



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:42 AM UTC

PDB ID : 4LNL / pdb_00004lnl
Title : Structure of Escherichia coli Threonine Aldolase in Complex with Allo-Thr
Authors : Safo, M.K.
Deposited on : 2013-07-11
Resolution : 2.10 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

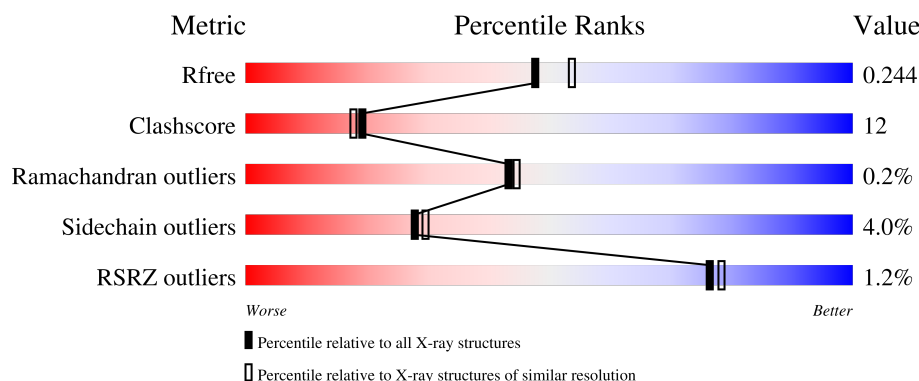
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	333	% 78% 20% .
1	B	333	2% 73% 23% .

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	2BO	A	402[A]	-	X	-	-
7	PLG	B	403	-	X	-	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5667 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 Low-specificity L-threonine aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	1	0
			2553	1601	458	478	16			
1	B	332	Total	C	N	O	S	0	0	0
			2548	1598	458	476	16			

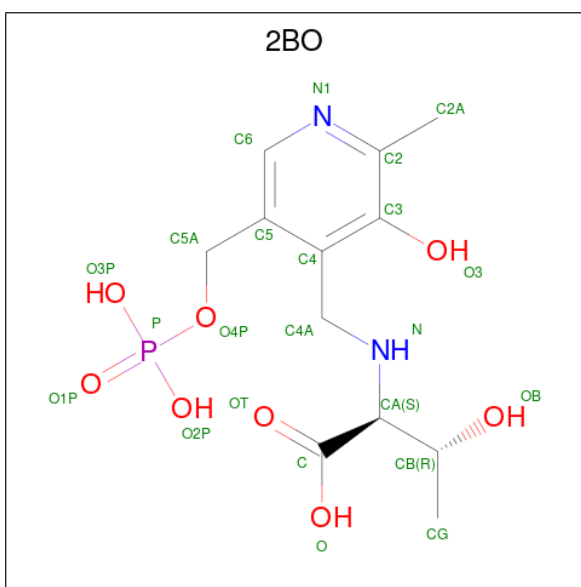
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	256	THR	ALA	conflict	UNP E7U392
A	257	ALA	THR	conflict	UNP E7U392
B	256	THR	ALA	conflict	UNP E7U392
B	257	ALA	THR	conflict	UNP E7U392

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

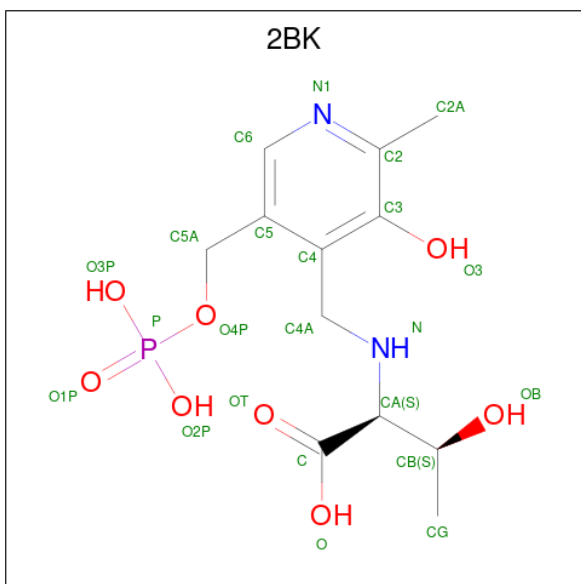
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	2	Total	Mg	0	0
			2	2		

- Molecule 3 is N-({3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}methyl)-L-threonine (CCD ID: 2BO) (formula: C₁₂H₁₉N₂O₈P).



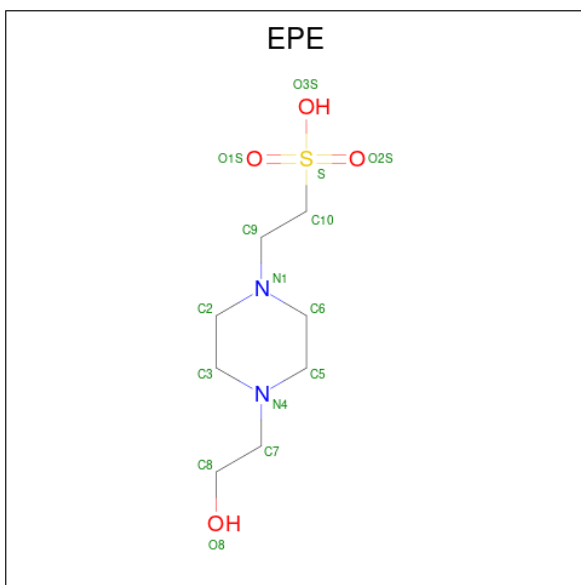
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	1
			23	12	2	8	1		

- Molecule 4 is N-({3-hydroxy-2-methyl-5-[(phosphonoxy)methyl]pyridin-4-yl}methyl)-L-allo-threonine (CCD ID: 2BK) (formula: $C_{12}H_{19}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	1
			23	12	2	8	1		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).

