	7.44	119.73	109.54
1	A	741	TRP	N-CA-C	7.17	119.04	108.14
1	A	517	THR	N-CA-C	7.12	118.32	110.13
1	A	248	VAL	N-CA-C	6.93	117.85	107.80
1	A	362	TRP	N-CA-C	-6.88	102.27	111.96
1	B	463	GLY	CA-C-N	6.78	128.17	120.85
1	B	463	GLY	C-N-CA	6.78	128.17	120.85
1	B	425	ALA	CA-C-N	-6.75	111.40	119.84
1	B	425	ALA	C-N-CA	-6.75	111.40	119.84
1	B	747	ASN	CA-C-N	-6.74	112.75	119.56
1	B	747	ASN	C-N-CA	-6.74	112.75	119.56
1	A	79	ASN	N-CA-C	-6.70	101.72	111.30
1	A	421	ASN	CA-C-N	-6.60	117.63	122.18
1	A	421	ASN	C-N-CA	-6.60	117.63	122.18
1	B	687	VAL	CB-CA-C	-6.59	100.15	110.69
1	B	137	LEU	N-CA-C	-6.53	105.06	113.16
1	A	313	ALA	N-CA-C	-6.49	97.65	108.75
1	A	471	GLU	N-CA-C	6.49	119.31	108.73
1	A	45	GLU	N-CA-C	6.44	119.31	110.24
1	B	366	PHE	CA-C-N	-6.34	113.42	120.14
1	B	366	PHE	C-N-CA	-6.34	113.42	120.14
1	A	50	ILE	CA-C-N	6.30	124.26	119.66
1	A	50	ILE	C-N-CA	6.30	124.26	119.66
1	A	580	ASN	CB-CA-C	-6.29	98.29	113.19
1	A	113	ILE	CA-C-N	-6.18	114.47	123.00
1	A	113	ILE	C-N-CA	-6.18	114.47	123.00
1	A	327	ARG	N-CA-C	6.12	118.27	107.61
1	A	475	VAL	CB-CA-C	-6.05	101.18	110.50
1	B	68	ILE	CB-CA-C	5.99	121.43	110.71
1	A	77	VAL	CB-CA-C	-5.94	105.36	112.19
1	A	61	GLU	N-CA-C	-5.90	104.79	112.23
1	B	250	LYS	N-CA-C	5.87	118.97	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	523	ASP	N-CA-C	-5.80	97.52	107.61
1	B	183	ASN	N-CA-C	5.77	120.47	112.45
1	B	698	ASP	CB-CA-C	-5.74	98.99	110.42
1	A	248	VAL	CB-CA-C	5.64	119.20	110.96
1	A	90	GLU	CA-C-N	5.61	125.98	119.47
1	A	90	GLU	C-N-CA	5.61	125.98	119.47
1	B	556	VAL	CB-CA-C	5.60	116.80	110.41
1	B	146	SER	N-CA-C	5.58	118.08	110.55
1	A	735	ARG	CB-CA-C	5.55	118.69	110.14
1	A	362	TRP	CA-CB-CG	5.53	124.11	113.60
1	B	331	VAL	N-CA-C	5.53	116.44	108.48
1	B	212	PHE	N-CA-C	5.52	118.09	108.76
1	A	660	THR	N-CA-C	-5.49	107.24	114.04
1	A	51	PRO	O-C-N	5.47	123.82	121.31
1	B	148	THR	CA-C-N	-5.46	114.96	120.31
1	B	148	THR	C-N-CA	-5.46	114.96	120.31
1	B	744	VAL	N-CA-C	5.43	116.40	108.53
1	B	473	GLU	N-CA-C	5.41	117.41	109.24
1	A	87	GLY	N-CA-C	5.40	118.33	111.85
1	A	708	GLU	N-CA-C	-5.39	101.57	109.50
1	A	653	LYS	CA-C-N	5.39	126.58	119.84
1	A	653	LYS	C-N-CA	5.39	126.58	119.84
1	A	561	PRO	N-CA-C	-5.39	102.65	111.21
1	A	524	ASP	N-CA-C	-5.28	99.49	108.26
1	B	233	ALA	CA-C-N	-5.28	115.95	123.08
1	B	233	ALA	C-N-CA	-5.28	115.95	123.08
1	B	676	GLU	N-CA-C	5.28	117.10	108.76
1	A	328	LYS	CB-CA-C	-5.28	101.63	110.29
1	A	176	ASN	N-CA-C	-5.25	105.64	111.36
1	A	77	VAL	N-CA-C	5.25	116.58	111.91
1	A	136	GLN	CA-C-N	-5.24	113.90	122.54
1	A	136	GLN	C-N-CA	-5.24	113.90	122.54
1	A	125	VAL	N-CA-C	5.24	116.12	108.53
1	A	55	LEU	N-CA-C	-5.23	105.58	111.28
1	B	50	ILE	CA-C-N	5.23	125.77	120.38
1	B	50	ILE	C-N-CA	5.23	125.77	120.38
1	B	320	SER	N-CA-C	5.22	116.22	108.86
1	A	683	PRO	N-CA-C	5.17	123.11	112.47
2	C	4	ALA	N-CA-C	5.15	125.43	111.00
1	B	79	ASN	N-CA-C	5.13	115.77	108.54
1	A	381	SER	N-CA-C	5.11	117.75	111.82
1	A	222	ILE	N-CA-C	5.08	113.03	107.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ALA	N-CA-C	-5.05	105.85	111.36
1	A	704	VAL	CB-CA-C	5.04	119.56	111.29
1	A	460	TYR	N-CA-C	5.04	116.90	108.99
1	B	229	VAL	N-CA-C	5.02	119.48	112.50

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	ILE	Peptide
1	B	208	TYR	Peptide
1	B	698	ASP	Peptide
2	C	3	DSN	Peptide
2	C	7	DAS	Peptide

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	6114	0	5788	196	0
1	B	5994	0	5675	183	0
2	C	57	0	38	11	0
3	A	72	0	114	17	0
4	A	30	0	0	2	0
4	B	20	0	0	2	0
5	C	26	0	14	1	0
6	C	1	0	0	0	0
All	All	12314	0	11629	384	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 16.

