



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:26 PM UTC

PDB ID : 2Y5D / pdb_00002y5d
Title : Crystal structure of C296A mutant of the box pathway encoded ALDH from Burkholderia xenovorans LB400
Authors : Bains, J.; Leon, R.; Temke, K.G.; Boulanger, M.J.
Deposited on : 2011-01-12
Resolution : 1.40 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

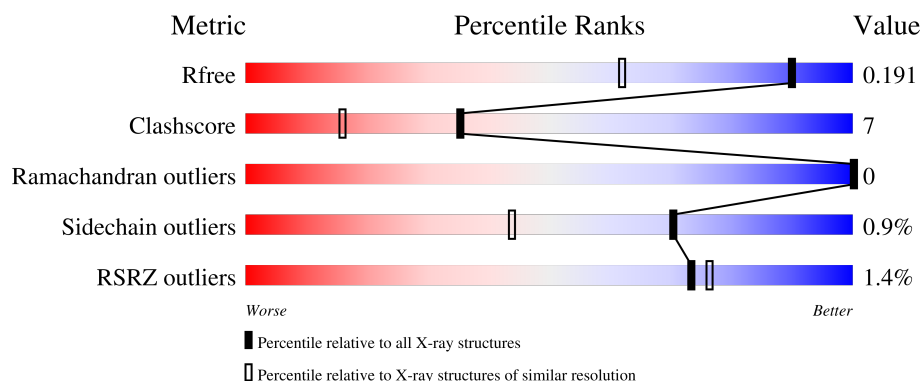
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (1.40-1.40)

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	534	
1	B	534	

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
3	P6G	A	1524	-	X	-	-
3	P6G	B	1532	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9349 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 ALDEHYDE DEHYDROGENASE (BOX PATHWAY).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	521	Total	C	N	O	S	0	1	0
			3845	2413	695	728	9			
1	B	527	Total	C	N	O	S	0	0	0
			3884	2440	702	733	9			

There are 8 discrepancies between the modelled and reference sequences:

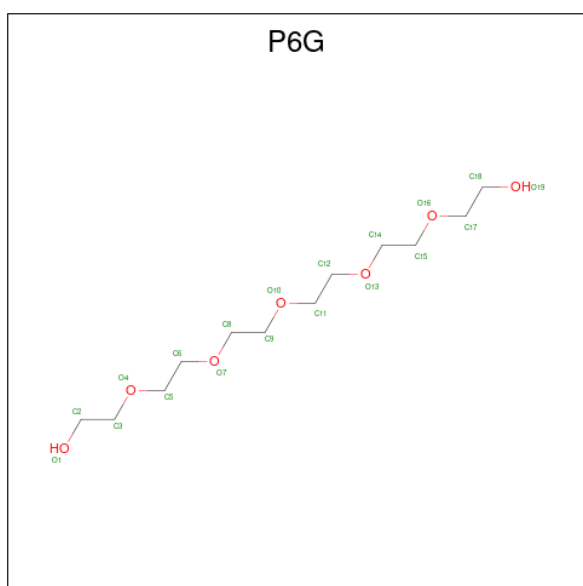
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q13WK4
A	-1	SER	-	expression tag	UNP Q13WK4
A	0	HIS	-	expression tag	UNP Q13WK4
A	296	ALA	CYS	engineered mutation	UNP Q13WK4
B	-2	GLY	-	expression tag	UNP Q13WK4
B	-1	SER	-	expression tag	UNP Q13WK4
B	0	HIS	-	expression tag	UNP Q13WK4
B	296	ALA	CYS	engineered mutation	UNP Q13WK4

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			19	12	7		
3	B	1	Total	C	O	0	0
			19	12	7		

- # NAP

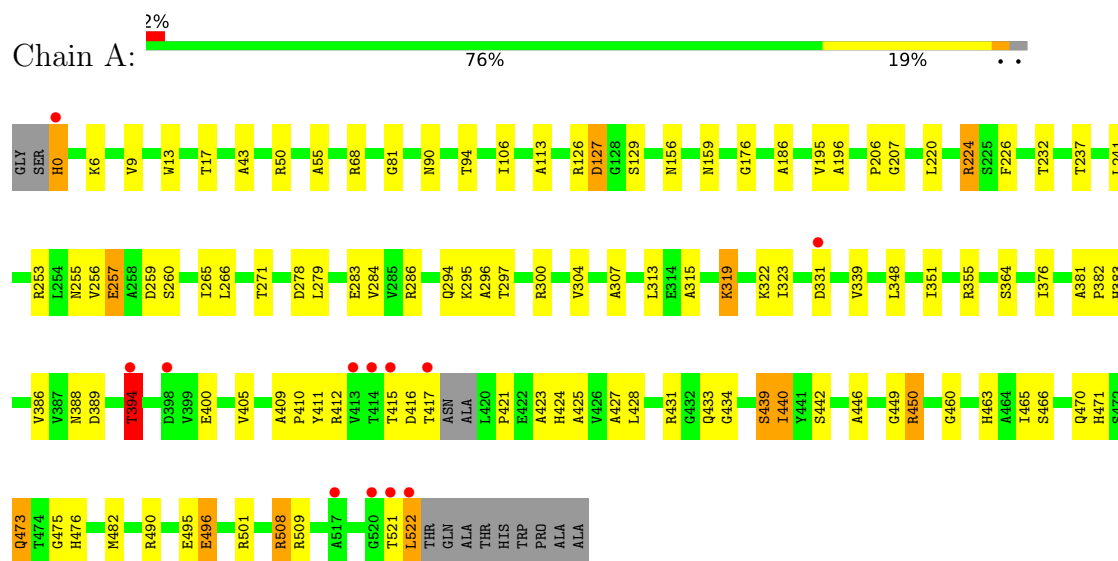
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	730	Total O 730 730	0	0
5	B	744	Total O 744 744	0	0

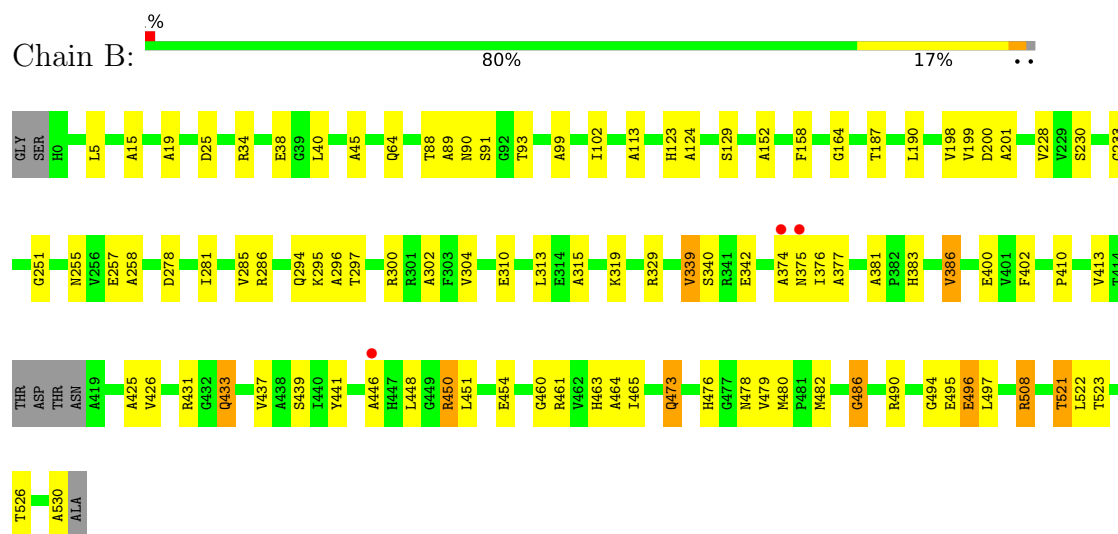
3 Residue-property plots

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: ALDEHYDE DEHYDROGENASE (BOX PATHWAY)