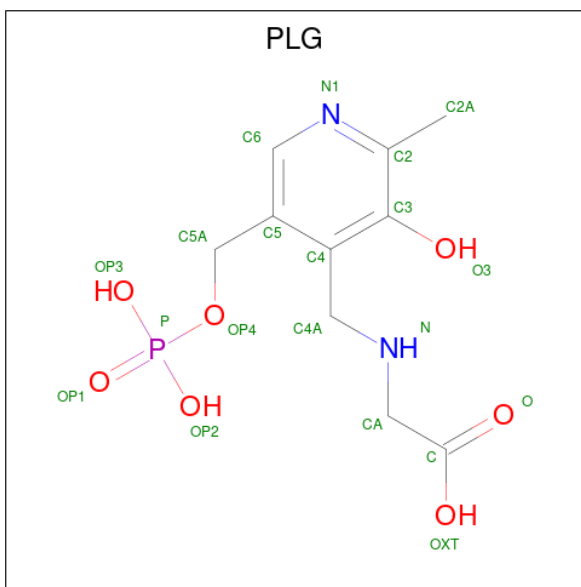


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is N-GLYCINE-[3-HYDROXY-2-METHYL-5-PHOSPHONOOXYMETHYL-PYRIDIN-4-YL-METHANE] (CCD ID: PLG) (formula: C₁₀H₁₅N₂O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	P	0	0
			20	10	2	7	1		

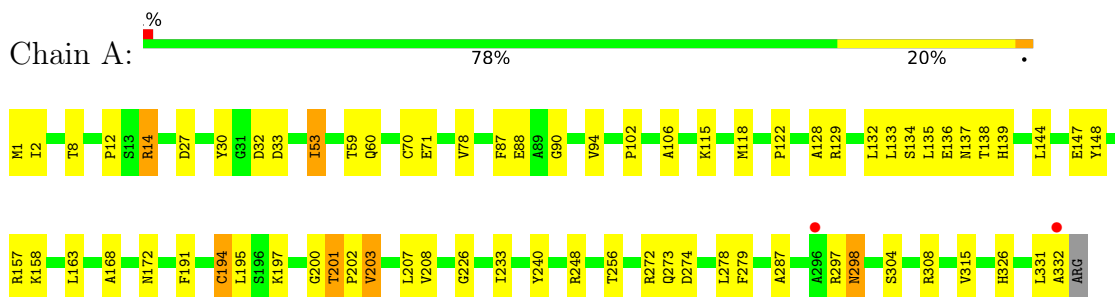
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	248	Total	O	0	0
			248	248		
8	B	218	Total	O	0	0
			218	218		

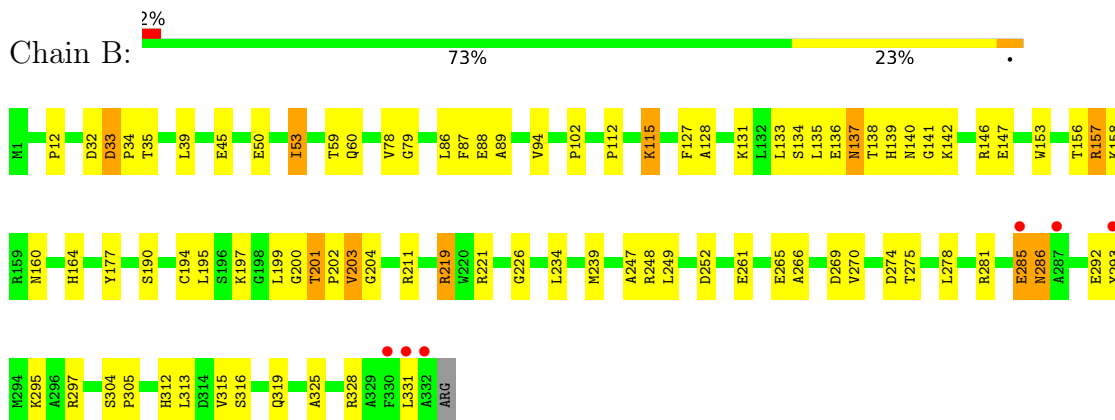
3 Residue-property plots

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: Low-specificity L-threonine aldolase



• Molecule 1: Low-specificity L-threonine aldolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.40Å 100.89Å 176.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.05 – 2.10 29.05 – 2.10	Depositor EDS
% Data completeness (in resolution range)	92.8 (29.05-2.10) 92.9 (29.05-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.182 , 0.243 0.183 , 0.244	Depositor DCC
R_{free} test set	1881 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5667	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.27% 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: EPE, CL, MG, PLG, 2BK, 2BO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.92	15/2601 (0.6%)	1.03	16/3522 (0.5%)
1	B	1.01	20/2592 (0.8%)	1.07	17/3510 (0.5%)
All	All	0.97	35/5193 (0.7%)	1.05	33/7032 (0.5%)