All (384) 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:189:MET:HE2	1:B:189:MET:HA	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:ARG:HG2	1:B:396:ARG:HH11	1.18	1.02
1:B:696:ILE:HG23	1:B:704:VAL:HG12	1.42	1.01
1:B:772:THR:HG22	1:B:774:LYS:H	1.20	0.99
1:B:363:SER:HB3	1:B:431:MET:CE	1.98	0.94
1:A:53:GLN:OE1	1:A:57:SER:HB2	1.68	0.93
1:B:698:ASP:HB3	1:B:700:SER:H	1.33	0.91
1:A:805:ARG:HD2	3:A:1817[A]:N8E:H031	1.52	0.90
1:B:396:ARG:HG2	1:B:396:ARG:NH1	1.83	0.89
1:B:536:ARG:HD2	1:B:546:PHE:CZ	2.09	0.88
1:A:772:THR:HG21	1:B:291:TYR:OH	1.78	0.83
1:A:777:ALA:HB1	3:A:1817[B]:N8E:H192	1.61	0.82
1:B:363:SER:CB	1:B:431:MET:HE1	2.09	0.82
1:A:133:THR:HG21	1:A:159:VAL:HG21	1.62	0.81
1:B:154:THR:OG1	1:B:247:GLU:OE1	1.99	0.81
1:B:363:SER:HB2	2:C:8:AHO:HC71	1.60	0.81
1:B:363:SER:HB3	1:B:431:MET:HE1	1.60	0.80
1:A:694:LYS:HE2	1:A:708:GLU:CD	2.06	0.80
1:B:792:ASN:HB3	1:B:800:SER:HB2	1.65	0.77
1:A:694:LYS:HE2	1:A:708:GLU:OE1	1.85	0.77
1:B:772:THR:HG22	1:B:774:LYS:N	2.00	0.76
3:A:1817[B]:N8E:H031	1:B:805:ARG:HD2	1.66	0.76
1:B:560:ASN:HB3	1:B:561:PRO:HD2	1.68	0.75
2:C:6:ORN:HG3	2:C:7:DAS:N	1.99	0.75
1:A:443:ILE:HG13	1:A:510:ILE:CD1	2.16	0.75
1:B:646:GLU:O	1:B:662:ALA:O	2.04	0.75
1:A:722:LYS:HG3	1:A:723:GLY:H	1.52	0.75
1:A:805:ARG:NH1	3:A:1817[A]:N8E:H013	2.01	0.74
1:A:603:SER:O	1:A:659:ILE:HD11	1.88	0.74
1:B:363:SER:CB	1:B:431:MET:CE	2.66	0.74
1:A:291:TYR:OH	1:B:772:THR:HG21	1.86	0.74
1:A:811:THR:CG2	3:A:1817[A]:N8E:H232	2.17	0.74
1:B:370:ASP:HA	1:B:434:TRP:O	1.88	0.73
1:B:341:ASN:HB2	1:B:342:PRO:HD2	1.70	0.73
1:A:443:ILE:HG13	1:A:510:ILE:HD13	1.69	0.72
1:B:255:LEU:O	1:B:550:ARG:HD2	1.88	0.72
1:B:470:ARG:HH12	1:B:540:THR:HA	1.54	0.72
1:B:540:THR:HG22	1:B:541:ASP:H	1.55	0.72
1:B:189:MET:HA	1:B:189:MET:CE	2.18	0.71
1:A:204:ARG:HG3	1:A:391:TRP:CH2	2.25	0.71
1:B:142:GLU:HB2	1:B:174:ARG:HG2	1.71	0.71
1:B:189:MET:HE2	1:B:189:MET:CA	2.18	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:ARG:HH21	1:A:555:ARG:HD2	1.56	0.70
1:A:805:ARG:HH11	3:A:1817[A]:N8E:H013	1.56	0.70
1:A:262:LEU:HD21	1:A:613:GLY:HA3	1.74	0.70
1:A:244:ASP:O	1:A:245:ARG:HB3	1.91	0.70
1:A:792:ASN:HB3	1:A:800:SER:HB2	1.72	0.69
1:A:214:ILE:HG12	1:A:264:ALA:HB3	1.74	0.69
1:A:222:ILE:HD11	1:A:415:GLN:NE2	2.08	0.69
1:A:165:THR:O	1:A:621:LYS:NZ	2.25	0.68
1:A:188:VAL:HG11	1:A:246:VAL:CG1	2.24	0.68
1:B:681:LEU:HD22	1:B:687:VAL:HG13	1.76	0.68
1:B:698:ASP:HB3	1:B:700:SER:N	2.06	0.68
1:B:737:GLN:O	1:B:759:ASP:HB2	1.94	0.68
1:A:742:GLN:HG3	1:A:793:ILE:O	1.94	0.67
1:B:696:ILE:CG2	1:B:704:VAL:HG12	2.22	0.67
1:A:615:ASN:HD21	1:A:617:GLU:HB2	1.60	0.67
1:A:392:GLU:HG2	1:A:424:HIS:HB3	1.77	0.66
1:A:260:GLY:HA2	1:A:594:MET:HE2	1.76	0.66
1:A:554:TYR:CD2	1:A:595:PRO:HG2	2.30	0.66
1:B:418:HIS:HE1	4:B:1821:PO4:O1	1.79	0.66
1:A:174:ARG:CZ	1:A:177:MET:HE2	2.26	0.65
1:A:99:LEU:O	1:A:102:THR:HG23	1.96	0.65
1:A:716:TYR:CD1	1:A:733:GLY:HA3	2.31	0.65
1:A:157:ARG:HB3	1:A:475:VAL:HG11	1.77	0.65
1:B:152:ILE:HD12	1:B:169:ILE:HG12	1.78	0.64
1:A:411:VAL:HG13	1:A:462:THR:HG22	1.80	0.64
1:A:454:SER:OG	1:A:483:SER:HB2	1.98	0.64
1:B:564:ARG:CG	1:B:564:ARG:HH11	2.11	0.64
1:A:722:LYS:HG3	1:A:723:GLY:N	2.13	0.63
1:B:459:ILE:HG13	1:B:459:ILE:O	1.98	0.63
1:A:281:VAL:HG23	1:A:815:PHE:CZ	2.33	0.63
1:A:371:SER:OG	1:A:436:ALA:HA	1.97	0.63
1:A:208:TYR:HA	1:A:212:PHE:O	1.99	0.63
1:A:297:VAL:HG12	3:A:1816:N8E:H162	1.81	0.63
3:A:1817[B]:N8E:H052	1:B:805:ARG:HD2	1.81	0.63
2:C:7:DAS:HA	2:C:9:SER:HB3	1.81	0.62
1:A:53:GLN:OE1	1:A:57:SER:CB	2.45	0.62
1:B:323:ASP:HB2	1:B:381:SER:O	1.98	0.62
1:A:186:ASP:OD1	1:A:207:TYR:OH	2.13	0.62
1:A:771:ILE:HG12	1:B:809:PHE:CD1	2.34	0.62
1:B:540:THR:HG22	1:B:541:ASP:N	2.14	0.61
3:A:1817[A]:N8E:H221	1:B:811:THR:OG1	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:LEU:CD2	1:A:475:VAL:HG22	2.31	0.61
1:A:188:VAL:HG11	1:A:246:VAL:HG11	1.82	0.61
1:A:132:ILE:HG23	1:A:133:THR:H	1.66	0.61
1:A:410:TRP:CD2	1:A:463:GLY:HA3	2.36	0.61
1:A:811:THR:HG21	3:A:1817[A]:N8E:H232	1.83	0.60
1:B:772:THR:CG2	1:B:773:ASP:N	2.64	0.60
1:A:470:ARG:NH1	1:A:538:ASN:OD1	2.33	0.60
1:B:694:LYS:HE3	1:B:708:GLU:OE1	2.01	0.60
1:B:669:LYS:O	1:B:696:ILE:HA	2.02	0.60
1:A:777:ALA:HB1	3:A:1817[B]:N8E:C19	2.32	0.60
1:A:132:ILE:CG2	1:A:133:THR:H	2.15	0.60