• Molecule 1: ALDEHYDE DEHYDROGENASE (BOX PATHWAY)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.00Å 67.70Å 77.54Å 111.09° 90.62° 113.36°	Depositor
Resolution (Å)	31.33 – 1.40 31.33 – 1.40	Depositor EDS
% Data completeness (in resolution range)	96.0 (31.33-1.40) 91.0 (31.33-1.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.160 , 0.193 0.159 , 0.191	Depositor DCC
R_{free} test set	8938 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	12.5	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9349	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.95% 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: NAP, GOL, P6G

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	1.97	67/3918 (1.7%)	1.58	31/5334 (0.6%)
1	B	1.91	61/3958 (1.5%)	1.59	24/5392 (0.4%)
All	All	1.94	128/7876 (1.6%)	1.59	55/10726 (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

All (128) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	425	ALA	CA-CB	-11.94	1.34	1.53
1	A	224	ARG	CG-CD	-10.28	1.21	1.52
1	A	271	THR	CA-CB	10.17	1.66	1.53
1	A	440	ILE	N-CA	8.60	1.56	1.46
1	A	427	ALA	N-CA	-8.39	1.36	1.46
1	A	394	THR	C-O	8.23	1.33	1.23
1	B	34	ARG	CA-C	-7.79	1.43	1.52
1	B	340	SER	CA-C	-7.60	1.43	1.52
1	A	427	ALA	CA-CB	7.44	1.65	1.53
1	B	129	SER	C-O	7.22	1.33	1.23
1	A	304	VAL	CA-C	7.18	1.60	1.52
1	A	410	PRO	C-O	-7.13	1.15	1.23
1	A	442	SER	N-CA	7.10	1.54	1.45
1	A	473	GLN	N-CA	7.07	1.54	1.46
1	B	464	ALA	CA-CB	-7.04	1.43	1.53
1	B	508	ARG	CD-NE	-7.00	1.36	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	206	PRO	N-CA	-6.95	1.38	1.47
1	B	494	GLY	N-CA	6.89	1.51	1.44
1	B	376	ILE	CA-C	6.85	1.59	1.52
1	B	523	THR	N-CA	-6.81	1.38	1.46
1	B	201	ALA	C-O	6.75	1.32	1.24
1	A	13	TRP	C-O	6.74	1.32	1.24
1	B	482	MET	SD-CE	-6.73	1.62	1.79
1	B	90	ASN	CG-OD1	6.63	1.36	1.23
1	B	451	LEU	CA-C	6.62	1.61	1.52
1	A	9	VAL	C-O	6.59	1.30	1.24
1	B	315	ALA	N-CA	-6.57	1.38	1.46
1	B	90	ASN	CG-ND2	-6.56	1.19	1.33
1	B	454	GLU	N-CA	-6.55	1.37	1.46
1	B	496	GLU	CD-OE2	-6.48	1.13	1.25
1	B	441	TYR	N-CA	6.47	1.54	1.46
1	A	411	TYR	N-CA	6.39	1.53	1.45
1	B	45	ALA	C-O	6.38	1.31	1.24
1	A	127	ASP	CA-C	-6.38	1.44	1.53
1	A	465	ILE	CA-C	6.25	1.60	1.52
1	B	38	GLU	N-CA	6.22	1.54	1.46
1	A	466	SER	C-N	6.22	1.41	1.33
1	A	50	ARG	N-CA	6.18	1.53	1.46
1	A	295	LYS	CA-C	-6.15	1.45	1.52
1	A	496	GLU	CD-OE2	-6.14	1.13	1.25
1	B	93	THR	N-CA	6.13	1.53	1.45
1	B	433	GLN	CG-CD	-6.08	1.36	1.52
1	B	152	ALA	CA-C	-6.07	1.45	1.52
1	A	43	ALA	CA-CB	6.04	1.62	1.53
1	A	405	VAL	CA-CB	-6.01	1.46	1.54
1	A	50	ARG	CZ-NH1	6.01	1.41	1.32
1	A	156	ASN	CA-C	-6.00	1.45	1.52
1	B	230	SER	CA-C	-5.99	1.45	1.52
1	B	497	LEU	N-CA	5.97	1.53	1.46
1	A	94	THR	N-CA	5.96	1.53	1.45
1	A	382	PRO	C-O	5.96	1.31	1.23
1	A	55	ALA	CA-C	5.90	1.60	1.52
1	B	465	ILE	CA-C	5.90	1.59	1.52
1	A	237	THR	N-CA	-5.89	1.39	1.46
1	B	450	ARG	CA-CB	5.87	1.62	1.53
1	A	412	ARG	N-CA	5.82	1.53	1.46
1	B	523	THR	CA-C	5.82	1.60	1.52
1	B	486	GLY	CA-C	-5.80	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	228	VAL	C-O	5.78	1.29	1.24
1	A	195	VAL	CA-CB	-5.78	1.47	1.54
1	A	424	HIS	CA-C	5.77	1.60	1.52
1	B	124	ALA	C-O	5.75	1.30	1.23
1	A	421	PRO	N-CA	5.73	1.54	1.47
1	A	196	ALA	CA-C	-5.68	1.45	1.52
1	A	319	LYS	CA-C	5.64	1.60	1.52
1	A	482	MET	CG-SD	5.60	1.94	1.80
1	B	339	VAL	CA-CB	-5.58	1.47	1.54
1	B	5	LEU	N-CA	5.58	1.52	1.46
1	B	342	GLU	CD-OE1	5.57	1.35	1.25
1	A	364	SER	N-CA	5.56	1.52	1.46
1	B	187	THR	CA-C	-5.55	1.46	1.53
1	A	449	GLY	N-CA	5.54	1.52	1.45
1	B	433	GLN	N-CA	5.51	1.53	1.46
1	A	279	LEU	N-CA	5.50	1.53	1.46
1	B	374	ALA	CA-C	-5.50	1.45	1.52
1	B	190	LEU	N-CA	5.50	1.53	1.46
1	B	375	ASN	CB-CG	5.48	1.65	1.52
1	B	199	VAL	C-O	5.48	1.30	1.24
1	A	442	SER	C-N	5.48	1.42	1.33
1	A	315	ALA	CA-CB	5.48	1.61	1.53
1	A	307	ALA	N-CA	5.47	1.53	1.46
1	A	323	ILE	N-CA	5.47	1.53	1.46
1	B	329	ARG	NE-CZ	5.46	1.39	1.33
1	A	496	GLU	CA-CB	5.45	1.63	1.53
1	A	176	GLY	C-N	5.44	1.37	1.32
1	B	281	ILE	C-O	5.43	1.30	1.24
1	B	482	MET	CG-SD	5.41	1.94	1.80
1	B	200	ASP	CG-OD2	5.40	1.35	1.25
1	B	19	ALA	CA-CB	-5.36	1.44	1.53
1	A	156	ASN	N-CA	5.36	1.52	1.45
1	B	198	VAL	CA-CB	5.36	1.61	1.54
1	A	17	THR	CA-CB	5.35	1.61	1.53
1	A	81	GLY	N-CA	5.35	1.52	1.45
1	A	106	ILE	CA-CB	-5.34	1.47	1.54
1	B	302	ALA	N-CA	5.33	1.52	1.46
1	A	253	ARG	N-CA	5.32	1.52	1.46
1	B	286	ARG	C-O	5.32	1.30	1.24
1	A	257	GLU	CA-C	-5.32	1.46	1.52
1	A	186	ALA	CA-CB	-5.31	1.44	1.53
1	B	91	SER	CA-C	-5.31	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	425	ALA	N-CA	5.30	1.52	1.46
1	B	64	GLN	N-CA	5.29	1.52	1.46
1	B	187	THR	C-O	5.28	1.31	1.23
1	A	434	GLY	N-CA	5.26	1.53	1.45
1	A	257	GLU	C-O	5.26	1.30	1.24
1	A	424	HIS	CA-CB	5.25	1.61	1.53
1	A	129	SER	C-O	5.25	1.30	1.23
1	A	501	ARG	CZ-NH2	5.24	1.40	1.33
1	B	413	VAL	CA-CB	-5.23	1.48	1.54
1	B	526	THR	C-O	5.20	1.30	1.23
1	A	304	VAL	C-O	-5.19	1.20	1.24
1	A	90	ASN	CG-ND2	-5.17	1.22	1.33
1	B	295	LYS	N-CA	5.15	1.52	1.46
1	B	251	GLY	N-CA	5.13	1.52	1.45
1	A	266	LEU	CA-C	5.13	1.59	1.52
1	A	475	GLY	C-N	-5.12	1.27	1.33
1	B	446	ALA	N-CA	5.12	1.53	1.46
1	B	40	LEU	CA-CB	5.11	1.61	1.53
1	B	164	GLY	N-CA	5.10	1.52	1.45
1	B	152	ALA	C-O	5.10	1.29	1.24
1	A	284	VAL	CA-CB	5.08	1.60	1.54
1	B	473	GLN	CA-C	5.08	1.59	1.52
1	B	386	VAL	CA-C	-5.06	1.46	1.52
1	A	256	VAL	C-O	5.06	1.29	1.24
1	A	423	ALA	CA-CB	5.05	1.61	1.53
1	A	460	GLY	N-CA	5.04	1.52	1.45
1	A	482	MET	SD-CE	-5.00	1.67	1.79
1	B	377	ALA	C-N	-5.00	1.26	1.33