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	137	ASN	C-O	-20.08	1.01	1.24
1	B	137	ASN	C-O	-14.61	1.07	1.24
1	B	140	ASN	C-O	-12.43	1.07	1.23
1	B	134	SER	C-O	-11.18	1.10	1.24
1	B	136	GLU	C-O	-10.77	1.10	1.23
1	B	139	HIS	C-O	-10.12	1.12	1.24
1	B	136	GLU	CD-OE2	-9.69	1.06	1.25
1	A	139	HIS	C-O	-9.66	1.12	1.24
1	B	138	THR	C-O	-9.12	1.05	1.23
1	B	136	GLU	CD-OE1	-8.77	1.08	1.25
1	B	141	GLY	C-O	-8.54	1.12	1.23
1	A	135	LEU	C-O	-8.47	1.13	1.23
1	A	136	GLU	C-O	-8.08	1.14	1.24
1	B	134	SER	N-CA	-7.94	1.36	1.46
1	B	137	ASN	C-N	-7.94	1.22	1.33
1	A	139	HIS	N-CA	-7.54	1.36	1.46
1	A	135	LEU	N-CA	-7.52	1.36	1.45
1	A	134	SER	C-O	-7.33	1.15	1.24
1	A	136	GLU	CD-OE1	-6.96	1.12	1.25
1	A	138	THR	C-O	-6.79	1.09	1.23
1	B	142	LYS	CE-NZ	-6.58	1.29	1.49
1	B	135	LEU	C-O	-6.57	1.15	1.23
1	A	136	GLU	CD-OE2	-6.18	1.13	1.25
1	B	142	LYS	C-O	-6.17	1.16	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	137	ASN	C-N	-6.10	1.24	1.33
1	B	136	GLU	CA-C	6.10	1.59	1.52
1	A	134	SER	CA-C	6.05	1.59	1.52
1	A	137	ASN	CG-ND2	-6.05	1.20	1.33
1	B	140	ASN	CA-CB	-5.92	1.44	1.53
1	B	139	HIS	N-CA	-5.92	1.39	1.46
1	A	133	LEU	C-N	-5.86	1.25	1.33
1	B	133	LEU	C-N	-5.47	1.26	1.33
1	B	140	ASN	CG-OD1	-5.46	1.13	1.23
1	A	135	LEU	CG-CD2	-5.04	1.35	1.52
1	B	137	ASN	CG-OD1	-5.01	1.14	1.23

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	33	ASP	CA-C-N	9.49	129.59	119.05
1	B	33	ASP	C-N-CA	9.49	129.59	119.05
1	B	128	ALA	N-CA-C	-6.87	101.46	110.53
1	A	128	ALA	N-CA-C	-6.44	102.22	110.53
1	A	172	ASN	N-CA-C	-6.35	104.44	111.36
1	A	134	SER	CA-CB-OG	6.25	123.61	111.10
1	A	33	ASP	CA-C-N	6.20	125.93	119.05
1	A	33	ASP	C-N-CA	6.20	125.93	119.05
1	B	137	ASN	N-CA-C	6.16	118.99	108.02
1	B	249	LEU	N-CA-C	-6.11	104.73	111.82
1	A	87	PHE	N-CA-C	6.09	120.41	112.92
1	B	200	GLY	N-CA-C	5.80	123.36	115.30
1	B	135	LEU	N-CA-C	5.70	118.52	110.14
1	A	135	LEU	N-CA-C	5.66	118.92	110.14
1	B	89	ALA	N-CA-C	5.64	119.35	111.90
1	B	137	ASN	CA-C-N	5.57	131.73	121.70
1	B	137	ASN	C-N-CA	5.57	131.73	121.70
1	A	137	ASN	O-C-N	-5.52	115.83	123.12
1	A	122	PRO	N-CA-C	-5.49	103.18	111.41
1	A	70	CYS	N-CA-C	5.45	117.40	108.52
1	B	87	PHE	N-CA-C	5.42	119.59	112.92
1	B	137	ASN	O-C-N	-5.42	115.97	123.12
1	B	86	LEU	N-CA-C	5.36	119.90	112.45
1	A	200	GLY	N-CA-C	5.34	123.30	115.08
1	B	134	SER	N-CA-C	5.28	117.58	109.07
1	A	134	SER	N-CA-C	5.26	117.54	109.07
1	A	132	LEU	N-CA-C	5.23	117.76	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	ALA	N-CA-C	-5.22	103.79	110.53
1	B	247	ALA	N-CA-C	5.21	116.95	111.28
1	B	127	PHE	N-CA-C	5.19	118.19	110.14
1	B	94	VAL	N-CA-C	5.17	115.38	110.42
1	A	32	ASP	N-CA-C	5.10	118.54	112.72
1	A	137	ASN	N-CA-C	5.04	117.00	108.02

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2553	0	2552	47	0
1	B	2548	0	2550	72	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	23	0	15	2	0
4	A	23	0	15	2	0
5	A	15	0	18	2	0
5	B	15	0	18	1	0
6	A	1	0	0	0	0
7	B	20	0	11	2	0
8	A	248	0	0	5	0
8	B	218	0	0	7	0
All	All	5667	0	5179	121	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 12.