1:A:680:GLU:HG3	1:A:682:ALA:O	2.02	0.60
1:A:631:THR:HG22	1:A:677:ILE:HG13	1.84	0.59
1:B:694:LYS:NZ	1:B:708:GLU:O	2.35	0.59
1:B:303:GLU:H	1:B:303:GLU:CD	2.10	0.59
1:A:747:ASN:HB3	1:A:748:PRO:HD3	1.84	0.59
1:B:646:GLU:O	1:B:663:TYR:HA	2.01	0.59
1:A:158:LEU:HD21	1:A:475:VAL:HG22	1.84	0.59
1:A:797:THR:O	1:A:797:THR:HG22	2.02	0.59
1:B:324:HIS:CE1	1:B:383:ASN:HB3	2.38	0.59
1:A:807:LEU:HD11	3:A:1817[A]:N8E:H061	1.84	0.59
1:A:210:ARG:O	1:A:670:THR:HG21	2.02	0.59
1:A:646:GLU:O	1:A:662:ALA:O	2.21	0.59
1:A:707:TRP:CH2	1:A:793:ILE:HG13	2.38	0.59
1:B:470:ARG:NH1	1:B:540:THR:HA	2.17	0.59
1:A:132:ILE:CG2	1:A:133:THR:N	2.66	0.58
1:A:601:ARG:NH1	1:A:605:ASN:O	2.37	0.58
1:A:392:GLU:CG	1:A:424:HIS:HB3	2.33	0.58
1:A:277:PHE:O	1:A:278:LYS:HB3	2.03	0.58
1:A:792:ASN:O	1:A:799:ALA:HA	2.02	0.58
1:A:805:ARG:HD3	3:A:1817[A]:N8E:H052	1.85	0.58
1:A:127:LEU:HD11	1:A:581:ASP:HA	1.85	0.58
1:B:542:ASP:O	1:B:577:TYR:HA	2.03	0.58
1:A:512:LYS:HD2	4:A:1818:PO4:O1	2.03	0.58
1:A:79:ASN:OD1	1:A:79:ASN:N	2.37	0.57
1:B:50:ILE:HG23	1:B:53:GLN:NE2	2.19	0.57
1:B:141:THR:HG21	1:B:173:THR:HG22	1.87	0.57
1:A:443:ILE:CG1	1:A:510:ILE:CD1	2.82	0.57
1:B:536:ARG:HB2	1:B:546:PHE:CE1	2.39	0.57
1:A:587:ALA:HB2	1:A:618:ILE:HG13	1.87	0.57
1:B:694:LYS:HZ2	1:B:708:GLU:HG2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:380:ARG:HD3	1:B:788:THR:HB	1.85	0.57
1:A:738:GLY:HA2	1:A:759:ASP:HB3	1.86	0.56
1:B:494:ARG:O	1:B:495:ASN:C	2.48	0.56
1:A:46:VAL:HG12	1:A:47:GLU:N	2.19	0.56
1:B:554:TYR:CD2	1:B:595:PRO:HG2	2.40	0.56
2:C:3:DSN:OG	2:C:4:ALA:N	2.33	0.56
1:A:435:PRO:HD3	1:A:503:PHE:CE1	2.40	0.56
1:A:380:ARG:HD3	1:A:788:THR:HB	1.88	0.56
1:A:60:GLN:HE21	1:A:134:SER:HA	1.71	0.56
1:B:62:PHE:CZ	1:B:95:ILE:HB	2.40	0.56
1:B:174:ARG:NH2	1:B:178:ASP:OD1	2.38	0.56
1:B:262:LEU:HD23	1:B:592:ILE:HG22	1.87	0.55
1:B:375:ARG:NE	1:B:755:PHE:CZ	2.74	0.55
1:A:580:ASN:HB2	1:A:582:THR:H	1.70	0.55
1:A:391:TRP:HB2	1:A:427:LEU:HD21	1.87	0.55
1:B:77:VAL:O	1:B:78:ARG:C	2.49	0.55
1:B:156:THR:O	1:B:157:ARG:HB2	2.06	0.55
1:B:659:ILE:HG23	1:B:659:ILE:O	2.06	0.55
1:A:738:GLY:HA2	1:A:759:ASP:CB	2.37	0.55
1:A:177:MET:HE3	1:A:240:MET:HB3	1.88	0.55
1:A:517:THR:O	1:A:518:PRO:C	2.47	0.55
1:B:738:GLY:HA2	1:B:759:ASP:CB	2.37	0.55
1:B:311:ALA:HA	1:B:333:TYR:O	2.06	0.55
1:B:775:LEU:HD13	1:B:813:TRP:HB2	1.89	0.55
1:A:109:GLN:OE1	1:A:114:THR:HG22	2.07	0.54
1:A:408:ASN:HB3	1:A:410:TRP:H	1.71	0.54
1:A:75:GLU:HB2	1:A:78:ARG:NH2	2.22	0.54
1:A:736:TRP:HB2	1:A:761:TRP:CE3	2.43	0.54
1:A:75:GLU:OE1	1:A:75:GLU:N	2.40	0.54
2:C:3:DSN:N	5:C:1:PVE:H8	2.22	0.54
3:A:1817[B]:N8E:H052	1:B:805:ARG:CD	2.38	0.54
1:A:291:TYR:OH	1:B:772:THR:CG2	2.54	0.54
1:A:253:THR:O	1:A:257:THR:HB	2.06	0.54
1:A:410:TRP:CE2	1:A:463:GLY:HA3	2.43	0.54
1:B:380:ARG:HA	1:B:801:TYR:CD2	2.42	0.54
1:A:133:THR:HG21	1:A:159:VAL:CG2	2.34	0.53
1:A:458:ASP:OD2	1:A:479:SER:HB3	2.07	0.53
1:B:425:ALA:HB1	1:B:427:LEU:HD21	1.89	0.53
1:A:352:TYR:CD1	1:A:352:TYR:C	2.87	0.53
1:B:646:GLU:HA	1:B:663:TYR:CD2	2.44	0.53
1:B:772:THR:CG2	1:B:774:LYS:H	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:7:DAS:HA	2:C:9:SER:CB	2.39	0.53
1:A:199:ALA:HA	1:A:205:ASN:HD22	1.74	0.53
1:A:438:ASP:C	1:A:438:ASP:OD1	2.50	0.53
1:A:394:TYR:CZ	1:A:422:GLY:HA3	2.44	0.53
1:A:775:LEU:HD23	1:A:775:LEU:C	2.34	0.53
1:B:512:LYS:HG3	1:B:513:PRO:HD2	1.90	0.53
1:A:646:GLU:HG3	1:A:661:TYR:OH	2.08	0.52
1:A:722:LYS:HA	1:A:726:ASP:HB3	1.90	0.52
1:A:380:ARG:HA	1:A:801:TYR:CD2	2.45	0.52
1:A:556:VAL:HG22	1:A:563:ILE:HD12	1.91	0.52
1:B:446:GLN:OE1	1:B:448:TYR:OH	2.25	0.52
1:A:447:LYS:HB3	1:A:490:TYR:HB2	1.91	0.52
1:A:723:GLY:O	1:A:726:ASP:OD2	2.27	0.52
1:A:51:PRO:O	1:A:53:GLN:HG2	2.09	0.52
1:A:772:THR:HG22	1:A:774:LYS:H	1.73	0.52
1:B:76:GLU:HG2	1:B:117:VAL:HB	1.92	0.52
1:A:98:LEU:C	1:A:98:LEU:HD23	2.35	0.52
1:B:151:THR:HG22	1:B:161:THR:HG22	1.91	0.52
1:B:341:ASN:HB2	1:B:342:PRO:CD	2.38	0.52
1:B:198:SER:OG	1:B:206:ASN:HB3	2.10	0.51
1:B:50:ILE:HG12	1:B:61:GLU:HG2	1.92	0.51
1:B:716:TYR:CD1	1:B:733:GLY:HA3	2.46	0.51
1:A:527:ARG:NH2	1:A:555:ARG:HD2	2.25	0.51
1:B:764:ASP:CB	1:B:782:ASN:HA	2.41	0.51
1:A:193:PRO:O	1:A:250:LYS:HE2	2.11	0.51
1:A:228:ASN:OD1	1:A:230:GLY:N	2.44	0.51
1:A:394:TYR:CE1	1:A:422:GLY:HA3	2.46	0.51
1:A:770:GLN:NE2	1:A:772:THR:O	2.34	0.51
