



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 02:33 pm GMT

PDB ID : 2Y5D  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

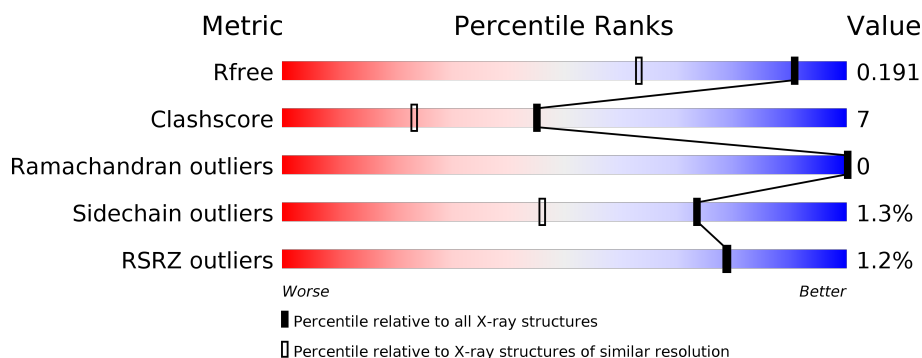
# 1 Overall quality at a glance ⓘ

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))
$R_{free}$	100719	1307 (1.40-1.40)
Clashscore	112137	1411 (1.40-1.40)
Ramachandran outliers	110173	1373 (1.40-1.40)
Sidechain outliers	110143	1372 (1.40-1.40)
RSRZ outliers	101464	1315 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>..</div> </div> </div>
1	B	534	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>..</div> </div> </div>

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	GOL	B	1531	-	-	-	X
3	P6G	A	1524	-	-	-	X
3	P6G	B	1532	-	-	X	X
4	NAP	A	1525	-	-	-	X
4	NAP	B	1533	-	-	-	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:

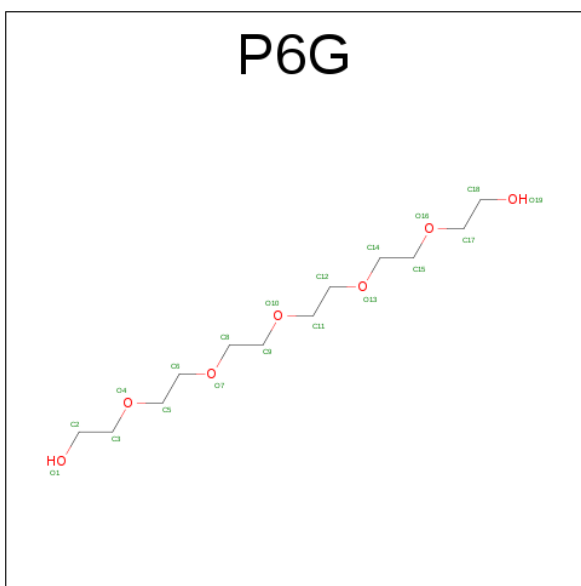
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q13WK4
A	-1	SER	-	EXPRESSION TAG	UNP Q13WK4
A	0	HIS	-	EXPRESSION TAG	UNP Q13WK4
A	296	ALA	CYS	ENGINEERED MUTATION	UNP Q13WK4
B	-2	GLY	-	EXPRESSION TAG	UNP Q13WK4
B	-1	SER	-	EXPRESSION TAG	UNP Q13WK4
B	0	HIS	-	EXPRESSION TAG	UNP Q13WK4
B	296	ALA	CYS	ENGINEERED MUTATION	UNP Q13WK4

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



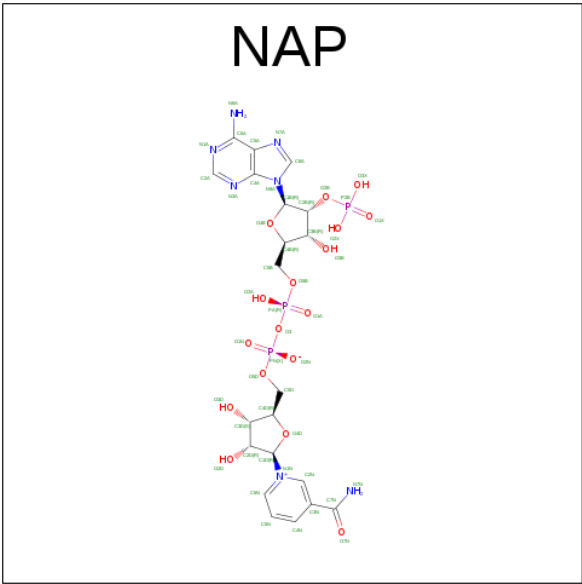
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is HEXAETHYLENE GLYCOL (three-letter code: 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		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
4	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