All (121) 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:60:GLN:HE22	1:B:226:GLY:HA3	1.25	1.01
1:A:60:GLN:HE22	1:A:226:GLY:HA3	1.28	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:PRO:HG3	1:B:202:PRO:HG3	1.55	0.89
1:B:285:GLU:HG2	1:B:286:ASN:ND2	1.89	0.86
1:B:59:THR:HG23	1:B:88:GLU:HG2	1.57	0.84
1:B:197:LYS:HZ1	7:B:403:PLG:H4A2	1.43	0.82
1:B:158:LYS:HE3	8:B:713:HOH:O	1.79	0.81
1:A:256:THR:HG23	1:A:278:LEU:HD22	1.65	0.79
1:B:35:THR:HG23	1:B:239:MET:HE2	1.69	0.73
1:B:50:GLU:HB3	1:B:211:ARG:HG3	1.73	0.70
1:B:297:ARG:HG2	1:B:297:ARG:HH11	1.55	0.70
1:A:195:LEU:O	1:A:201:THR:HB	1.94	0.67
1:B:297:ARG:HD2	1:B:297:ARG:N	2.08	0.67
1:B:197:LYS:NZ	7:B:403:PLG:H4A2	2.12	0.65
1:B:115:LYS:HG2	8:B:601:HOH:O	1.95	0.65
1:B:131:LYS:NZ	8:B:696:HOH:O	2.29	0.64
1:A:12:PRO:HG3	1:A:202:PRO:HG3	1.78	0.64
1:A:8:THR:HG22	1:A:197:LYS:HG2	1.79	0.63
1:B:115:LYS:HG3	8:B:709:HOH:O	1.99	0.62
1:B:12:PRO:CG	1:B:202:PRO:HG3	2.30	0.62
1:A:115:LYS:HA	1:A:118:MET:HE3	1.80	0.61
1:A:298:ASN:ND2	8:A:503:HOH:O	2.34	0.60
1:B:153:TRP:O	1:B:157:ARG:HD2	2.01	0.60
1:B:157:ARG:HH21	1:B:157:ARG:N	2.01	0.59
1:A:1:MET:HG3	1:A:298:ASN:ND2	2.17	0.58
1:B:53:ILE:HD11	1:B:221:ARG:HD3	1.85	0.58
1:A:78:VAL:O	1:A:102:PRO:HA	2.04	0.57
1:A:59:THR:HG23	1:A:88:GLU:HG2	1.86	0.57
1:B:297:ARG:HG2	1:B:297:ARG:NH1	2.20	0.57
1:A:53:ILE:HG23	1:A:207:LEU:HB3	1.87	0.56
1:A:248:ARG:HG3	1:A:248:ARG:HH11	1.69	0.56
1:B:286:ASN:HD22	1:B:286:ASN:N	2.03	0.56
1:B:78:VAL:HG22	1:B:79:GLY:N	2.20	0.55
1:B:164:HIS:HD2	1:B:190:SER:OG	1.90	0.55
1:B:248:ARG:NH2	1:B:252:ASP:OD1	2.40	0.55
1:B:195:LEU:O	1:B:201:THR:HB	2.07	0.55
1:A:129:ARG:NH2	8:A:649:HOH:O	2.32	0.54
1:B:248:ARG:NH1	1:B:313:LEU:HA	2.23	0.53
1:A:256:THR:HG22	1:A:273:GLN:HG2	1.90	0.53
1:A:1:MET:HG2	1:A:2:ILE:N	2.24	0.53
1:B:286:ASN:ND2	1:B:286:ASN:N	2.54	0.53
1:B:153:TRP:CZ3	1:B:157:ARG:NH1	2.77	0.53
1:A:202:PRO:C	1:A:203:VAL:HG12	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:LYS:HD2	1:B:295:LYS:C	2.34	0.52
1:B:316:SER:OG	1:B:319:GLN:HG3	2.09	0.52
1:A:60:GLN:NE2	1:A:226:GLY:HA3	2.12	0.51
1:A:90:GLY:O	1:A:94:VAL:HG23	2.10	0.51
1:B:195:LEU:C	1:B:201:THR:HB	2.36	0.51
1:B:248:ARG:HH12	1:B:313:LEU:HA	1.76	0.51
1:B:269:ASP:OD2	1:B:281:ARG:NH1	2.43	0.51
1:A:297:ARG:HG2	1:A:326:HIS:CE1	2.47	0.50
1:A:201:THR:HG23	1:A:202:PRO:HD2	1.92	0.50
1:A:195:LEU:C	1:A:201:THR:HB	2.37	0.49
1:A:326:HIS:HA	8:A:722:HOH:O	2.12	0.48
1:B:219:ARG:HH11	1:B:219:ARG:HG3	1.78	0.48
1:A:163:LEU:C	1:A:163:LEU:HD23	2.38	0.48
1:B:266:ALA:O	1:B:331:LEU:HD12	2.14	0.48
1:B:293:TYR:O	1:B:297:ARG:CD	2.61	0.48
1:B:304:SER:OG	1:B:305:PRO:HD2	2.14	0.48
1:B:53:ILE:HD11	1:B:221:ARG:CD	2.44	0.47
1:A:201:THR:HG22	1:A:203:VAL:H	1.80	0.47
1:B:35:THR:HG23	1:B:239:MET:CE	2.42	0.47