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	508	ARG	NE-CZ-NH1	-13.65	107.85	121.50
1	A	304	VAL	O-C-N	13.06	129.92	121.69
1	B	508	ARG	NE-CZ-NH2	12.70	130.63	119.20
1	B	508	ARG	CD-NE-CZ	9.18	137.25	124.40
1	A	389	ASP	CA-C-N	-8.49	110.98	119.56
1	A	389	ASP	C-N-CA	-8.49	110.98	119.56
1	B	508	ARG	CB-CG-CD	-8.03	92.83	111.30
1	B	102	ILE	O-C-N	7.83	130.32	121.94
1	B	375	ASN	N-CA-C	7.37	121.86	113.02
1	B	376	ILE	O-C-N	7.11	129.22	121.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	412	ARG	CG-CD-NE	-6.94	96.72	112.00
1	A	207	GLY	CA-C-O	-6.89	112.10	119.27
1	A	466	SER	CA-C-O	6.88	126.69	120.71
1	A	300	ARG	NE-CZ-NH2	-6.85	113.04	119.20
1	A	304	VAL	CA-C-N	-6.43	113.33	119.89
1	A	304	VAL	C-N-CA	-6.43	113.33	119.89
1	A	442	SER	CA-C-O	6.41	128.25	121.33
1	B	88	THR	N-CA-C	-6.39	104.23	111.07
1	A	351	ILE	N-CA-C	-6.29	104.62	110.53
1	A	279	LEU	CA-C-N	6.17	128.46	120.44
1	A	279	LEU	C-N-CA	6.17	128.46	120.44
1	A	428	LEU	O-C-N	6.10	128.58	122.12
1	B	374	ALA	CA-C-N	-6.05	112.15	122.56
1	B	374	ALA	C-N-CA	-6.05	112.15	122.56
1	A	279	LEU	CA-C-O	-5.88	114.31	120.55
1	B	426	VAL	N-CA-C	-5.86	104.80	110.72
1	B	508	ARG	CG-CD-NE	-5.82	99.19	112.00
1	A	113	ALA	N-CA-C	-5.79	104.88	111.07
1	B	374	ALA	N-CA-C	-5.71	105.57	112.54
1	B	15	ALA	N-CA-C	5.64	118.63	110.28
1	A	260	SER	N-CA-CB	-5.63	101.37	110.71
1	A	388	ASN	N-CA-C	5.54	118.24	111.82
1	B	448	LEU	CB-CA-C	-5.54	101.60	110.79
1	B	99	ALA	N-CA-C	5.53	118.06	111.71
1	A	265	ILE	CA-C-O	5.50	126.11	120.39
1	B	200	ASP	CB-CA-C	-5.49	100.47	110.63
1	A	259	ASP	CB-CA-C	-5.47	100.63	109.72
1	A	266	LEU	O-C-N	5.43	129.37	123.13
1	B	199	VAL	N-CA-C	-5.37	105.49	110.53
1	B	425	ALA	CA-C-O	-5.28	114.95	120.55
1	A	283	GLU	N-CA-C	-5.24	105.25	111.69
1	B	300	ARG	NE-CZ-NH2	-5.23	114.49	119.20
1	A	409	ALA	CA-C-O	5.22	125.66	120.28
1	A	439	SER	CA-C-O	5.20	127.04	121.16
1	A	348	LEU	CA-C-O	-5.19	115.05	120.55
1	A	522	LEU	CA-CB-CG	5.17	134.41	116.30
1	A	376	ILE	O-C-N	5.16	126.57	121.98
1	B	521	THR	CA-C-N	-5.11	111.99	120.68
1	B	521	THR	C-N-CA	-5.11	111.99	120.68
1	A	450	ARG	N-CA-C	5.04	116.85	111.36
1	B	113	ALA	N-CA-C	-5.04	105.79	111.28
1	A	431	ARG	N-CA-C	5.02	118.89	112.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	351	ILE	CA-C-O	-5.01	115.49	121.05
1	A	389	ASP	O-C-N	5.01	125.88	121.37
1	B	102	ILE	N-CA-C	5.00	115.12	110.42

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	508	ARG	Sidechain

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	3845	0	3860	52	0
1	B	3884	0	3890	47	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
3	A	19	0	26	8	0
3	B	19	0	26	11	0
4	A	48	0	25	5	0
4	B	48	0	24	7	0
5	A	730	0	0	32	0
5	B	744	0	0	23	0
All	All	9349	0	7867	116	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 7.