1:B:396:ARG:HH11	1:B:396:ARG:CG	2.00	0.51
1:B:156:THR:O	1:B:157:ARG:CB	2.60	0.50
1:B:736:TRP:HB2	1:B:761:TRP:CE3	2.47	0.50
2:C:6:ORN:CG	2:C:7:DAS:N	2.68	0.50
1:A:434:TRP:HB3	1:A:435:PRO:HA	1.92	0.50
1:B:646:GLU:HG3	1:B:661:TYR:OH	2.10	0.50
1:A:211:GLY:HA2	1:A:708:GLU:OE1	2.10	0.50
1:B:439:ASN:ND2	1:B:502:ASP:HA	2.27	0.50
1:A:218:GLN:NE2	1:A:267:ASN:HB2	2.27	0.50
1:A:611:ASP:OD1	1:A:640:GLU:OE2	2.30	0.50
1:B:174:ARG:NH2	1:B:177:MET:HB3	2.27	0.50
1:B:694:LYS:NZ	1:B:708:GLU:HG2	2.27	0.50
1:A:228:ASN:O	1:A:232:SER:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:GLU:O	1:A:647:ASP:HB3	2.12	0.50
1:A:362:TRP:HB3	1:A:431:MET:HE1	1.94	0.49
1:B:556:VAL:HG13	1:B:563:ILE:HB	1.94	0.49
1:B:625:LEU:O	1:B:628:ARG:HD3	2.12	0.49
1:A:147:TYR:HA	1:A:173:THR:OG1	2.12	0.49
1:B:467:PHE:HB3	1:B:472:HIS:CE1	2.47	0.49
1:B:249:LEU:O	1:B:264:ALA:HA	2.13	0.49
1:A:339:ASP:O	1:A:340:LEU:C	2.55	0.49
1:A:343:ASP:HB2	1:A:405:ASN:HB2	1.94	0.49
1:B:370:ASP:O	1:B:433:ASP:HB3	2.13	0.49
1:B:152:ILE:CD1	1:B:169:ILE:HG12	2.42	0.49
1:B:321:PHE:CE1	1:B:322:MET:HG3	2.46	0.49
1:A:401:ASN:ND2	1:A:415:GLN:HG2	2.27	0.49
1:B:70:VAL:HG13	1:B:113:ILE:CG1	2.43	0.49
1:B:694:LYS:HD2	1:B:694:LYS:C	2.38	0.49
1:A:189:MET:HA	1:A:189:MET:HE2	1.93	0.49
1:B:363:SER:HB2	2:C:8:AHO:C7	2.35	0.48
1:A:199:ALA:HA	1:A:205:ASN:ND2	2.28	0.48
1:A:811:THR:HG23	3:A:1817[A]:N8E:H232	1.95	0.48
1:B:436:ALA:HB1	1:B:437:PRO:CD	2.43	0.48
1:B:774:LYS:HE2	1:B:814:ASP:O	2.13	0.48
3:A:1817[B]:N8E:H031	1:B:805:ARG:HH11	1.78	0.48
1:B:470:ARG:HH12	1:B:540:THR:CA	2.25	0.48
1:A:666:ILE:HD12	1:A:698:ASP:HB2	1.94	0.48
1:B:735:ARG:NH2	1:B:737:GLN:OE1	2.30	0.48
1:B:50:ILE:HG23	1:B:53:GLN:HE21	1.78	0.48
1:B:50:ILE:HD12	1:B:85:ILE:HD11	1.94	0.48
1:B:470:ARG:NH2	1:B:541:ASP:OD1	2.43	0.48
1:B:609:GLU:HG3	1:B:610:PRO:HD2	1.96	0.48
1:A:46:VAL:CG1	1:A:47:GLU:N	2.76	0.47
1:B:214:ILE:CD1	1:B:264:ALA:HB3	2.44	0.47
1:B:532:TYR:HA	1:B:549:GLY:O	2.15	0.47
1:A:123:SER:O	1:A:124:SER:HB3	2.14	0.47
1:A:654:PRO:HG3	1:A:660:THR:O	2.15	0.47
1:A:746:ASN:C	1:A:746:ASN:OD1	2.57	0.47
1:A:576:VAL:HG22	1:A:586:TYR:HB3	1.96	0.47
1:A:275:HIS:O	1:A:300:PRO:HD3	2.14	0.47
1:A:435:PRO:HD3	1:A:503:PHE:CD1	2.49	0.47
1:A:496:TYR:CG	1:A:513:PRO:HB3	2.49	0.47
1:A:638:ILE:HB	1:A:670:THR:HB	1.95	0.47
1:A:502:ASP:OD2	1:A:505:ASN:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:764:ASP:HB3	1:B:782:ASN:HA	1.97	0.47
1:B:106:VAL:HG13	1:B:115:ILE:HD13	1.97	0.47
1:B:772:THR:HG22	1:B:773:ASP:N	2.30	0.47
1:B:653:LYS:HA	1:B:654:PRO:HD2	1.66	0.47
1:B:262:LEU:CD2	1:B:592:ILE:HG22	2.45	0.47
1:B:203:ASP:OD2	1:B:360:SER:OG	2.24	0.46
1:A:591:ASP:CG	1:A:592:ILE:N	2.73	0.46
1:B:363:SER:HB2	1:B:431:MET:HE1	1.92	0.46
1:A:704:VAL:O	1:A:705:SER:C	2.59	0.46
1:A:239:ASP:OD2	1:A:292:ARG:NH2	2.48	0.46
1:A:472:HIS:ND1	1:A:537:PHE:HA	2.31	0.46
1:B:417:ASP:O	1:B:455:ASN:HA	2.15	0.46
1:A:161:THR:OG1	1:A:164:GLU:HG3	2.16	0.46
1:B:162:PRO:O	1:B:163:ARG:C	2.57	0.46
1:A:174:ARG:NH1	1:A:177:MET:CE	2.79	0.46
1:A:435:PRO:HB3	1:A:503:PHE:CB	2.45	0.46
1:A:443:ILE:HG13	1:A:510:ILE:HD12	1.96	0.46
1:B:530:GLY:HA2	1:B:551:VAL:O	2.16	0.46
1:B:646:GLU:O	1:B:647:ASP:CB	2.64	0.46
1:A:271:LYS:NZ	1:A:296:ASP:OD2	2.44	0.46
1:B:50:ILE:HA	1:B:51:PRO:HD3	1.62	0.46
1:B:313:ALA:HA	1:B:331:VAL:O	2.16	0.46
1:A:313:ALA:HA	1:A:331:VAL:O	2.16	0.45
1:B:260:GLY:O	1:B:594:MET:HB2	2.16	0.45
1:A:691:TYR:C	1:A:691:TYR:CD2	2.93	0.45
1:A:772:THR:HG22	1:A:774:LYS:N	2.31	0.45
1:B:538:ASN:ND2	1:B:540:THR:O	2.49	0.45
1:A:443:ILE:CG1	1:A:510:ILE:HD12	2.47	0.45
1:B:564:ARG:HH11	1:B:564:ARG:HG3	1.82	0.45
1:B:614:GLN:OE1	1:B:641:GLU:OE2	2.33	0.45
1:A:184:ASN:C	1:A:184:ASN:OD1	2.57	0.45
1:B:320:SER:C	1:B:322:MET:N	2.75	0.45
1:A:681:LEU:HG	1:A:687:VAL:HG22	1.99	0.45
1:A:388:TRP:CH2	1:A:428:GLY:HA3	2.52	0.45
1:A:648:ALA:O	1:A:649:LEU:C	2.60	0.45
1:B:142:GLU:O	1:B:143:ASP:HB2	2.17	0.45
1:A:489:SER:HB2	1:A:520:GLN:HB3	1.99	0.45
1:A:325:TYR:OH	1:A:327:ARG:NH1	2.50	0.44
1:B:57:SER:O	1:B:58:ALA:C	2.60	0.44
1:B:231:TYR:HB3	1:B:423:TYR:CE1	2.53	0.44
1:B:237:LEU:O	1:B:238:SER:C	2.59	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:ARG:HG2	1:A:552:VAL:CG2	2.47	0.44
1:B:746:ASN:OD1	1:B:748:PRO:HD2	2.17	0.44
2:C:7:DAS:HA	2:C:9:SER:CA	2.47	0.44