1:A:279:PHE:CZ	1:A:308:ARG:HG3	2.50	0.47
1:A:240:TYR:C	1:A:240:TYR:CD1	2.92	0.47
3:A:402[A]:2BO:OB	3:A:402[A]:2BO:H5	2.15	0.47
4:A:403[B]:2BK:H8	4:A:403[B]:2BK:OB	2.15	0.47
1:B:60:GLN:NE2	1:B:226:GLY:HA3	2.09	0.47
1:B:78:VAL:O	1:B:102:PRO:HA	2.15	0.47
1:A:248:ARG:HG3	1:A:248:ARG:NH1	2.30	0.46
1:B:285:GLU:H	1:B:285:GLU:CD	2.23	0.46
1:A:157:ARG:HA	5:A:404:EPE:C8	2.45	0.46
1:B:33:ASP:HA	1:B:34:PRO:HD3	1.72	0.46
1:A:191:PHE:CE1	1:A:208:VAL:HB	2.52	0.45
1:A:1:MET:HG2	1:A:2:ILE:H	1.80	0.45
1:B:156:THR:OG1	1:B:157:ARG:NH2	2.50	0.45
1:B:285:GLU:CD	1:B:285:GLU:N	2.75	0.45
1:B:146:ARG:HG3	1:B:177:TYR:CE1	2.51	0.45
1:B:203:VAL:HG23	1:B:204:GLY:N	2.32	0.45
1:A:147:GLU:HG2	1:A:148:TYR:N	2.31	0.45
1:B:285:GLU:HG2	1:B:286:ASN:H	1.82	0.45
1:A:1:MET:HE2	1:A:298:ASN:CG	2.42	0.45
1:B:261:GLU:O	1:B:265:GLU:HG3	2.17	0.45
1:A:201:THR:HG23	1:A:202:PRO:CD	2.47	0.44
1:B:270:VAL:HG13	1:B:278:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:312:HIS:O	1:B:315:VAL:HG12	2.16	0.44
1:B:248:ARG:NH1	8:B:672:HOH:O	2.49	0.44
1:A:331:LEU:O	1:A:332:ALA:HB2	2.18	0.44
1:A:272:ARG:NH1	1:A:274:ASP:OD2	2.48	0.44
1:B:274:ASP:O	1:B:275:THR:C	2.60	0.43
1:B:199:LEU:HD23	1:B:199:LEU:HA	1.85	0.43
1:A:168:ALA:HA	1:A:194:CYS:HB2	2.00	0.43
1:B:285:GLU:HG2	1:B:286:ASN:N	2.33	0.43
1:B:201:THR:CG2	1:B:203:VAL:O	2.65	0.43
1:B:295:LYS:HE2	1:B:295:LYS:HB3	1.87	0.43
1:B:160:ASN:HD22	5:B:404:EPE:H71	1.82	0.43
1:A:201:THR:HG22	1:A:203:VAL:N	2.34	0.42
1:B:112:PRO:HB2	1:B:115:LYS:HB2	2.01	0.42
1:A:14:ARG:NE	8:A:625:HOH:O	2.21	0.42
1:B:32:ASP:O	1:B:34:PRO:HD3	2.20	0.42
1:B:285:GLU:CG	1:B:286:ASN:H	2.32	0.42
1:A:1:MET:HE2	1:A:298:ASN:ND2	2.34	0.42
1:A:71[B]:GLU:OE1	8:A:596:HOH:O	2.22	0.42
1:A:202:PRO:C	1:A:203:VAL:CG1	2.93	0.42
1:A:157:ARG:HA	5:A:404:EPE:H82	2.02	0.41
1:B:39:LEU:HD13	1:B:239:MET:HG2	2.01	0.41
1:B:78:VAL:CG2	1:B:79:GLY:N	2.83	0.41
1:B:194:CYS:SG	1:B:197:LYS:HE2	2.61	0.41
1:A:197:LYS:NZ	4:A:403[B]:2BK:H9	2.35	0.41
1:A:197:LYS:NZ	3:A:402[A]:2BO:H6	2.35	0.41
1:B:201:THR:HA	1:B:202:PRO:HD3	1.93	0.41
1:A:27:ASP:HB3	1:A:30:TYR:HD2	1.86	0.41
1:A:147:GLU:HG2	1:A:148:TYR:H	1.85	0.41
1:B:147:GLU:H	1:B:147:GLU:CD	2.29	0.41
1:B:304:SER:OG	1:B:305:PRO:CD	2.69	0.41
1:B:325:ALA:HA	8:B:502:HOH:O	2.21	0.41
1:B:203:VAL:HG13	1:B:234:LEU:HD22	2.03	0.40
1:B:292:GLU:HA	1:B:295:LYS:HE2	2.02	0.40
1:A:315:VAL:HG13	1:A:315:VAL:O	2.20	0.40
1:B:203:VAL:HA	8:B:593:HOH:O	2.22	0.40
1:B:201:THR:HG23	1:B:202:PRO:HD2	2.03	0.40
1:B:312:HIS:H	1:B:315:VAL:CG1	2.35	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	331/333 (99%)	320 (97%)	10 (3%)	1 (0%)	36	36
1	B	330/333 (99%)	313 (95%)	17 (5%)	0	100	100
All	All	661/666 (99%)	633 (96%)	27 (4%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	287	ALA