All (116) 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)
3:B:1532:P6G:C8	3:B:1532:P6G:O7	1.71	1.36
1:B:278:ASP:HB3	5:B:2475:HOH:O	1.31	1.31
1:B:530:ALA:C	5:B:2732:HOH:O	1.76	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:MET:HG2	5:B:2682:HOH:O	1.47	1.14
3:A:1524:P6G:H111	5:A:2259:HOH:O	1.51	1.08
1:A:400:GLU:OE2	5:A:2611:HOH:O	1.72	1.04
3:B:1532:P6G:C8	3:B:1532:P6G:C6	2.35	1.04
1:A:509[B]:ARG:NH2	5:A:2709:HOH:O	1.65	1.01
4:B:1533:NAP:H4N	5:B:2739:HOH:O	0.82	0.98
1:A:416:ASP:HB3	5:A:2630:HOH:O	1.67	0.92
1:A:0:HIS:ND1	1:A:0:HIS:O	2.04	0.89
1:B:310:GLU:HG2	5:B:2495:HOH:O	1.72	0.88
1:A:490:ARG:NE	5:A:2682:HOH:O	2.12	0.82
3:B:1532:P6G:H111	5:B:2269:HOH:O	1.78	0.82
1:B:450:ARG:NH2	5:B:2662:HOH:O	2.11	0.82
1:A:255:ASN:HD21	1:A:495:GLU:H	1.28	0.81
1:B:255:ASN:HD21	1:B:495:GLU:H	1.28	0.79
1:B:480:MET:HE1	3:B:1532:P6G:C12	2.16	0.76
1:A:68:ARG:NH1	5:A:2181:HOH:O	2.19	0.74
1:A:127:ASP:OD2	1:A:509[A]:ARG:NH1	2.21	0.74
3:B:1532:P6G:C8	3:B:1532:P6G:H62	2.17	0.74
1:B:383:HIS:HE1	5:B:2565:HOH:O	1.76	0.68
1:B:522:LEU:C	1:B:522:LEU:HD12	2.18	0.68
3:A:1524:P6G:H142	5:A:2721:HOH:O	1.92	0.68
1:A:522:LEU:HG	5:A:2304:HOH:O	1.93	0.68
1:A:417:THR:HA	5:A:2629:HOH:O	1.95	0.66
1:A:159:ASN:OD1	4:A:1525:NAP:H5N	1.95	0.66
1:B:480:MET:HE1	3:B:1532:P6G:H122	1.78	0.66
1:A:415:THR:C	5:A:2628:HOH:O	2.39	0.65
1:A:0:HIS:ND1	1:A:0:HIS:C	2.55	0.64
1:B:439:SER:OG	1:B:476:HIS:HD2	1.81	0.64
1:A:313:LEU:HD21	1:A:386:VAL:HG22	1.81	0.63
1:A:294:GLN:HE22	1:A:339:VAL:H	1.48	0.61
1:A:439:SER:OG	1:A:476:HIS:HD2	1.84	0.61
4:B:1533:NAP:C4N	5:B:2739:HOH:O	1.66	0.61
1:A:381:ALA:O	1:A:383:HIS:HD2	1.84	0.60
3:A:1524:P6G:H121	5:A:2720:HOH:O	2.02	0.59
1:B:490:ARG:NE	5:B:2690:HOH:O	2.36	0.59
1:A:415:THR:HG22	5:A:2627:HOH:O	2.03	0.58
1:B:294:GLN:HE22	1:B:339:VAL:H	1.48	0.58
1:A:6:LYS:NZ	5:A:2030:HOH:O	2.34	0.57
1:A:278:ASP:CG	5:A:2473:HOH:O	2.47	0.57
1:B:508:ARG:CD	5:B:2713:HOH:O	2.52	0.57
1:A:257:GLU:OE2	1:A:496:GLU:HG3	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:ARG:HD3	5:B:2713:HOH:O	2.04	0.56
1:B:480:MET:HE2	3:B:1532:P6G:H112	1.88	0.55
1:B:463:HIS:HE1	1:B:473:GLN:OE1	1.90	0.55
1:A:355:ARG:HG2	5:A:2558:HOH:O	2.06	0.55
1:A:296:ALA:HB2	4:A:1525:NAP:C2N	2.37	0.55
1:A:509[B]:ARG:NH1	5:A:2707:HOH:O	2.39	0.53
4:A:1525:NAP:C2D	5:A:2723:HOH:O	2.56	0.53
1:A:490:ARG:CD	5:A:2682:HOH:O	2.52	0.53
1:A:232:THR:CG2	4:A:1525:NAP:C3N	2.87	0.53
1:A:286:ARG:NH1	5:A:2480:HOH:O	2.24	0.53
1:B:381:ALA:O	1:B:383:HIS:HD2	1.92	0.52
1:B:313:LEU:HD21	1:B:386:VAL:HG22	1.90	0.52
4:A:1525:NAP:H2D	5:A:2723:HOH:O	2.09	0.51
1:B:123:HIS:HE1	5:B:2292:HOH:O	1.92	0.51
1:A:313:LEU:HD21	1:A:386:VAL:CG2	2.39	0.51
1:B:257:GLU:OE2	1:B:496:GLU:HG3	2.10	0.51
1:A:220:LEU:HD11	1:A:241:LEU:HG	1.93	0.50
1:A:297:THR:O	1:A:476:HIS:HE1	1.95	0.50
1:B:490:ARG:HD3	5:B:2690:HOH:O	2.10	0.50
1:A:226:PHE:HE2	5:B:2648:HOH:O	1.95	0.49
1:A:490:ARG:HD3	5:A:2682:HOH:O	2.11	0.49
1:B:400:GLU:OE2	5:B:2615:HOH:O	2.19	0.49
1:B:478:ASN:ND2	5:B:2681:HOH:O	2.46	0.49
1:A:255:ASN:HD21	1:A:495:GLU:N	2.03	0.49
3:A:1524:P6G:H152	5:A:2720:HOH:O	2.11	0.49
1:A:446:ALA:HB1	1:B:521:THR:HG21	1.95	0.48
1:A:463:HIS:HE1	1:A:473:GLN:OE1	1.97	0.48
3:B:1532:P6G:O7	3:B:1532:P6G:C9	2.54	0.48
1:A:297:THR:O	1:A:476:HIS:CE1	2.66	0.48
1:A:433:GLN:HA	1:A:433:GLN:HE21	1.79	0.47
1:B:296:ALA:HB2	4:B:1533:NAP:C3N	2.45	0.47
3:A:1524:P6G:H122	5:A:2259:HOH:O	2.14	0.47
1:A:126:ARG:NH2	5:A:2305:HOH:O	2.44	0.46
1:B:433:GLN:HG3	1:B:490:ARG:NH2	2.30	0.46
1:B:233:GLY:O	1:B:258:ALA:HA	2.16	0.46
1:A:439:SER:OG	1:A:476:HIS:CD2	2.67	0.46
1:B:310:GLU:CG	5:B:2495:HOH:O	2.46	0.46
1:A:446:ALA:CB	1:B:521:THR:HG21	2.46	0.46
1:A:490:ARG:CZ	5:A:2682:HOH:O	2.60	0.46
1:B:297:THR:O	1:B:476:HIS:HE1	1.99	0.45
3:A:1524:P6G:H121	3:A:1524:P6G:H152	1.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:PHE:CE1	4:B:1533:NAP:H2D	2.51	0.45
1:B:490:ARG:CD	5:B:2690:HOH:O	2.64	0.45
1:B:479:VAL:O	3:B:1532:P6G:H112	2.17	0.45
1:A:416:ASP:CB	5:A:2630:HOH:O	2.42	0.44
1:A:381:ALA:O	1:A:383:HIS:CD2	2.68	0.44
1:A:470:GLN:HG3	1:A:471:HIS:N	2.31	0.44
4:B:1533:NAP:H6N	5:B:2744:HOH:O	2.16	0.44
3:A:1524:P6G:C11	5:A:2259:HOH:O	2.32	0.44
1:A:439:SER:CB	1:A:476:HIS:HD2	2.31	0.44
1:A:322:LYS:HE2	5:A:2512:HOH:O	2.18	0.44
1:A:400:GLU:HA	5:A:2616:HOH:O	2.16	0.44
1:B:297:THR:O	1:B:476:HIS:CE1	2.71	0.43
1:B:25:ASP:HA	1:B:89:ALA:O	2.18	0.43
3:A:1524:P6G:C12	5:A:2259:HOH:O	2.67	0.43
1:B:508:ARG:HD2	5:B:2713:HOH:O	2.15	0.43
1:B:158:PHE:CD2	4:B:1533:NAP:H51N	2.54	0.42
1:B:460:GLY:HA3	1:B:486:GLY:O	2.18	0.42
1:B:437:VAL:HA	1:B:461:ARG:O	2.19	0.42
1:B:304:VAL:O	1:B:410:PRO:HA	2.19	0.42
1:A:394:THR:HG21	5:A:2607:HOH:O	2.20	0.42
1:B:439:SER:CB	1:B:476:HIS:HD2	2.33	0.42
3:B:1532:P6G:C6	3:B:1532:P6G:H82	2.41	0.42
1:B:158:PHE:CE2	4:B:1533:NAP:H51N	2.55	0.42
1:B:439:SER:OG	1:B:476:HIS:CD2	2.68	0.41
1:A:68:ARG:HG3	1:A:68:ARG:HH11	1.85	0.41
1:A:450:ARG:HG2	5:B:2380:HOH:O	2.21	0.41
1:B:285:VAL:HG11	1:B:319:LYS:HG2	2.03	0.40
1:B:480:MET:HE1	3:B:1532:P6G:H121	1.98	0.40
1:A:440:ILE:HD13	1:A:440:ILE:HG21	1.91	0.40
1:A:521:THR:OG1	5:A:2714:HOH:O	2.21	0.40
1:B:278:ASP:CG	5:B:2472:HOH:O	2.64	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	518/534 (97%)	508 (98%)	10 (2%)	0	100	100
1	B	523/534 (98%)	515 (98%)	8 (2%)	0	100	100
All	All	1041/1068 (98%)	1023 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	391/398 (98%)	385 (98%)	6 (2%)	57	26
1	B	393/398 (99%)	392 (100%)	1 (0%)	86	70
All	All	784/796 (98%)	777 (99%)	7 (1%)	70	44