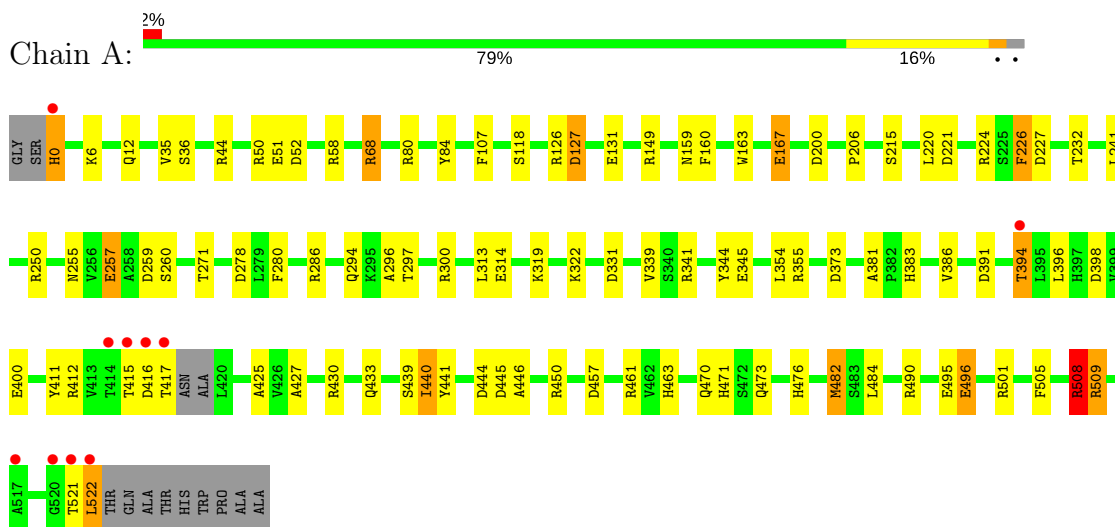
- Molecule 5 is water.

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

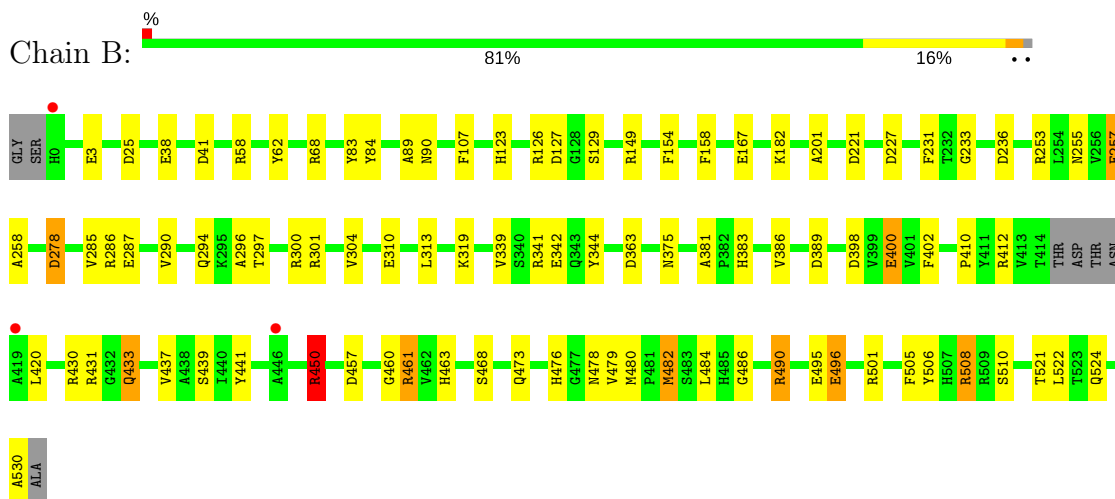
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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)