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	261/261 (100%)	251 (96%)	10 (4%)	29	32
1	B	260/261 (100%)	249 (96%)	11 (4%)	26	28
All	All	521/522 (100%)	500 (96%)	21 (4%)	28	29

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	53	ILE
1	A	144	LEU
1	A	158	LYS
1	A	194	CYS

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Mol	Chain	Res	Type
1	A	201	THR
1	A	203	VAL
1	A	233	ILE
1	A	298	ASN
1	A	304	SER
1	B	45	GLU
1	B	53	ILE
1	B	115	LYS
1	B	137	ASN
1	B	157	ARG
1	B	201	THR
1	B	203	VAL
1	B	219	ARG
1	B	285	GLU
1	B	286	ASN
1	B	328	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	60	GLN
1	A	137	ASN
1	A	245	ASN
1	A	286	ASN
1	A	298	ASN
1	A	302	ASN
1	B	37	ASN
1	B	60	GLN
1	B	137	ASN
1	B	160	ASN
1	B	164	HIS
1	B	210	ASN
1	B	245	ASN
1	B	286	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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$
7	PLG	B	403	-	20,20,20	4.36	8 (40%)	26,28,28	3.58	12 (46%)
5	EPE	A	404	-	15,15,15	1.47	2 (13%)	19,20,20	1.10	1 (5%)
3	2BO	A	402[A]	-	23,23,23	4.08	11 (47%)	30,33,33	2.76	14 (46%)
4	2BK	A	403[B]	-	23,23,23	4.04	10 (43%)	30,33,33	2.74	13 (43%)
5	EPE	B	404	-	15,15,15	1.65	4 (26%)	19,20,20	1.34	2 (10%)

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
7	PLG	B	403	-	-	5/12/12/12	0/1/1/1
5	EPE	A	404	-	-	1/9/19/19	0/1/1/1
3	2BO	A	402[A]	-	-	6/19/19/19	0/1/1/1
4	2BK	A	403[B]	-	-	5/19/19/19	0/1/1/1
5	EPE	B	404	-	-	2/9/19/19	0/1/1/1

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	403	PLG	C5-C4	13.54	1.59	1.40
3	A	402[A]	2BO	C5-C4	13.46	1.59	1.40
4	A	403[B]	2BK	C5-C4	13.46	1.59	1.40
7	B	403	PLG	C3-C2	9.68	1.51	1.41
3	A	402[A]	2BO	C3-C2	8.09	1.49	1.41
4	A	403[B]	2BK	C3-C2	8.09	1.49	1.41
3	A	402[A]	2BO	C3-C4	6.09	1.49	1.40
4	A	403[B]	2BK	C3-C4	6.09	1.49	1.40
3	A	402[A]	2BO	C2-N1	5.29	1.43	1.33
4	A	403[B]	2BK	C2-N1	5.29	1.43	1.33
7	B	403	PLG	C2-N1	5.07	1.42	1.33
7	B	403	PLG	C3-C4	5.01	1.47	1.40
5	B	404	EPE	C6-N1	4.37	1.58	1.46
7	B	403	PLG	C6-N1	4.06	1.42	1.34
5	A	404	EPE	C6-N1	3.99	1.57	1.46
3	A	402[A]	2BO	C6-N1	3.79	1.42	1.34
4	A	403[B]	2BK	C6-N1	3.79	1.42	1.34
3	A	402[A]	2BO	C4A-N	-2.96	1.38	1.46
4	A	403[B]	2BK	C4A-N	-2.96	1.38	1.46
3	A	402[A]	2BO	CA-N	2.96	1.52	1.46
4	A	403[B]	2BK	CA-N	2.96	1.52	1.46
3	A	402[A]	2BO	CG-CB	2.69	1.59	1.51
3	A	402[A]	2BO	C5A-C5	2.61	1.57	1.50
4	A	403[B]	2BK	C5A-C5	2.61	1.57	1.50
7	B	403	PLG	C5A-C5	2.36	1.57	1.50
3	A	402[A]	2BO	O-C	-2.29	1.23	1.30
4	A	403[B]	2BK	O-C	-2.29	1.23	1.30
7	B	403	PLG	P-OP3	-2.25	1.46	1.54
3	A	402[A]	2BO	P-O2P	-2.16	1.46	1.54
4	A	403[B]	2BK	P-O2P	-2.16	1.46	1.54
5	B	404	EPE	C10-S	2.14	1.80	1.77
5	B	404	EPE	C3-N4	2.14	1.52	1.46
5	B	404	EPE	C7-N4	2.12	1.52	1.47
5	A	404	EPE	C10-S	2.11	1.80	1.77
7	B	403	PLG	C4A-C4	-2.08	1.48	1.52