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	224	ARG
1	A	319	LYS
1	A	331	ASP
1	A	394	THR
1	A	508	ARG
1	B	431	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	12	GLN
1	A	90	ASN

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Mol	Chain	Res	Type
1	A	142	GLN
1	A	255	ASN
1	A	343	GLN
1	A	346	ASN
1	A	383	HIS
1	A	433	GLN
1	A	463	HIS
1	A	476	HIS
1	A	478	ASN
1	B	8	HIS
1	B	123	HIS
1	B	142	GLN
1	B	255	ASN
1	B	294	GLN
1	B	346	ASN
1	B	383	HIS
1	B	463	HIS
1	B	476	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 ligands 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	GOL	B	1531	-	5,5,5	1.06	0	5,5,5	0.54	0
4	NAP	B	1533	-	50,52,52	3.58	20 (40%)	71,80,80	3.23	34 (47%)
3	P6G	B	1532	-	18,18,18	2.23	5 (27%)	17,17,17	1.88	5 (29%)
2	GOL	A	1523	-	5,5,5	0.79	0	5,5,5	0.72	0
3	P6G	A	1524	-	18,18,18	2.31	9 (50%)	17,17,17	2.41	7 (41%)
4	NAP	A	1525	-	50,52,52	2.42	19 (38%)	71,80,80	3.26	24 (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
2	GOL	B	1531	-	-	0/4/4/4	-
4	NAP	B	1533	-	-	10/35/67/67	0/5/5/5
3	P6G	B	1532	-	-	5/16/16/16	-
2	GOL	A	1523	-	-	0/4/4/4	-
3	P6G	A	1524	-	-	9/16/16/16	-
4	NAP	A	1525	-	-	8/35/67/67	0/5/5/5

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1533	NAP	C2N-N1N	13.26	1.49	1.35
4	B	1533	NAP	C7N-N7N	9.41	1.50	1.33
4	A	1525	NAP	O4D-C1D	8.45	1.52	1.40
4	B	1533	NAP	C2N-C3N	6.80	1.49	1.39
3	B	1532	P6G	O7-C8	6.69	1.71	1.42
4	B	1533	NAP	C3N-C7N	6.64	1.60	1.50
4	B	1533	NAP	O4D-C1D	6.58	1.49	1.40
4	B	1533	NAP	O5D-C5D	-5.80	1.22	1.44
4	A	1525	NAP	C5A-N7A	-5.69	1.28	1.39
4	B	1533	NAP	P2B-O2B	5.67	1.69	1.59
4	B	1533	NAP	C6N-C5N	-4.94	1.28	1.38
4	A	1525	NAP	PN-O1N	4.47	1.66	1.50
4	B	1533	NAP	C5A-N7A	-4.36	1.31	1.39
4	B	1533	NAP	O4D-C4D	-4.15	1.35	1.45
3	A	1524	P6G	O7-C8	4.13	1.60	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1524	P6G	O10-C11	3.91	1.59	1.42
4	A	1525	NAP	C8A-N9A	-3.78	1.31	1.37
4	A	1525	NAP	C4N-C3N	3.63	1.44	1.39
3	B	1532	P6G	O13-C14	3.53	1.57	1.42
4	B	1533	NAP	O7N-C7N	-3.50	1.17	1.24
4	B	1533	NAP	PA-O3	-3.25	1.56	1.59
4	B	1533	NAP	PN-O1N	3.24	1.62	1.50
4	A	1525	NAP	O4B-C4B	-3.22	1.37	1.45
4	B	1533	NAP	C2A-N3A	-3.18	1.28	1.33
3	A	1524	P6G	C12-C11	3.17	1.65	1.49
4	B	1533	NAP	C8A-N9A	-3.16	1.32	1.37
4	A	1525	NAP	PN-O2N	-3.15	1.40	1.55
3	A	1524	P6G	O7-C6	3.15	1.55	1.42
4	A	1525	NAP	C4A-N3A	-3.14	1.28	1.34
4	A	1525	NAP	C4A-N9A	-3.06	1.31	1.37
4	A	1525	NAP	PN-O3	3.00	1.62	1.59
3	A	1524	P6G	O13-C14	2.98	1.55	1.42
4	B	1533	NAP	PN-O2N	-2.87	1.42	1.55
4	A	1525	NAP	P2B-O3X	-2.76	1.44	1.54
3	A	1524	P6G	O4-C3	2.71	1.53	1.42
3	A	1524	P6G	O1-C2	2.66	1.55	1.42
4	A	1525	NAP	O2D-C2D	2.64	1.49	1.43
3	B	1532	P6G	O1-C2	2.57	1.55	1.42
4	B	1533	NAP	C5N-C4N	-2.55	1.34	1.38
4	A	1525	NAP	C2N-N1N	2.48	1.37	1.35
3	A	1524	P6G	O4-C5	2.44	1.52	1.42
4	A	1525	NAP	C8A-N7A	2.41	1.36	1.31
4	B	1533	NAP	C4A-N3A	-2.38	1.30	1.34
3	B	1532	P6G	O4-C3	2.38	1.52	1.42
4	A	1525	NAP	C2N-C3N	2.36	1.42	1.39
4	A	1525	NAP	C6N-N1N	-2.32	1.30	1.35
3	A	1524	P6G	O10-C9	2.31	1.52	1.42
4	B	1533	NAP	C5D-C4D	2.30	1.58	1.51
4	A	1525	NAP	C5A-C4A	-2.26	1.35	1.39
4	A	1525	NAP	P2B-O2B	2.20	1.63	1.59
4	B	1533	NAP	C4A-N9A	-2.12	1.33	1.37
4	A	1525	NAP	C2D-C3D	2.07	1.59	1.53
3	B	1532	P6G	C3-C2	2.04	1.60	1.49