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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) 78.6 (31.33-1.40)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	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 (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	12.5	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	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 <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, NAP, 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	1.60	33/3918 (0.8%)	1.47	47/5334 (0.9%)
1	B	1.54	26/3958 (0.7%)	1.53	56/5392 (1.0%)
All	All	1.57	59/7876 (0.7%)	1.50	103/10726 (1.0%)

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

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

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	224	ARG	CG-CD	-12.14	1.21	1.51
1	B	496	GLU	CD-OE2	-11.46	1.13	1.25
1	A	496	GLU	CD-OE2	-10.87	1.13	1.25
1	B	342	GLU	CD-OE1	9.34	1.35	1.25
1	A	425	ALA	CA-CB	-8.46	1.34	1.52
1	A	496	GLU	CB-CG	-7.65	1.37	1.52
1	A	411	TYR	CE2-CZ	7.33	1.48	1.38
1	A	51	GLU	CG-CD	-7.16	1.41	1.51
1	A	131	GLU	CB-CG	-6.88	1.39	1.52
1	B	167	GLU	CD-OE2	6.87	1.33	1.25
1	B	510	SER	CB-OG	6.82	1.51	1.42
1	A	226	PHE	CD1-CE1	6.81	1.52	1.39
1	A	36	SER	CB-OG	6.80	1.51	1.42
1	B	375	ASN	CB-CG	6.39	1.65	1.51
1	B	62	TYR	CE1-CZ	6.38	1.46	1.38
1	A	314	GLU	CG-CD	6.32	1.61	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	50	ARG	CZ-NH1	6.25	1.41	1.33
1	B	433	GLN	CG-CD	-6.18	1.36	1.51
1	A	107	PHE	CG-CD2	6.04	1.47	1.38
1	A	427	ALA	CA-CB	5.93	1.65	1.52
1	B	290	VAL	CB-CG2	5.88	1.65	1.52
1	B	508	ARG	CD-NE	-5.88	1.36	1.46
1	A	215	SER	CA-CB	5.88	1.61	1.52
1	A	12	GLN	CG-CD	5.83	1.64	1.51
1	A	411	TYR	CE1-CZ	5.78	1.46	1.38
1	B	257	GLU	CB-CG	5.76	1.63	1.52
1	B	278	ASP	CB-CG	5.72	1.63	1.51
1	A	445	ASP	CB-CG	5.72	1.63	1.51
1	B	496	GLU	CB-CG	-5.65	1.41	1.52
1	B	508	ARG	CG-CD	5.64	1.66	1.51
1	A	501	ARG	CZ-NH2	5.55	1.40	1.33
1	B	90	ASN	CG-OD1	5.55	1.36	1.24
1	B	450	ARG	CG-CD	5.52	1.65	1.51
1	A	35	VAL	CB-CG1	5.52	1.64	1.52
1	A	314	GLU	CB-CG	5.50	1.62	1.52
1	B	441	TYR	CE1-CZ	-5.49	1.31	1.38
1	A	163	TRP	CG-CD1	5.49	1.44	1.36
1	A	394	THR	C-O	5.36	1.33	1.23
1	B	90	ASN	CG-ND2	-5.35	1.19	1.32
1	B	344	TYR	CE2-CZ	5.32	1.45	1.38
1	A	118	SER	CB-OG	5.30	1.49	1.42
1	B	506	TYR	CG-CD1	5.28	1.46	1.39
1	B	468	SER	CB-OG	5.25	1.49	1.42
1	A	482	MET	CG-SD	5.23	1.94	1.81
1	B	129	SER	C-O	5.23	1.33	1.23
1	A	271	THR	CA-CB	5.21	1.66	1.53
1	A	257	GLU	CB-CG	5.20	1.62	1.52
1	B	524	GLN	CB-CG	-5.19	1.38	1.52
1	B	38	GLU	CD-OE2	5.15	1.31	1.25
1	A	430	ARG	CG-CD	5.12	1.64	1.51
1	B	3	GLU	CG-CD	5.10	1.59	1.51
1	A	440	ILE	N-CA	5.10	1.56	1.46
1	A	345	GLU	CG-CD	5.09	1.59	1.51
1	A	167	GLU	CG-CD	-5.08	1.44	1.51
1	A	427	ALA	N-CA	-5.07	1.36	1.46
1	A	505	PHE	CG-CD2	-5.07	1.31	1.38
1	B	482	MET	CG-SD	5.05	1.94	1.81
1	B	201	ALA	C-O	5.05	1.32	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	206	PRO	N-CA	-5.02	1.38	1.47