1:B:431:MET:HE2	1:B:431:MET:HB3	1.65	0.44
1:A:318:LYS:HG3	1:A:318:LYS:O	2.18	0.44
1:A:731:GLY:O	1:A:766:MET:N	2.50	0.44
1:B:396:ARG:NH1	1:B:396:ARG:CG	2.61	0.44
1:B:470:ARG:NH1	1:B:539:VAL:O	2.48	0.44
1:B:50:ILE:CG2	1:B:53:GLN:HE21	2.31	0.44
1:B:570:ILE:HG23	1:B:591:ASP:HB3	1.99	0.44
1:A:258:GLY:HA2	1:A:550:ARG:HD3	2.00	0.44
1:A:262:LEU:HD23	1:A:592:ILE:HG22	2.00	0.44
1:A:392:GLU:O	1:A:392:GLU:HG3	2.18	0.44
1:B:366:PHE:CE2	1:B:799:ALA:HB3	2.52	0.44
1:A:222:ILE:HD11	1:A:415:GLN:CD	2.43	0.44
1:B:564:ARG:C	1:B:564:ARG:HD3	2.43	0.44
1:B:646:GLU:O	1:B:647:ASP:HB3	2.18	0.44
1:B:681:LEU:HD13	1:B:687:VAL:HG22	1.99	0.44
1:A:295:LEU:O	1:A:312:VAL:HA	2.18	0.43
1:A:408:ASN:HB3	1:A:410:TRP:HB2	2.00	0.43
1:A:482:PHE:CD2	1:A:527:ARG:HG3	2.54	0.43
1:A:152:ILE:HA	1:A:152:ILE:HD13	1.68	0.43
1:B:392:GLU:HB2	1:B:424:HIS:O	2.17	0.43
1:A:171:VAL:HG22	1:A:247:GLU:HB3	1.99	0.43
1:B:386:ALA:N	1:B:428:GLY:O	2.46	0.43
1:A:174:ARG:CZ	4:A:1823:PO4:O2	2.67	0.43
1:A:615:ASN:ND2	1:A:617:GLU:HB2	2.32	0.43
1:B:199:ALA:O	1:B:792:ASN:HB2	2.19	0.43
1:B:320:SER:C	1:B:322:MET:H	2.25	0.43
1:A:148:THR:OG1	1:A:149:PRO:HD2	2.19	0.43
1:A:207:TYR:O	1:A:214:ILE:HD12	2.18	0.43
1:A:550:ARG:HG2	1:A:552:VAL:HG22	2.01	0.43
1:B:419:LYS:HG3	1:B:420:ILE:N	2.33	0.43
1:A:236:THR:H	1:A:236:THR:HG22	1.53	0.43
1:A:175:GLN:O	1:A:175:GLN:HG3	2.18	0.42
1:B:738:GLY:HA2	1:B:759:ASP:HB2	2.01	0.42
1:B:772:THR:HG23	1:B:773:ASP:H	1.83	0.42
1:A:411:VAL:HG13	1:A:462:THR:CG2	2.48	0.42
1:A:667:LYS:HB2	1:A:699:ASP:OD1	2.19	0.42
1:B:183:ASN:O	1:B:240:MET:HB2	2.19	0.42
1:B:215:ASN:ND2	1:B:227:ARG:O	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:771:ILE:H	1:B:771:ILE:HG13	1.26	0.42
1:B:772:THR:HB	1:B:775:LEU:HB3	2.00	0.42
2:C:5:AHO:HC73	2:C:5:AHO:HC52	1.91	0.42
1:A:640:GLU:CD	1:A:643:ARG:HB2	2.45	0.42
1:A:298:SER:HB2	1:A:310:ARG:HG3	2.01	0.42
1:B:797:THR:HG22	1:B:797:THR:O	2.19	0.42
1:A:286:GLY:O	1:A:287:SER:C	2.62	0.42
1:A:349:GLY:HA2	3:A:1816:N8E:H051	2.00	0.42
1:A:431:MET:HE2	1:A:431:MET:HB3	1.94	0.42
1:B:681:LEU:HD13	1:B:687:VAL:CG2	2.49	0.42
1:B:73:ARG:O	1:B:74:PRO:C	2.62	0.42
1:B:778:SER:HB2	1:B:810:SER:HB3	2.01	0.42
1:B:176:ASN:C	1:B:176:ASN:HD22	2.27	0.42
1:B:479:SER:O	1:B:529:LEU:HA	2.20	0.42
1:A:62:PHE:CZ	1:A:95:ILE:HB	2.55	0.42
1:A:279:GLY:HA3	1:A:296:ASP:O	2.20	0.42
1:B:273:PRO:HB2	1:B:308:ARG:HB3	2.01	0.42
1:A:70:VAL:CG1	1:A:115:ILE:HD13	2.50	0.41
1:A:689:ALA:HA	1:A:714:SER:O	2.19	0.41
1:B:738:GLY:O	1:B:739:LYS:C	2.63	0.41
1:B:764:ASP:HB2	1:B:782:ASN:HA	2.02	0.41
1:A:132:ILE:HG22	1:A:133:THR:N	2.35	0.41
1:B:472:HIS:HD2	1:B:538:ASN:H	1.68	0.41
1:B:388:TRP:CZ2	1:B:513:PRO:HD3	2.55	0.41
1:B:465:PHE:N	1:B:465:PHE:CD1	2.89	0.41
2:C:7:DAS:HA	2:C:9:SER:O	2.21	0.41
1:A:646:GLU:HA	1:A:663:TYR:CD2	2.54	0.41
1:B:271:LYS:HD3	1:B:310:ARG:NH2	2.35	0.41
1:B:540:THR:CG2	1:B:541:ASP:H	2.28	0.41
1:A:132:ILE:HD13	1:A:132:ILE:HA	1.94	0.41
1:B:99:LEU:HD22	1:B:104:ALA:HB3	2.03	0.41
1:B:370:ASP:HA	1:B:434:TRP:C	2.44	0.41
1:B:780:ASN:O	1:B:807:LEU:HA	2.20	0.41
1:A:596:GLN:NE2	1:A:609:GLU:O	2.53	0.41
1:A:625:LEU:O	1:A:628:ARG:HB2	2.21	0.41
1:B:431:MET:HG3	1:B:444:VAL:CG2	2.50	0.41
1:A:594:MET:HA	1:A:595:PRO:HD3	1.90	0.41
1:B:375:ARG:HE	1:B:755:PHE:HZ	1.60	0.41
1:B:418:HIS:CD2	1:B:455:ASN:HD21	2.39	0.41
1:B:438:ASP:OD1	1:B:438:ASP:N	2.48	0.41
1:B:614:GLN:NE2	1:B:641:GLU:OE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:ASN:HB2	1:B:276:GLU:OE1	2.21	0.41
1:B:254:GLY:N	1:B:592:ILE:HD12	2.35	0.41
1:A:188:VAL:HG11	1:A:246:VAL:HG13	2.01	0.40
1:A:669:LYS:O	1:A:696:ILE:HA	2.21	0.40
1:B:190:ARG:NH2	4:B:1819:PO4:O3	2.55	0.40
1:A:136:GLN:HE22	1:A:462:THR:HG21	1.86	0.40
1:B:325:TYR:OH	1:B:327:ARG:HD3	2.21	0.40
1:A:716:TYR:CE1	1:A:733:GLY:HA3	2.57	0.40
1:B:489:SER:HB2	1:B:520:GLN:HB3	2.03	0.40
1:B:656:ASN:HA	1:B:657:PRO:HD2	1.93	0.40
1:A:470:ARG:HD3	1:A:538:ASN:O	2.22	0.40
1:B:161:THR:HG23	1:B:164:GLU:OE1	2.22	0.40
1:A:341:ASN:OD1	1:A:341:ASN:C	2.64	0.40
1:B:486:GLU:HA	1:B:522:ILE:O	2.21	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	770/772 (100%)	706 (92%)	57 (7%)	7 (1%)	14	48
1	B	750/772 (97%)	689 (92%)	52 (7%)	9 (1%)	10	40
2	C	1/7 (14%)	1 (100%)	0	0	100	100
All	All	1521/1551 (98%)	1396 (92%)	109 (7%)	16 (1%)	11	43