All (70) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1525	NAP	C5N-C4N-C3N	-13.09	107.50	120.36
4	B	1533	NAP	O7N-C7N-C3N	-11.40	105.65	119.60
4	B	1533	NAP	C4D-O4D-C1D	-8.81	101.86	109.92
4	A	1525	NAP	C4D-O4D-C1D	-8.64	102.01	109.92
4	A	1525	NAP	C2N-C3N-C4N	7.08	126.49	118.26
4	A	1525	NAP	O4B-C1B-N9A	7.06	121.66	108.09
4	B	1533	NAP	C3N-C7N-N7N	7.01	126.38	117.74
4	B	1533	NAP	C2N-N1N-C1D	6.76	134.05	119.13
4	B	1533	NAP	C6N-N1N-C2N	-6.74	116.14	121.88
4	A	1525	NAP	C6N-N1N-C2N	-6.55	116.31	121.88
4	A	1525	NAP	O7N-C7N-N7N	6.07	131.38	122.62
4	A	1525	NAP	C3N-C7N-N7N	-6.06	110.28	117.74
4	A	1525	NAP	C5A-C4A-N3A	-5.95	118.52	126.72
4	B	1533	NAP	N3A-C2A-N1A	-5.84	119.74	128.58
3	A	1524	P6G	O4-C5-C6	-5.19	86.69	110.35
3	A	1524	P6G	C11-O10-C9	5.12	135.69	113.26
4	B	1533	NAP	C6N-N1N-C1D	-5.12	109.67	119.73
4	A	1525	NAP	O4D-C4D-C3D	-5.04	95.16	105.15
4	B	1533	NAP	C5A-C4A-N3A	-4.97	119.87	126.72
4	A	1525	NAP	C2A-N3A-C4A	4.88	123.74	111.83
4	A	1525	NAP	N3A-C2A-N1A	-4.82	121.28	128.58
4	A	1525	NAP	C6N-C5N-C4N	4.73	126.26	119.45
4	B	1533	NAP	O3X-P2B-O2X	4.62	125.14	107.80
4	A	1525	NAP	N9A-C8A-N7A	-4.41	107.68	113.94
4	B	1533	NAP	O4D-C4D-C3D	-4.38	96.45	105.15
4	B	1533	NAP	C5D-C4D-C3D	4.36	130.90	115.21
4	B	1533	NAP	C2A-N3A-C4A	4.31	122.35	111.83
4	B	1533	NAP	C5N-C6N-N1N	4.10	125.97	120.38
4	B	1533	NAP	O2X-P2B-O1X	-3.93	95.50	110.83
3	B	1532	P6G	C8-O7-C6	-3.91	96.16	113.26
4	B	1533	NAP	O3D-C3D-C2D	-3.67	100.06	111.82
4	B	1533	NAP	O2N-PN-O3	3.66	117.15	107.27
3	B	1532	P6G	C17-O16-C15	3.53	128.69	113.26
3	B	1532	P6G	C5-O4-C3	-3.34	98.65	113.26
4	A	1525	NAP	C5A-N7A-C8A	3.24	108.54	103.45
4	B	1533	NAP	C4N-C3N-C7N	-3.24	112.25	121.06
4	B	1533	NAP	O7N-C7N-N7N	3.15	127.17	122.62
4	B	1533	NAP	O3D-C3D-C4D	3.14	120.11	111.08
4	B	1533	NAP	N9A-C8A-N7A	-3.11	109.53	113.94
4	A	1525	NAP	C4A-C5A-N7A	-3.10	107.04	110.58
3	A	1524	P6G	O13-C12-C11	3.10	124.46	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1525	NAP	C5A-C4A-N9A	3.09	109.18	105.81
4	B	1533	NAP	O2A-PA-O3	-3.08	98.95	107.27
4	A	1525	NAP	C5N-C6N-N1N	3.05	124.54	120.38
4	B	1533	NAP	C4A-C5A-N7A	-3.02	107.13	110.58
4	A	1525	NAP	N3A-C4A-N9A	3.02	132.30	127.17
4	B	1533	NAP	C5A-N7A-C8A	2.97	108.11	103.45
4	B	1533	NAP	C6N-C5N-C4N	2.90	123.62	119.45
4	A	1525	NAP	O5B-C5B-C4B	2.80	118.53	108.99
4	B	1533	NAP	C2N-C3N-C4N	2.73	121.44	118.26
4	A	1525	NAP	O3X-P2B-O2X	2.72	118.01	107.80
3	A	1524	P6G	C5-O4-C3	-2.72	101.36	113.26
3	A	1524	P6G	O7-C8-C9	2.63	122.33	110.35
4	B	1533	NAP	C5A-C4A-N9A	2.62	108.67	105.81
3	B	1532	P6G	O4-C5-C6	-2.49	99.00	110.35
3	A	1524	P6G	C8-O7-C6	-2.47	102.43	113.26
3	B	1532	P6G	O16-C17-C18	-2.47	99.22	110.11
4	B	1533	NAP	N3A-C4A-N9A	2.47	131.37	127.17
4	B	1533	NAP	PN-O5D-C5D	-2.43	107.43	121.35
4	B	1533	NAP	O3-PA-O1A	2.43	118.00	110.70
4	A	1525	NAP	O3B-C3B-C4B	-2.39	104.21	111.08
3	A	1524	P6G	O7-C6-C5	2.38	121.22	110.35
4	A	1525	NAP	C2N-C3N-C7N	-2.36	112.66	119.46
4	A	1525	NAP	O2A-PA-O3	-2.34	100.94	107.27
4	B	1533	NAP	C2N-C3N-C7N	2.33	126.17	119.46
4	A	1525	NAP	O3D-C3D-C4D	2.26	117.58	111.08
4	B	1533	NAP	O4D-C4D-C5D	2.25	116.53	109.33
4	B	1533	NAP	O3-PN-O1N	-2.22	104.03	110.70
4	B	1533	NAP	C2D-C3D-C4D	-2.17	98.42	102.61
4	B	1533	NAP	C2B-C1B-N9A	2.12	117.24	113.75

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1525	NAP	C5B-O5B-PA-O2A
4	A	1525	NAP	O4D-C4D-C5D-O5D
4	A	1525	NAP	C3D-C4D-C5D-O5D
4	B	1533	NAP	C5B-O5B-PA-O1A
4	B	1533	NAP	C5B-O5B-PA-O3
4	B	1533	NAP	C5D-O5D-PN-O3
4	B	1533	NAP	C3D-C4D-C5D-O5D
3	A	1524	P6G	O10-C11-C12-O13

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Mol	Chain	Res	Type	Atoms
3	B	1532	P6G	O4-C5-C6-O7
4	B	1533	NAP	O4D-C4D-C5D-O5D
3	A	1524	P6G	O1-C2-C3-O4
3	A	1524	P6G	O4-C5-C6-O7
3	B	1532	P6G	O1-C2-C3-O4
4	A	1525	NAP	C3B-C4B-C5B-O5B
3	B	1532	P6G	O13-C14-C15-O16
3	A	1524	P6G	O16-C17-C18-O19
3	B	1532	P6G	O16-C17-C18-O19
3	A	1524	P6G	C15-C14-O13-C12
4	A	1525	NAP	O4B-C4B-C5B-O5B
3	A	1524	P6G	C5-C6-O7-C8
4	B	1533	NAP	PA-O3-PN-O5D
4	B	1533	NAP	C4D-C5D-O5D-PN
4	B	1533	NAP	C5B-O5B-PA-O2A
4	B	1533	NAP	C5D-O5D-PN-O1N
3	A	1524	P6G	O7-C8-C9-O10
4	A	1525	NAP	C4D-C5D-O5D-PN
3	A	1524	P6G	C12-C11-O10-C9
4	A	1525	NAP	PA-O3-PN-O5D
3	B	1532	P6G	C12-C11-O10-C9
4	B	1533	NAP	PA-O3-PN-O2N
3	A	1524	P6G	O13-C14-C15-O16
4	A	1525	NAP	PA-O3-PN-O2N