All (103) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	508	ARG	NE-CZ-NH1	-24.90	107.85	120.30
1	B	508	ARG	NE-CZ-NH2	20.66	130.63	120.30
1	A	300	ARG	NE-CZ-NH2	-14.53	113.04	120.30
1	A	509[A]	ARG	NE-CZ-NH1	-12.56	114.02	120.30
1	A	509[B]	ARG	NE-CZ-NH1	-12.56	114.02	120.30
1	A	509[A]	ARG	NE-CZ-NH2	11.99	126.30	120.30
1	A	509[B]	ARG	NE-CZ-NH2	11.99	126.30	120.30
1	B	127	ASP	CB-CG-OD1	11.70	128.83	118.30
1	B	300	ARG	NE-CZ-NH2	-11.62	114.49	120.30
1	B	68	ARG	NE-CZ-NH2	-10.07	115.27	120.30
1	B	508	ARG	CD-NE-CZ	9.75	137.25	123.60
1	A	501	ARG	NE-CZ-NH2	-9.71	115.45	120.30
1	B	341	ARG	NE-CZ-NH1	9.67	125.14	120.30
1	B	126	ARG	NE-CZ-NH1	9.57	125.08	120.30
1	B	126	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	A	501	ARG	NE-CZ-NH1	9.26	124.93	120.30
1	B	83	TYR	CB-CG-CD1	9.15	126.49	121.00
1	A	391	ASP	CB-CG-OD1	9.08	126.47	118.30
1	B	278	ASP	CB-CG-OD1	9.06	126.46	118.30
1	A	344	TYR	CB-CG-CD1	8.35	126.01	121.00
1	A	522	LEU	CA-CB-CG	8.31	134.41	115.30
1	B	341	ARG	NE-CZ-NH2	-8.17	116.22	120.30
1	B	58	ARG	NE-CZ-NH1	8.04	124.32	120.30
1	B	149	ARG	NE-CZ-NH2	-8.01	116.30	120.30
1	B	490	ARG	NE-CZ-NH1	7.97	124.29	120.30
1	B	501	ARG	NE-CZ-NH2	-7.97	116.31	120.30
1	B	221	ASP	CB-CG-OD1	7.86	125.37	118.30
1	B	301	ARG	NE-CZ-NH2	-7.74	116.43	120.30
1	A	221	ASP	CB-CG-OD1	7.66	125.19	118.30
1	A	398	ASP	CB-CG-OD2	7.53	125.08	118.30
1	A	227	ASP	CB-CG-OD2	-7.51	111.54	118.30
1	B	278	ASP	CB-CG-OD2	-7.45	111.59	118.30
1	B	430	ARG	NE-CZ-NH1	-7.42	116.59	120.30
1	B	412	ARG	NE-CZ-NH2	-7.39	116.61	120.30
1	A	522	LEU	CB-CG-CD2	7.35	123.49	111.00
1	B	420	LEU	CB-CG-CD1	-7.30	98.59	111.00
1	B	508	ARG	CB-CG-CD	-7.22	92.83	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	412	ARG	CG-CD-NE	-7.18	96.72	111.80
1	A	58	ARG	NE-CZ-NH1	7.07	123.84	120.30
1	B	461	ARG	NE-CZ-NH1	6.99	123.79	120.30
1	A	412	ARG	NE-CZ-NH2	-6.88	116.86	120.30
1	A	80	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	A	149	ARG	NE-CZ-NH2	-6.79	116.90	120.30
1	B	83	TYR	CB-CG-CD2	-6.77	116.94	121.00
1	A	508	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	A	68	ARG	NE-CZ-NH2	-6.65	116.98	120.30
1	A	505	PHE	CB-CG-CD1	-6.63	116.16	120.80
1	B	68	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	41	ASP	CB-CG-OD1	6.56	124.21	118.30
1	A	344	TYR	CB-CG-CD2	-6.49	117.10	121.00
1	B	505	PHE	CB-CG-CD2	-6.47	116.27	120.80
1	B	398	ASP	CB-CG-OD2	6.47	124.12	118.30
1	A	80	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	A	127	ASP	CB-CG-OD1	6.37	124.04	118.30
1	A	52	ASP	CB-CG-OD1	6.23	123.91	118.30
1	A	396	LEU	CB-CG-CD1	6.18	121.50	111.00
1	A	200	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	B	482	MET	CG-SD-CE	6.13	110.02	100.20
1	B	441	TYR	CB-CG-CD1	-6.13	117.32	121.00
1	A	260	SER	N-CA-CB	-6.09	101.37	110.50
1	A	44	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	B	508	ARG	CG-CD-NE	-6.00	99.19	111.80
1	A	444	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	484	LEU	CB-CG-CD1	-5.92	100.93	111.00
1	B	457	ASP	CB-CG-OD1	5.90	123.61	118.30
1	A	52	ASP	CB-CG-OD2	-5.88	113.00	118.30
1	A	441	TYR	CZ-CE2-CD2	-5.82	114.56	119.80
1	B	484	LEU	CB-CG-CD1	-5.82	101.11	111.00
1	B	505	PHE	CD1-CG-CD2	5.73	125.75	118.30
1	A	167	GLU	OE1-CD-OE2	-5.71	116.45	123.30
1	B	167	GLU	CG-CD-OE1	5.70	129.70	118.30
1	A	373	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	B	154	PHE	CB-CG-CD2	-5.68	116.83	120.80
1	B	286	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	84	TYR	CZ-CE2-CD2	-5.62	114.74	119.80
1	B	253	ARG	NE-CZ-NH1	-5.60	117.50	120.30
1	B	58	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	A	341	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	461	ARG	NE-CZ-NH1	5.52	123.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	344	TYR	CZ-CE2-CD2	-5.48	114.87	119.80
1	B	236	ASP	CB-CG-OD2	-5.46	113.39	118.30
1	B	301	ARG	NE-CZ-NH1	5.45	123.03	120.30
1	A	259	ASP	CB-CG-OD1	5.40	123.16	118.30
1	B	227	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	B	400	GLU	OE1-CD-OE2	-5.36	116.86	123.30
1	B	505	PHE	CG-CD2-CE2	-5.34	114.92	120.80
1	B	287	GLU	OE1-CD-OE2	5.34	129.70	123.30
1	A	508	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	B	107	PHE	CB-CG-CD1	5.30	124.51	120.80
1	A	250	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	A	354	LEU	CB-CG-CD1	-5.27	102.04	111.00
1	B	363	ASP	CB-CG-OD2	-5.19	113.63	118.30
1	A	441	TYR	CG-CD1-CE1	-5.18	117.15	121.30
1	A	160	PHE	CG-CD2-CE2	-5.17	115.11	120.80
1	B	167	GLU	OE1-CD-OE2	-5.12	117.16	123.30
1	B	84	TYR	CB-CG-CD2	-5.11	117.94	121.00
1	A	280	PHE	CB-CG-CD1	5.10	124.37	120.80
1	B	496	GLU	CG-CD-OE1	5.09	128.49	118.30
1	B	430	ARG	NE-CZ-NH2	5.09	122.85	120.30
1	B	389	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	231	PHE	CB-CG-CD1	-5.08	117.25	120.80
1	A	84	TYR	CB-CG-CD1	5.03	124.02	121.00
1	A	457	ASP	CB-CG-OD1	5.01	122.81	118.30