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	SER
1	A	408	ASN
1	B	408	ASN

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Mol	Chain	Res	Type
1	B	647	ASP
1	B	699	ASP
1	A	324	HIS
1	A	340	LEU
1	A	646	GLU
1	B	78	ARG
1	B	323	ASP
1	A	245	ARG
1	B	370	ASP
1	B	562	THR
1	B	495	ASN
1	A	653	LYS
1	B	254	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	650/650 (100%)	561 (86%)	89 (14%)	3	17
1	B	637/650 (98%)	550 (86%)	87 (14%)	3	17
2	C	1/1 (100%)	1 (100%)	0	100	100
All	All	1288/1301 (99%)	1112 (86%)	176 (14%)	3	17

All (176) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	68	ILE
1	A	71	LEU
1	A	79	ASN
1	A	83	SER
1	A	93	GLN
1	A	113	ILE
1	A	114	THR
1	A	123	SER

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Mol	Chain	Res	Type
1	A	132	ILE
1	A	133	THR
1	A	143	ASP
1	A	152	ILE
1	A	154	THR
1	A	196	THR
1	A	204	ARG
1	A	213	SER
1	A	215	ASN
1	A	232	SER
1	A	236	THR
1	A	246	VAL
1	A	248	VAL
1	A	257	THR
1	A	265	THR
1	A	276	GLU
1	A	278	LYS
1	A	295	LEU
1	A	307	VAL
1	A	312	VAL
1	A	326	GLU
1	A	329	THR
1	A	331	VAL
1	A	343	ASP
1	A	348	VAL
1	A	362	TRP
1	A	372	GLN
1	A	392	GLU
1	A	408	ASN
1	A	411	VAL
1	A	417	ASP
1	A	454	SER
1	A	459	ILE
1	A	461	LEU
1	A	466	GLN
1	A	475	VAL
1	A	494	ARG
1	A	499	THR
1	A	504	ILE
1	A	522	ILE
1	A	528	GLN
1	A	539	VAL

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Mol	Chain	Res	Type
1	A	542	ASP
1	A	551	VAL
1	A	556	VAL
1	A	557	THR
1	A	564	ARG
1	A	566	SER
1	A	578	ASP
1	A	580	ASN
1	A	596	GLN
1	A	601	ARG
1	A	606	LYS
1	A	609	GLU
1	A	618	ILE
1	A	620	ILE
1	A	633	LEU
1	A	641	GLU
1	A	645	GLU
1	A	652	SER
1	A	654	PRO
1	A	659	ILE
1	A	660	THR
1	A	669	LYS
1	A	676	GLU
1	A	683	PRO
1	A	687	VAL
1	A	704	VAL
1	A	714	SER
1	A	720	LYS
1	A	727	LYS
1	A	729	THR
1	A	730	VAL
1	A	744	VAL
1	A	758	GLU
1	A	771	ILE
1	A	772	THR
1	A	788	THR
1	A	792	ASN
1	A	811	THR
1	B	57	SER
1	B	61	GLU
1	B	68	ILE
1	B	73	ARG

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Mol	Chain	Res	Type
1	B	76	GLU
1	B	88	LYS
1	B	96	THR
1	B	106	VAL
1	B	107	ASP
1	B	117	VAL
1	B	137	LEU
1	B	140	ILE
1	B	142	GLU
1	B	148	THR
1	B	157	ARG
1	B	161	THR
1	B	163	ARG
1	B	168	SER
1	B	169	ILE
1	B	177	MET
1	B	189	MET
1	B	236	THR
1	B	240	MET
1	B	250	LYS
1	B	253	THR
1	B	265	THR
1	B	270	ARG
1	B	292	ARG
1	B	303	GLU
1	B	323	ASP
1	B	329	THR
1	B	330	SER
1	B	331	VAL
1	B	360	SER
1	B	396	ARG
1	B	411	VAL
1	B	443	ILE
1	B	447	LYS
1	B	459	ILE
1	B	462	THR
1	B	465	PHE
1	B	476	VAL
1	B	493	LEU
1	B	495	ASN
1	B	504	ILE
1	B	509	ASP

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Mol	Chain	Res	Type
1	B	510	ILE
1	B	512	LYS
1	B	517	THR
1	B	524	ASP
1	B	533	MET
1	B	551	VAL
1	B	556	VAL
1	B	562	THR
1	B	564	ARG
1	B	576	VAL
1	B	596	GLN
1	B	601	ARG
1	B	604	SER
1	B	615	ASN
1	B	618	ILE
1	B	624	TYR
1	B	628	ARG
1	B	633	LEU
1	B	641	GLU
1	B	645	GLU
1	B	646	GLU
1	B	655	THR
1	B	671	LYS
1	B	687	VAL
1	B	694	LYS
1	B	702	LYS
1	B	704	VAL
1	B	714	SER
1	B	720	LYS
1	B	722	LYS
1	B	739	LYS
1	B	742	GLN
1	B	744	VAL
1	B	750	SER
1	B	771	ILE
1	B	772	THR
1	B	788	THR
1	B	791	THR
1	B	792	ASN
1	B	810	SER
1	B	815	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	136	GLN
1	A	183	ASN
1	A	191	HIS
1	A	205	ASN
1	A	218	GLN
1	A	401	ASN
1	A	408	ASN
1	A	415	GLN
1	A	424	HIS
1	A	455	ASN
1	A	492	ASN
1	A	495	ASN
1	A	505	ASN
1	A	580	ASN
1	A	596	GLN
1	A	615	ASN
1	A	737	GLN
1	B	53	GLN
1	B	60	GLN
1	B	176	ASN
1	B	183	ASN
1	B	401	ASN
1	B	415	GLN
1	B	418	HIS
1	B	472	HIS
1	B	538	ASN
1	B	544	ASN
1	B	560	ASN
1	B	596	GLN
1	B	605	ASN
1	B	614	GLN
1	B	615	ASN
1	B	630	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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	AHO	C	8	6,2	9,11,12	7.85	1 (11%)	4,13,15	2.14	1 (25%)
2	ORN	C	6	2	6,7,8	0.94	0	2,7,9	0.89	0
2	AHO	C	5	6,2	9,11,12	7.53	1 (11%)	4,13,15	1.52	1 (25%)

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	AHO	C	8	6,2	-	4/11/12/14	-
2	ORN	C	6	2	-	1/5/6/8	-
2	AHO	C	5	6,2	-	5/11/12/14	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	8	AHO	O2-N2	-23.50	1.22	1.40
2	C	5	AHO	O2-N2	-22.43	1.23	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	8	AHO	O2-N2-C5	4.13	123.45	113.76
2	C	5	AHO	O2-N2-C5	2.74	120.18	113.76

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	5	AHO	C4-C3-CA-C
2	C	5	AHO	C4-C5-N2-O2
2	C	5	AHO	C4-C5-N2-C6
2	C	6	ORN	NE-CD-CG-CB
2	C	5	AHO	C7-C6-N2-O2
2	C	8	AHO	C7-C6-N2-O2
2	C	8	AHO	C3-C4-C5-N2
2	C	8	AHO	CA-C3-C4-C5
2	C	5	AHO	O3-C6-N2-O2
2	C	8	AHO	O3-C6-N2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	8	AHO	2	0
2	C	6	ORN	2	0
2	C	5	AHO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 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	PO4	A	1820	-	4,4,4	0.82	0	6,6,6	1.04	0
3	N8E	A	1817[B]	-	23,23,23	0.78	0	22,22,22	0.71	0
4	PO4	A	1819	-	4,4,4	0.93	0	6,6,6	1.24	1 (16%)
4	PO4	B	1818	-	4,4,4	0.37	0	6,6,6	1.50	1 (16%)
4	PO4	B	1819	-	4,4,4	1.11	0	6,6,6	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PO4	A	1823	-	4,4,4	1.18	0	6,6,6	0.52	0
4	PO4	A	1822	-	4,4,4	0.98	0	6,6,6	0.58	0
3	N8E	A	1816	-	23,23,23	0.63	0	22,22,22	0.56	0
4	PO4	A	1818	-	4,4,4	0.75	0	6,6,6	0.98	0
3	N8E	A	1817[A]	-	23,23,23	0.81	0	22,22,22	0.67	0
4	PO4	B	1820	-	4,4,4	0.69	0	6,6,6	1.03	0
4	PO4	B	1821	-	4,4,4	0.90	0	6,6,6	0.67	0
5	PVE	C	1	6,2	27,28,29	2.62	5 (18%)	31,40,42	3.89	14 (45%)
4	PO4	A	1821	-	4,4,4	0.68	0	6,6,6	1.45	2 (33%)

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
3	N8E	A	1816	-	-	10/21/21/21	-
3	N8E	A	1817[A]	-	-	13/21/21/21	-
3	N8E	A	1817[B]	-	-	14/21/21/21	-
5	PVE	C	1	6,2	-	9/11/21/23	0/2/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	1	PVE	C20-C18	10.70	1.72	1.51
5	C	1	PVE	OXT-C15	-4.27	1.24	1.42
5	C	1	PVE	C5-C6	4.23	1.41	1.37
5	C	1	PVE	C21-C22	2.67	1.56	1.50
5	C	1	PVE	C9-N1	-2.28	1.37	1.39