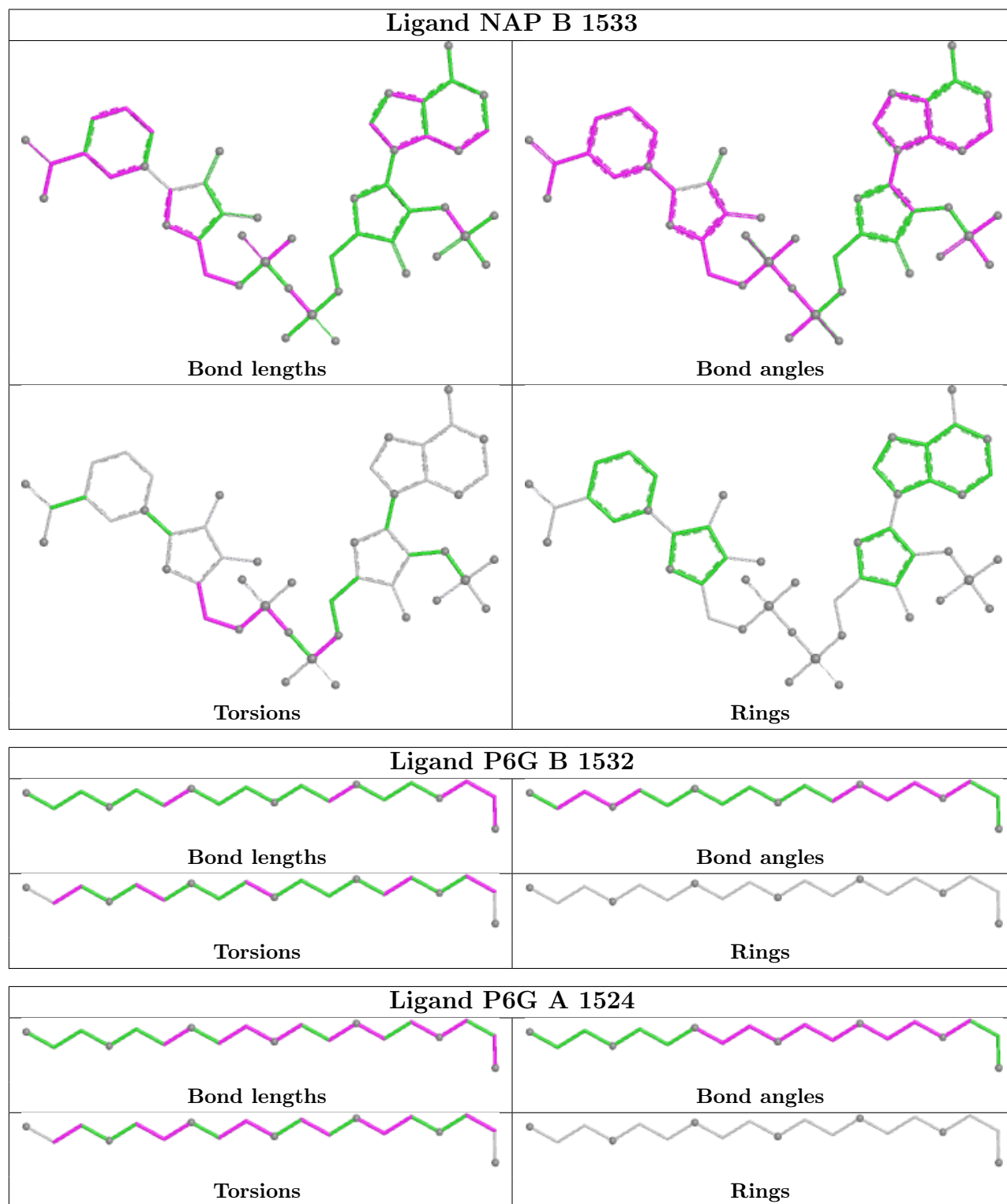
There are no ring outliers.

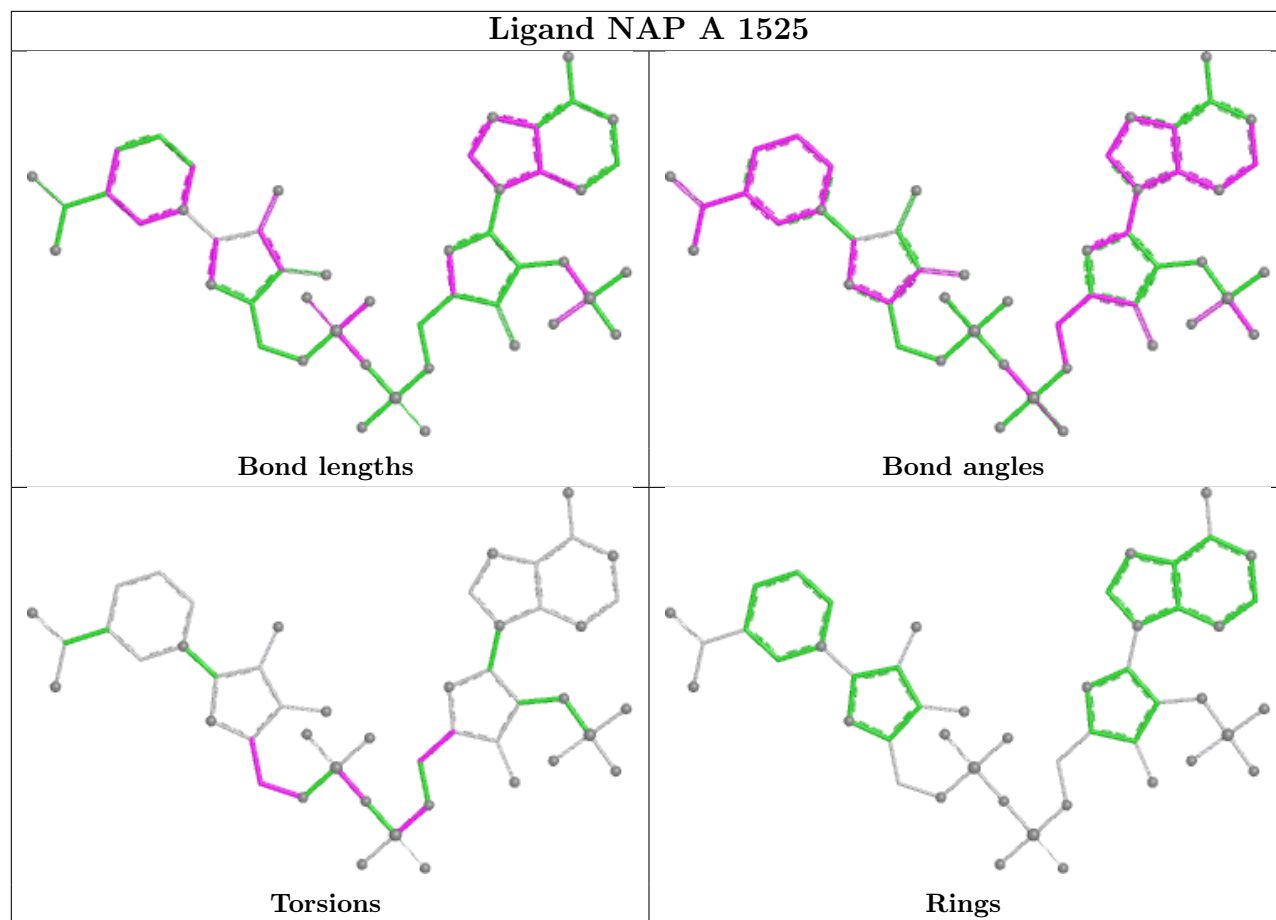
4 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1533	NAP	7	0
3	B	1532	P6G	11	0
3	A	1524	P6G	8	0
4	A	1525	NAP	5	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	521/534 (97%)	-0.24	12 (2%) 61 63	8, 13, 27, 59	1 (0%)
1	B	527/534 (98%)	-0.45	3 (0%) 85 88	8, 12, 22, 36	0
All	All	1048/1068 (98%)	-0.35	15 (1%) 73 76	8, 12, 25, 59	1 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	522	LEU	7.2
1	A	417	THR	3.7
1	A	0	HIS	3.2
1	A	520	GLY	3.0
1	A	415	THR	2.7
1	A	521	THR	2.7
1	B	374	ALA	2.6
1	A	414	THR	2.5
1	B	375	ASN	2.5
1	B	446	ALA	2.4
1	A	517	ALA	2.4
1	A	394	THR	2.2
1	A	413	VAL	2.2
1	A	398	ASP	2.2
1	A	331	ASP	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](#)