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	53	0
1	B	3884	0	3890	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	33	0
5	B	744	0	0	22	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:O7	3:B:1532:P6G:C8	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	1.25
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:C6	3:B:1532:P6G:C8	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:HE2	3:B:1532:P6G:H112	1.64	0.79
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:H62	3:B:1532:P6G:C8	2.17	0.74
1:B:383:HIS:HE1	5:B:2565:HOH:O	1.76	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:ASN:OD1	4:A:1525:NAP:H5N	1.95	0.66
1:B:522:LEU:HD12	1:B:522:LEU:C	2.18	0.65
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
1:A:415:THR:C	5:A:2628:HOH:O	2.39	0.60
3:A:1524:P6G:H121	5:A:2720:HOH:O	2.02	0.59
1:A:0:HIS:C	1:A:0:HIS:ND1	2.55	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: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
1:B:508:ARG:HD3	5:B:2713:HOH:O	2.04	0.56
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:A:278:ASP:CG	5:A:2473:HOH:O	2.47	0.53
1:B:480:MET:HE2	3:B:1532:P6G:C11	2.35	0.52
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1524:P6G:H152	5:A:2720:HOH:O	2.11	0.49
1:A:255:ASN:HD21	1:A:495:GLU:N	2.03	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:HE21	1:A:433:GLN:HA	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:H152	3:A:1524:P6G:H121	1.56	0.45
1:A:470:GLN:HG3	1:A:471:HIS:N	2.31	0.45
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
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:480:MET:CE	3:B:1532:P6G:C12	2.95	0.43
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:H82	3:B:1532:P6G:C6	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:PHE:CE2	4:B:1533:NAP:H51N	2.55	0.42
1:A:416:ASP:N	5:A:2628:HOH:O	2.53	0.41
1:B:439:SER:OG	1:B:476:HIS:CD2	2.68	0.41
1:B:480:MET:HE2	3:B:1532:P6G:C12	2.51	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:A:440:ILE:HG21	1:A:440:ILE:HD13	1.91	0.40
1:A:521:THR:OG1	5:A:2714:HOH: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	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 [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	391/398 (98%)	385 (98%)	6 (2%)	70	40
1	B	393/398 (99%)	389 (99%)	4 (1%)	80	57
All	All	784/796 (98%)	774 (99%)	10 (1%)	73	46