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1	PVE	C20-C18-N17	-14.13	90.01	114.59
5	C	1	PVE	O19-C18-C20	9.85	139.86	122.02
5	C	1	PVE	C13-C12-N11	-6.49	100.39	110.04
5	C	1	PVE	C20-C21-C22	4.86	126.57	113.67
5	C	1	PVE	C13-C14-N1	3.45	113.63	108.29
5	C	1	PVE	C12-C13-C14	-3.27	107.88	110.44
5	C	1	PVE	OXT-C15-C14	3.24	124.57	112.09
5	C	1	PVE	O24-C22-C21	2.97	123.39	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1818	PO4	O4-P-O3	2.95	117.09	107.91
5	C	1	PVE	C8-C7-C6	2.60	121.53	119.87
4	A	1819	PO4	O4-P-O2	2.60	115.99	107.91
5	C	1	PVE	C10-C9-N1	2.60	120.72	118.51
5	C	1	PVE	O24-C22-O23	-2.56	116.75	123.33
5	C	1	PVE	C3-N17-C18	2.27	134.22	126.61
4	A	1821	PO4	O4-P-O3	2.24	114.89	107.91
5	C	1	PVE	O19-C18-N17	2.19	127.56	123.64
4	A	1821	PO4	O4-P-O1	-2.17	103.27	110.95
5	C	1	PVE	C3-C2-N11	-2.11	117.48	122.87

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1	PVE	C18-C20-C21-C22
5	C	1	PVE	C13-C14-C15-OXT
3	A	1817[A]	N8E	O15-C16-C17-O18
3	A	1817[A]	N8E	O18-C19-C20-O21
3	A	1817[B]	N8E	O18-C19-C20-O21
3	A	1817[A]	N8E	O09-C10-C11-O12
3	A	1817[B]	N8E	O15-C16-C17-O18
3	A	1816	N8E	O12-C13-C14-O15
3	A	1817[B]	N8E	C06-C07-C08-O09
3	A	1817[B]	N8E	O12-C13-C14-O15
3	A	1816	N8E	O21-C22-C23-O24
3	A	1817[A]	N8E	O12-C13-C14-O15
3	A	1817[B]	N8E	C02-C03-C04-C05
3	A	1817[B]	N8E	O21-C22-C23-O24
5	C	1	PVE	O19-C18-C20-C21
3	A	1816	N8E	O15-C16-C17-O18
3	A	1817[A]	N8E	C02-C03-C04-C05
3	A	1817[B]	N8E	C10-C11-O12-C13
5	C	1	PVE	N1-C14-C15-OXT
3	A	1817[B]	N8E	C20-C19-O18-C17
3	A	1817[B]	N8E	C23-C22-O21-C20
3	A	1817[B]	N8E	C19-C20-O21-C22
3	A	1817[A]	N8E	C20-C19-O18-C17
3	A	1817[A]	N8E	C14-C13-O12-C11
3	A	1817[B]	N8E	C03-C04-C05-C06
3	A	1817[B]	N8E	C13-C14-O15-C16
3	A	1817[B]	N8E	O09-C10-C11-O12

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Mol	Chain	Res	Type	Atoms
3	A	1817[A]	N8E	O21-C22-C23-O24
3	A	1816	N8E	C16-C17-O18-C19
3	A	1817[A]	N8E	C03-C04-C05-C06
3	A	1817[A]	N8E	C17-C16-O15-C14
3	A	1816	N8E	C07-C08-O09-C10
3	A	1817[A]	N8E	C10-C11-O12-C13
3	A	1816	N8E	C04-C05-C06-C07
3	A	1816	N8E	C19-C20-O21-C22
5	C	1	PVE	C2-C3-N17-C18
5	C	1	PVE	C4-C3-N17-C18
3	A	1817[A]	N8E	C01-C02-C03-C04
3	A	1816	N8E	O09-C10-C11-O12
5	C	1	PVE	N17-C18-C20-C21
3	A	1816	N8E	C14-C13-O12-C11
3	A	1816	N8E	C17-C16-O15-C14
3	A	1817[A]	N8E	C05-C06-C07-C08
3	A	1817[B]	N8E	C11-C10-O09-C08
5	C	1	PVE	C20-C21-C22-O23
5	C	1	PVE	C20-C21-C22-O24

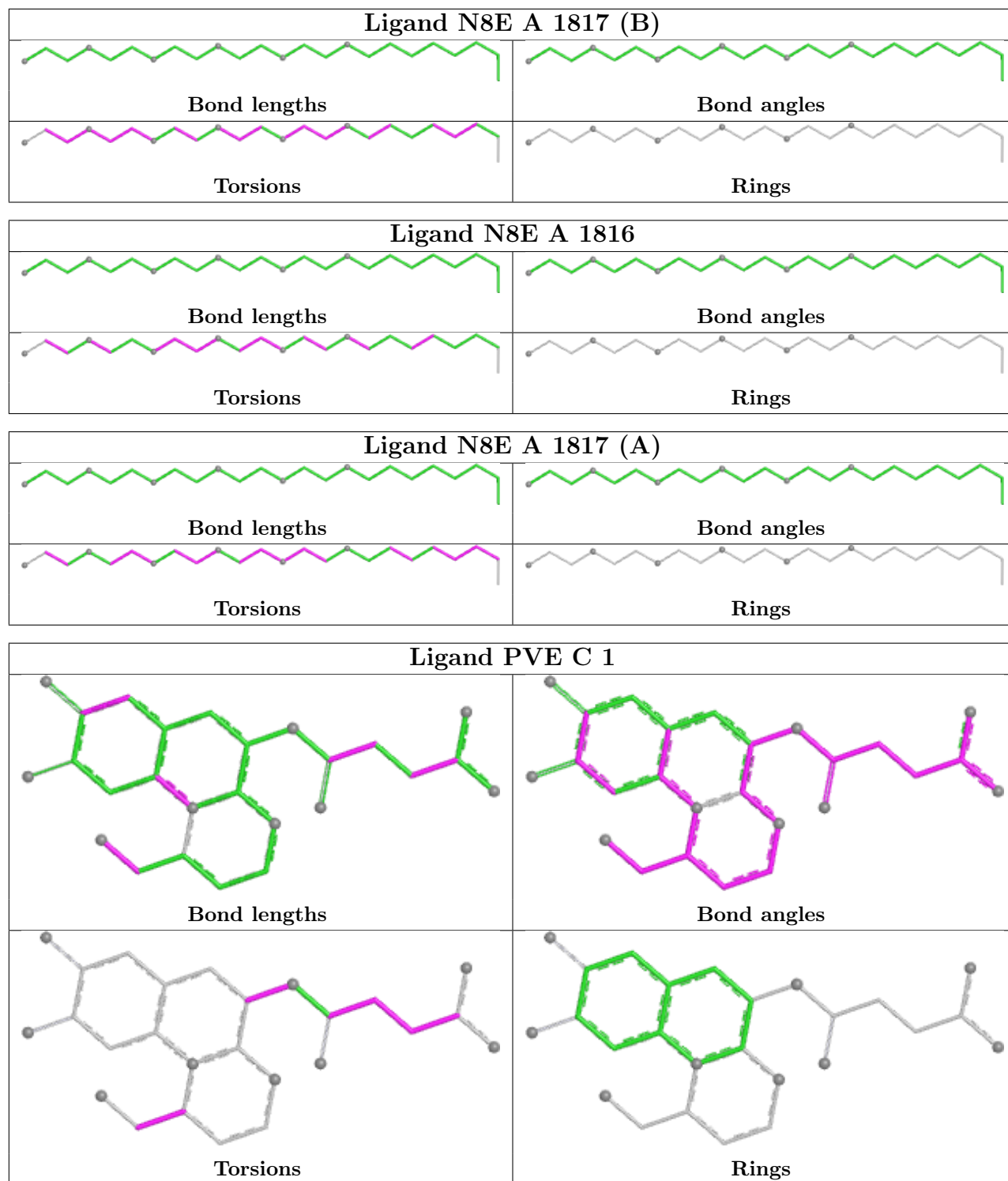
There are no ring outliers.