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	403	PLG	C4A-N-CA	12.07	126.78	112.72
7	B	403	PLG	C2A-C2-C3	7.43	129.49	120.80
3	A	402[A]	2BO	C2A-C2-C3	7.16	129.18	120.80
4	A	403[B]	2BK	C2A-C2-C3	7.16	129.18	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402[A]	2BO	C4A-N-CA	5.92	128.08	114.63
4	A	403[B]	2BK	C4A-N-CA	5.92	128.08	114.63
3	A	402[A]	2BO	C6-N1-C2	5.09	128.42	119.20
4	A	403[B]	2BK	C6-N1-C2	5.09	128.42	119.20
7	B	403	PLG	C6-N1-C2	4.89	128.07	119.20
7	B	403	PLG	C4-C4A-N	4.26	119.37	111.50
7	B	403	PLG	C3-C2-N1	-4.25	115.60	120.96
3	A	402[A]	2BO	C3-C2-N1	-4.19	115.67	120.96
4	A	403[B]	2BK	C3-C2-N1	-4.19	115.67	120.96
7	B	403	PLG	C4A-C4-C5	3.89	123.99	119.75
4	A	403[B]	2BK	CG-CB-CA	3.85	119.90	112.29
3	A	402[A]	2BO	OB-CB-CG	-3.71	98.59	109.68
3	A	402[A]	2BO	C5-C6-N1	-3.61	117.96	123.83
4	A	403[B]	2BK	C5-C6-N1	-3.61	117.96	123.83
7	B	403	PLG	C5-C6-N1	-3.54	118.06	123.83
3	A	402[A]	2BO	C4A-C4-C5	3.38	123.43	119.75
4	A	403[B]	2BK	C4A-C4-C5	3.38	123.43	119.75
5	A	404	EPE	C9-N1-C6	3.35	120.18	111.24
5	B	404	EPE	C9-N1-C6	3.34	120.13	111.24
3	A	402[A]	2BO	C6-C5-C4	3.33	120.58	118.06
4	A	403[B]	2BK	C6-C5-C4	3.33	120.58	118.06
7	B	403	PLG	C6-C5-C4	3.31	120.56	118.06
3	A	402[A]	2BO	O-C-OT	-2.86	117.59	124.08
4	A	403[B]	2BK	O-C-OT	-2.86	117.59	124.08
3	A	402[A]	2BO	O3-C3-C4	2.85	126.44	118.18
4	A	403[B]	2BK	O3-C3-C4	2.85	126.44	118.18
7	B	403	PLG	O3-C3-C4	2.65	125.87	118.18
5	B	404	EPE	O3S-S-C10	-2.65	100.82	106.00
3	A	402[A]	2BO	C3-C4-C5	-2.60	116.37	118.73
4	A	403[B]	2BK	C3-C4-C5	-2.60	116.37	118.73
7	B	403	PLG	C3-C4-C5	-2.44	116.52	118.73
3	A	402[A]	2BO	O3-C3-C2	-2.42	112.56	117.58
4	A	403[B]	2BK	O3-C3-C2	-2.42	112.56	117.58
7	B	403	PLG	O3-C3-C2	-2.24	112.94	117.58
3	A	402[A]	2BO	CG-CB-CA	2.12	116.47	112.29
3	A	402[A]	2BO	O-C-CA	2.06	121.30	114.15
4	A	403[B]	2BK	O-C-CA	2.06	121.30	114.15
7	B	403	PLG	OP4-C5A-C5	2.04	113.17	109.36

There are no chirality outliers.

All (19) torsion outliers are listed below:

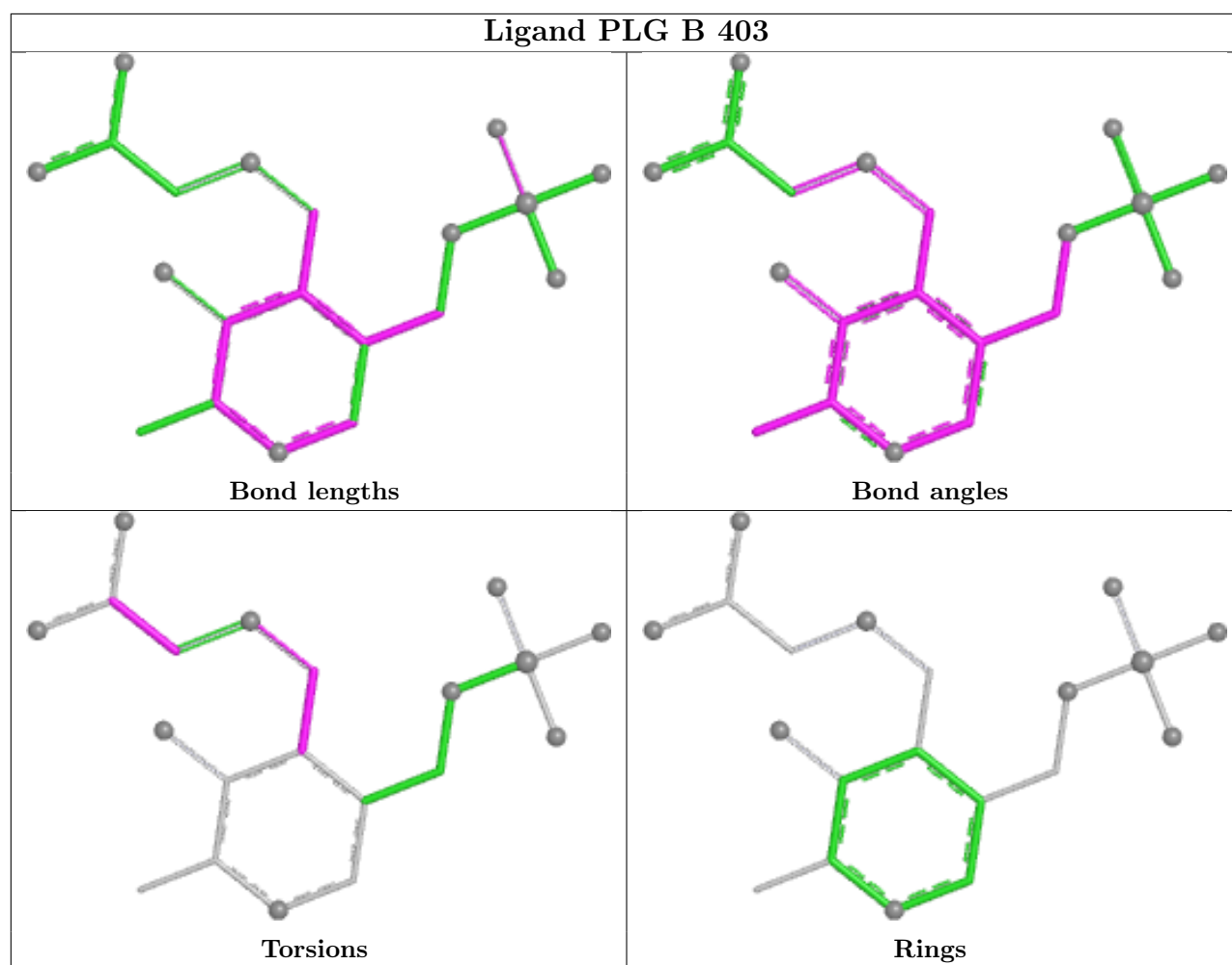
Mol	Chain	Res	Type	Atoms
3	A	402[A]	2BO	C5-C4-C4A-N
3	A	402[A]	2BO	CB-CA-N-C4A
4	A	403[B]	2BK	C5-C4-C4A-N
4	A	403[B]	2BK	CB-CA-N-C4A
7	B	403	PLG	C5-C4-C4A-N
5	B	404	EPE	C8-C7-N4-C3
7	B	403	PLG	C4-C4A-N-CA
7	B	403	PLG	OXT-C-CA-N
7	B	403	PLG	O-C-CA-N
3	A	402[A]	2BO	C4-C4A-N-CA
4	A	403[B]	2BK	C4-C4A-N-CA
3	A	402[A]	2BO	C-CA-N-C4A
4	A	403[B]	2BK	C-CA-N-C4A
5	B	404	EPE	C8-C7-N4-C5
3	A	402[A]	2BO	C3-C4-C4A-N
4	A	403[B]	2BK	C3-C4-C4A-N
7	B	403	PLG	C3-C4-C4A-N
3	A	402[A]	2BO	C-CA-CB-CG
5	A	404	EPE	C8-C7-N4-C5