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	167	GLU
1	A	319	LYS
1	A	331	ASP
1	A	482	MET
1	A	508	ARG
1	B	182	LYS
1	B	431	ARG
1	B	450	ARG
1	B	482	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	ASN
1	A	255	ASN
1	A	294	GLN
1	A	343	GLN
1	A	346	ASN
1	A	383	HIS
1	A	392	ASN
1	A	433	GLN
1	A	463	HIS
1	A	476	HIS
1	A	478	ASN
1	A	513	GLN
1	B	90	ASN
1	B	123	HIS
1	B	249	GLN
1	B	255	ASN
1	B	294	GLN
1	B	383	HIS
1	B	463	HIS
1	B	476	HIS

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Mol	Chain	Res	Type
1	B	478	ASN
1	B	513	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	A	1523	-	5,5,5	0.74	0	5,5,5	0.61	0
3	P6G	A	1524	-	18,18,18	2.31	9 (50%)	17,17,17	2.41	7 (41%)
4	NAP	A	1525	-	44,52,52	2.27	15 (34%)	51,80,80	3.19	16 (31%)
2	GOL	B	1531	-	5,5,5	1.02	0	5,5,5	0.46	0
3	P6G	B	1532	-	18,18,18	2.24	5 (27%)	17,17,17	1.88	5 (29%)
4	NAP	B	1533	-	44,52,52	3.03	18 (40%)	51,80,80	3.41	20 (39%)

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	A	1523	-	-	0/4/4/4	0/0/0/0
3	P6G	A	1524	-	-	0/16/16/16	0/0/0/0
4	NAP	A	1525	-	-	0/27/67/67	0/5/5/5
2	GOL	B	1531	-	-	0/4/4/4	0/0/0/0
3	P6G	B	1532	-	-	0/16/16/16	0/0/0/0
4	NAP	B	1533	-	-	0/27/67/67	0/5/5/5