8 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1817[B]	N8E	6	0
4	B	1819	PO4	1	0
4	A	1823	PO4	1	0
3	A	1816	N8E	2	0
4	A	1818	PO4	1	0
3	A	1817[A]	N8E	9	0
4	B	1821	PO4	1	0
5	C	1	PVE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	772/772 (100%)	-0.27	10 (1%) 75 53	15, 27, 40, 58	0
1	B	754/772 (97%)	-0.09	9 (1%) 76 55	19, 33, 47, 58	0
2	C	2/7 (28%)	1.69	0 100 100	46, 46, 46, 50	0
All	All	1528/1551 (98%)	-0.18	19 (1%) 76 55	15, 30, 45, 58	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	123	SER	6.1
1	A	44	GLN	3.8
1	A	599	TRP	3.1
1	A	87	GLY	3.0
1	B	698	ASP	2.7
1	B	471	GLU	2.6
1	B	773	ASP	2.6
1	B	155	ALA	2.6
1	A	121	ALA	2.5
1	A	276	GLU	2.5
1	A	79	ASN	2.5
1	B	699	ASP	2.4
1	A	379	SER	2.4
1	A	124	SER	2.3
1	B	533	MET	2.2
1	B	154	THR	2.1
1	A	122	ASP	2.1
1	B	109	GLN	2.1
1	B	78	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
2	ORN	C	6	8/9	0.79	0.17	47,48,48,50	0
2	DAS	C	7	8/9	0.85	0.18	45,49,49,52	0
2	AHO	C	5	12/13	0.94	0.12	37,41,46,46	0
2	DSN	C	3	6/7	0.95	0.14	44,44,44,45	0
2	AHO	C	8	12/13	0.97	0.07	36,40,49,49	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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. 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.

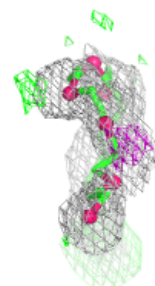
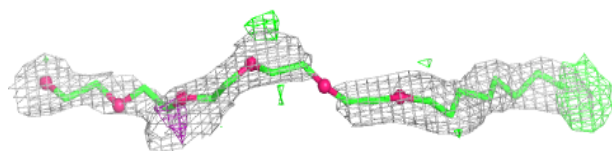
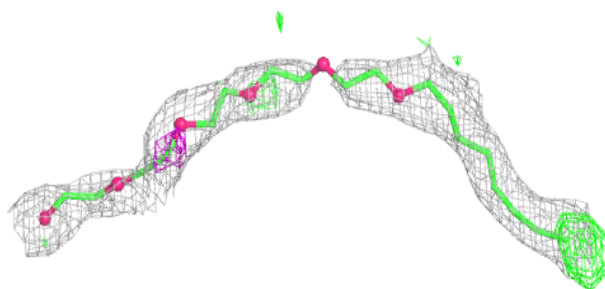
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	N8E	A	1817[A]	24/24	0.81	0.21	2,9,12,15	24
3	N8E	A	1817[B]	24/24	0.81	0.21	2,7,12,14	24
4	PO4	A	1821	5/5	0.86	0.15	62,63,63,63	0
4	PO4	A	1822	5/5	0.87	0.18	84,84,86,87	0
3	N8E	A	1816	24/24	0.88	0.15	47,49,81,82	0
4	PO4	B	1818	5/5	0.89	0.18	55,56,57,58	0
4	PO4	B	1820	5/5	0.92	0.14	64,64,66,67	0
4	PO4	A	1818	5/5	0.93	0.14	48,49,51,51	0
4	PO4	B	1821	5/5	0.94	0.12	42,44,45,47	0
4	PO4	B	1819	5/5	0.95	0.12	40,43,44,45	0
5	PVE	C	1	26/27	0.95	0.10	35,37,52,53	5
4	PO4	A	1820	5/5	0.96	0.12	66,66,66,66	0
4	PO4	A	1823	5/5	0.97	0.13	59,60,61,61	0
4	PO4	A	1819	5/5	0.98	0.12	28,29,33,34	0
6	FE	C	2	1/1	1.00	0.04	33,33,33,33	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

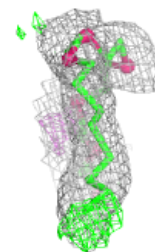
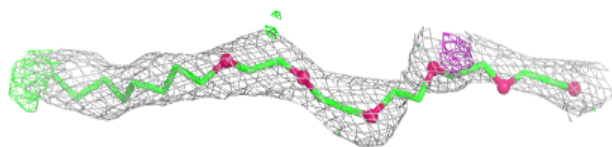
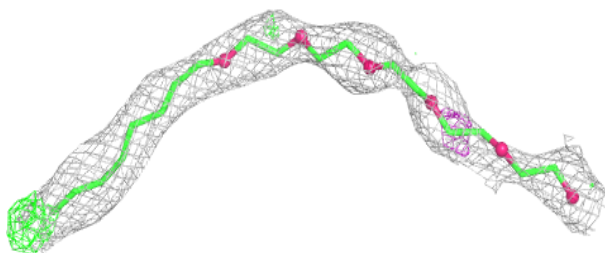
Electron density around N8E A 1817 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



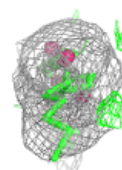
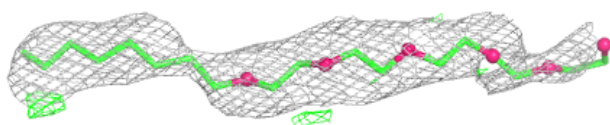
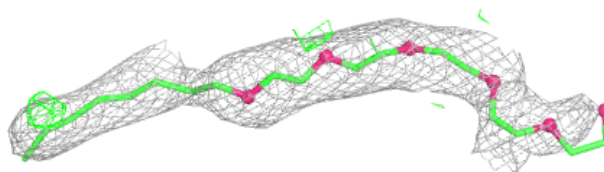
Electron density around N8E A 1817 (B):

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and green (positive)

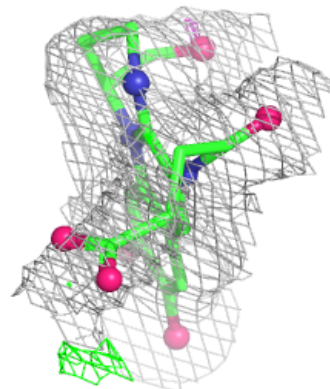
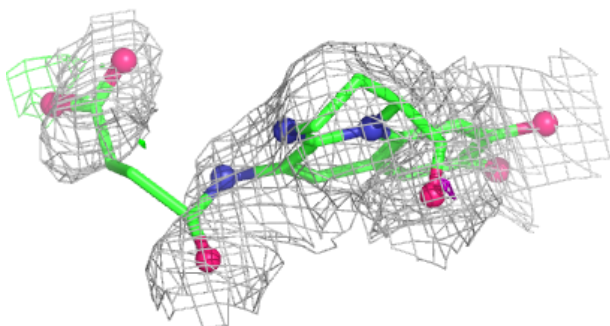
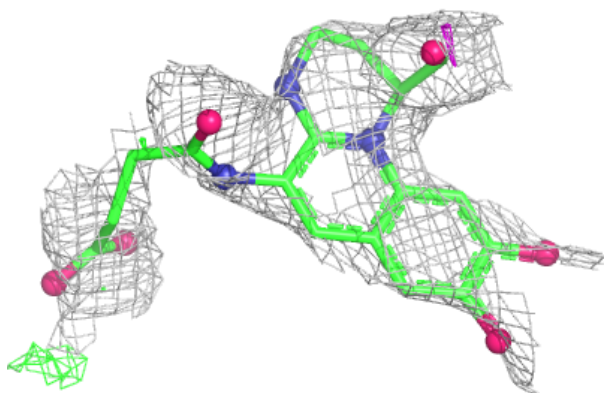


Electron density around N8E A 1816:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around PVE C 1:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.