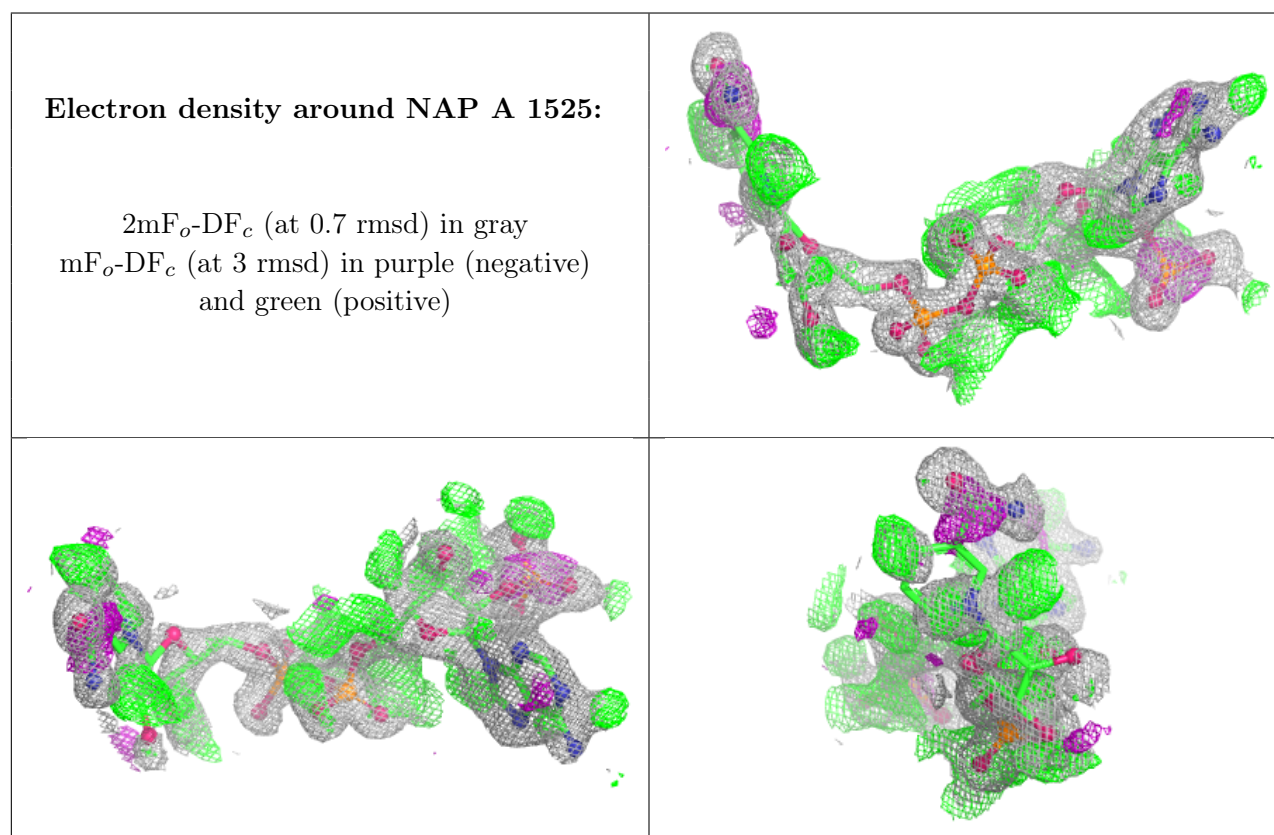
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

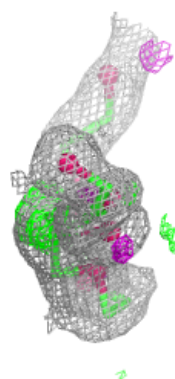
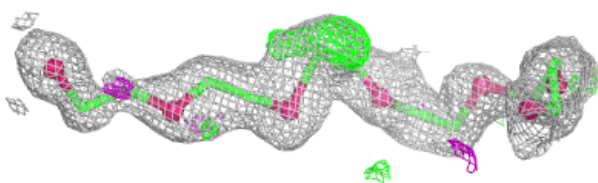
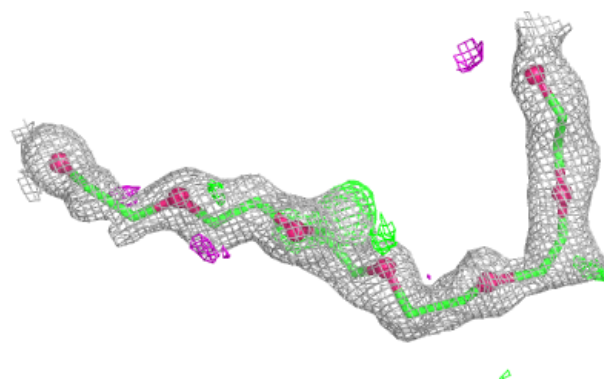
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAP	A	1525	48/48	0.87	0.15	8,21,33,37	23
3	P6G	B	1532	19/19	0.88	0.12	16,32,39,42	0
3	P6G	A	1524	19/19	0.88	0.12	15,31,39,41	0
4	NAP	B	1533	48/48	0.89	0.13	6,16,26,27	23
2	GOL	A	1523	6/6	0.97	0.06	9,13,16,16	0
2	GOL	B	1531	6/6	0.97	0.08	9,13,14,16	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.

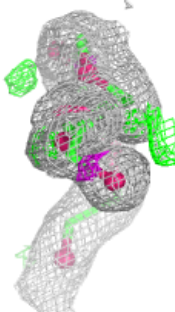
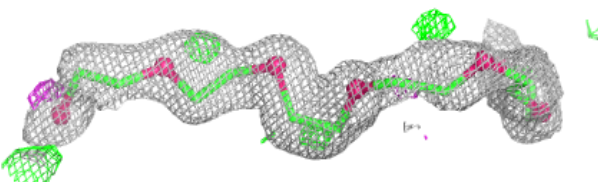
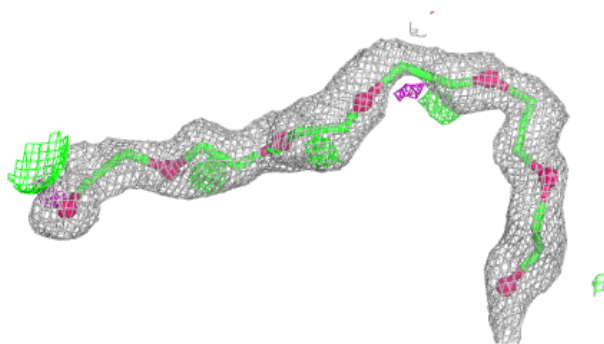


Electron density around P6G B 1532:

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

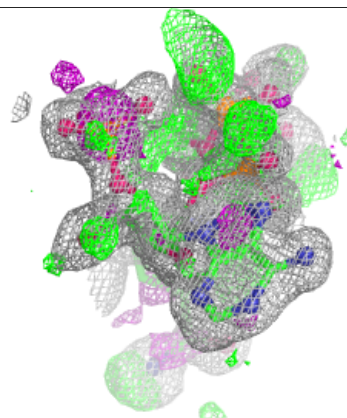
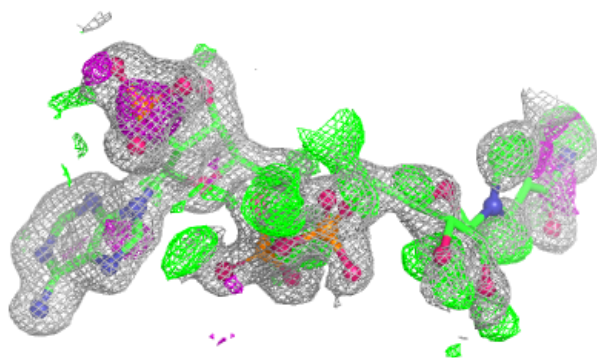
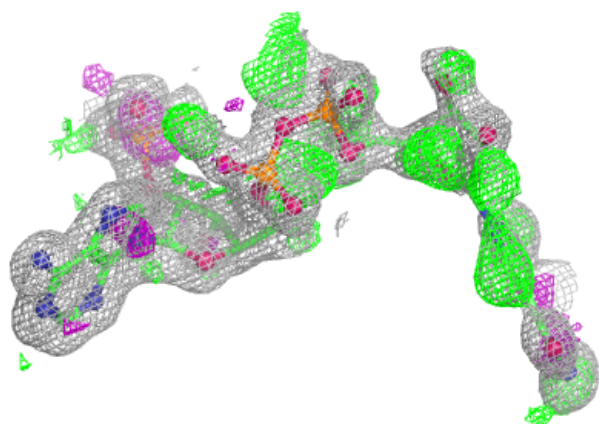
**Electron density around P6G A 1524:**

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



Electron density around NAP B 1533:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.