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1533	NAP	O5D-C5D	-5.58	1.22	1.44
4	A	1525	NAP	C4A-N3A	-4.77	1.28	1.35
4	B	1533	NAP	C6N-C5N	-4.66	1.28	1.38
4	B	1533	NAP	O4D-C4D	-4.09	1.35	1.45
4	B	1533	NAP	C4A-N3A	-3.80	1.30	1.35
4	B	1533	NAP	O7N-C7N	-3.19	1.17	1.24
4	A	1525	NAP	O4B-C4B	-3.17	1.37	1.45
4	A	1525	NAP	C5A-N7A	-3.16	1.28	1.39
4	A	1525	NAP	PN-O2N	-2.86	1.40	1.55
4	B	1533	NAP	PN-O2N	-2.60	1.42	1.55
4	A	1525	NAP	P2B-O3X	-2.50	1.44	1.54
4	B	1533	NAP	C5A-N7A	-2.44	1.31	1.39
4	A	1525	NAP	C5A-C4A	-2.41	1.35	1.40
4	B	1533	NAP	C2A-N3A	-2.37	1.28	1.32
4	B	1533	NAP	C5N-C4N	-2.27	1.34	1.38
4	A	1525	NAP	C6N-N1N	-2.11	1.30	1.35
4	B	1533	NAP	C5A-C4A	-2.06	1.35	1.40
3	B	1532	P6G	C3-C2	2.07	1.60	1.49
4	A	1525	NAP	C2D-C3D	2.10	1.59	1.53
4	B	1533	NAP	C5D-C4D	2.17	1.58	1.51
4	A	1525	NAP	P2B-O2B	2.19	1.63	1.59
3	A	1524	P6G	O10-C9	2.34	1.52	1.42
3	B	1532	P6G	O4-C3	2.41	1.52	1.42
3	A	1524	P6G	O4-C5	2.47	1.52	1.42
4	A	1525	NAP	C2N-C3N	2.47	1.42	1.39
3	B	1532	P6G	O1-C2	2.49	1.55	1.42
3	A	1524	P6G	O1-C2	2.57	1.55	1.42
3	A	1524	P6G	O4-C3	2.74	1.53	1.42
4	B	1533	NAP	C2D-C1D	2.82	1.58	1.53
4	A	1525	NAP	O2D-C2D	2.84	1.49	1.43
4	B	1533	NAP	PN-O1N	2.97	1.62	1.50
3	A	1524	P6G	O13-C14	3.01	1.55	1.42
3	A	1524	P6G	C12-C11	3.09	1.65	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1524	P6G	O7-C6	3.18	1.55	1.42
4	A	1525	NAP	C4N-C3N	3.40	1.44	1.39
3	B	1532	P6G	O13-C14	3.57	1.57	1.42
4	A	1525	NAP	C2D-C1D	3.68	1.59	1.53
3	A	1524	P6G	O10-C11	3.95	1.59	1.42
4	A	1525	NAP	PN-O1N	4.10	1.66	1.50
3	A	1524	P6G	O7-C8	4.17	1.60	1.42
4	B	1533	NAP	P2B-O2B	5.67	1.69	1.59
4	B	1533	NAP	O4D-C1D	5.98	1.49	1.41
4	B	1533	NAP	C3N-C7N	6.41	1.60	1.50
3	B	1532	P6G	O7-C8	6.75	1.71	1.42
4	B	1533	NAP	C2N-C3N	7.09	1.49	1.39
4	A	1525	NAP	O4D-C1D	7.76	1.52	1.41
4	B	1533	NAP	C7N-N7N	8.86	1.50	1.33

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1533	NAP	O7N-C7N-C3N	-11.95	105.65	119.62
4	A	1525	NAP	C5N-C4N-C3N	-10.92	107.50	120.35
4	B	1533	NAP	N3A-C2A-N1A	-10.47	119.74	128.86
4	A	1525	NAP	N3A-C2A-N1A	-8.70	121.28	128.86
4	B	1533	NAP	C4D-O4D-C1D	-7.43	101.86	109.77
4	A	1525	NAP	C4D-O4D-C1D	-7.29	102.01	109.77
4	A	1525	NAP	C3N-C7N-N7N	-6.57	110.28	117.77
4	B	1533	NAP	C3N-C2N-N1N	-6.12	114.26	120.43
3	A	1524	P6G	O4-C5-C6	-5.16	86.69	110.41
4	A	1525	NAP	O4D-C4D-C3D	-5.04	95.16	105.17
4	B	1533	NAP	O4D-C4D-C3D	-4.38	96.45	105.17
3	B	1532	P6G	C8-O7-C6	-3.96	96.16	113.30
4	B	1533	NAP	O2X-P2B-O1X	-3.83	95.50	110.50
4	B	1533	NAP	O3D-C3D-C2D	-3.67	100.06	111.83
3	B	1532	P6G	C5-O4-C3	-3.38	98.65	113.30
4	B	1533	NAP	C4N-C3N-C7N	-3.32	112.25	121.07
3	A	1524	P6G	C5-O4-C3	-2.76	101.36	113.30
3	A	1524	P6G	C8-O7-C6	-2.51	102.43	113.30
3	B	1532	P6G	O4-C5-C6	-2.48	99.00	110.41
4	A	1525	NAP	C4A-C5A-N7A	-2.46	107.04	109.41
3	B	1532	P6G	O16-C17-C18	-2.37	99.22	110.15
4	B	1533	NAP	C4A-C5A-N7A	-2.36	107.13	109.41
4	A	1525	NAP	O3B-C3B-C4B	-2.35	104.21	111.09
4	A	1525	NAP	C2N-C3N-C7N	-2.30	112.66	119.34

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1533	NAP	C2D-C3D-C4D	-2.16	98.42	102.62
4	B	1533	NAP	O4D-C4D-C5D	2.11	116.53	109.40
4	A	1525	NAP	C4B-O4B-C1B	2.17	112.08	109.77
4	A	1525	NAP	O3D-C3D-C4D	2.22	117.58	111.09
4	B	1533	NAP	C2N-C3N-C7N	2.35	126.17	119.34
3	A	1524	P6G	O7-C6-C5	2.35	121.22	110.41
4	A	1525	NAP	O3X-P2B-O2X	2.58	118.01	107.61
3	A	1524	P6G	O7-C8-C9	2.60	122.33	110.41
4	A	1525	NAP	O5B-C5B-C4B	2.69	118.53	109.00
4	A	1525	NAP	C5N-C6N-N1N	2.69	124.54	120.40
4	B	1533	NAP	C6N-C5N-C4N	2.78	123.62	119.44
4	B	1533	NAP	C2N-C3N-C4N	2.79	121.44	118.26
3	A	1524	P6G	O13-C12-C11	3.06	124.46	110.41
4	B	1533	NAP	O3D-C3D-C4D	3.09	120.11	111.09
4	B	1533	NAP	O7N-C7N-N7N	3.22	127.17	122.58
3	B	1532	P6G	C17-O16-C15	3.55	128.69	113.30
4	B	1533	NAP	C5N-C6N-N1N	3.62	125.97	120.40
4	B	1533	NAP	C5D-C4D-C3D	4.10	130.90	115.29
4	B	1533	NAP	O3X-P2B-O2X	4.34	125.14	107.61
4	A	1525	NAP	C6N-C5N-C4N	4.52	126.26	119.44
3	A	1524	P6G	C11-O10-C9	5.17	135.69	113.30
4	A	1525	NAP	O7N-C7N-N7N	6.19	131.38	122.58
4	A	1525	NAP	C2N-C3N-C4N	7.21	126.49	118.26
4	B	1533	NAP	C3N-C7N-N7N	7.53	126.38	117.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1524	P6G	8	0
4	A	1525	NAP	5	0
3	B	1532	P6G	11	0
4	B	1533	NAP	7	0

## 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	521/534 (97%)	-0.27	10 (1%) 67 68	8, 13, 27, 59	0
1	B	527/534 (98%)	-0.42	3 (0%) 89 88	8, 12, 22, 36	0
All	All	1048/1068 (98%)	-0.35	13 (1%) 79 78	8, 12, 25, 59	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	417	THR	5.0
1	A	0	HIS	4.2
1	A	520	GLY	4.0
1	A	415	THR	4.0
1	A	416	ASP	3.7
1	A	394	THR	3.2
1	A	522	LEU	3.2
1	A	521	THR	3.0
1	A	414	THR	2.4
1	B	446	ALA	2.4
1	B	0	HIS	2.3
1	B	419	ALA	2.1
1	A	517	ALA	2.0

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAP	A	1525	48/48	0.85	0.20	7.27	8,21,33,37	23
4	NAP	B	1533	48/48	0.87	0.16	5.20	6,16,26,27	23
3	P6G	B	1532	19/19	0.84	0.14	3.74	16,32,39,42	0
3	P6G	A	1524	19/19	0.86	0.13	2.72	15,31,39,41	0
2	GOL	B	1531	6/6	0.96	0.09	2.30	9,13,14,16	0
2	GOL	A	1523	6/6	0.97	0.06	-0.46	9,13,16,16	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.