There are no ring outliers.

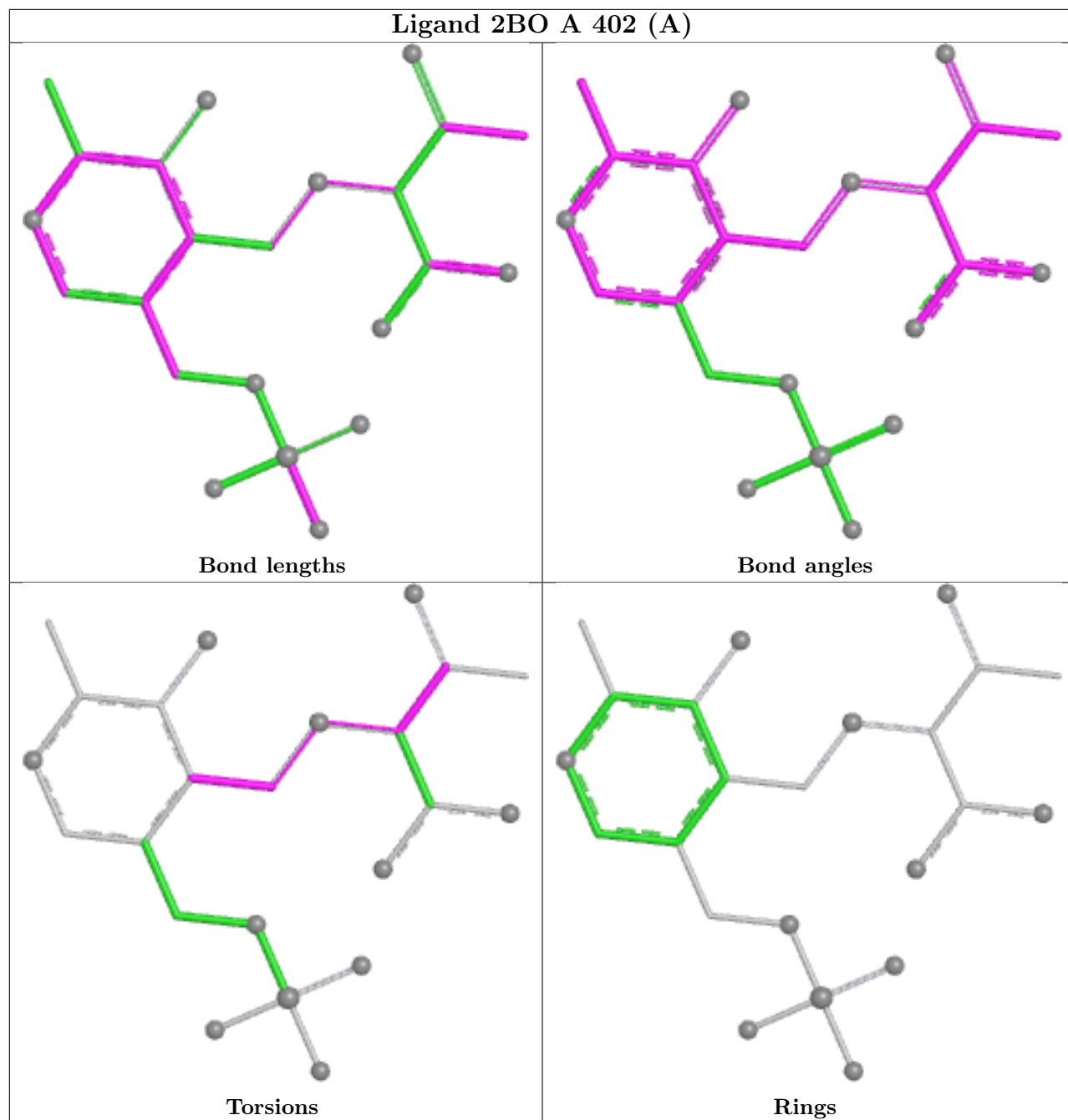
5 monomers are involved in 9 short contacts:

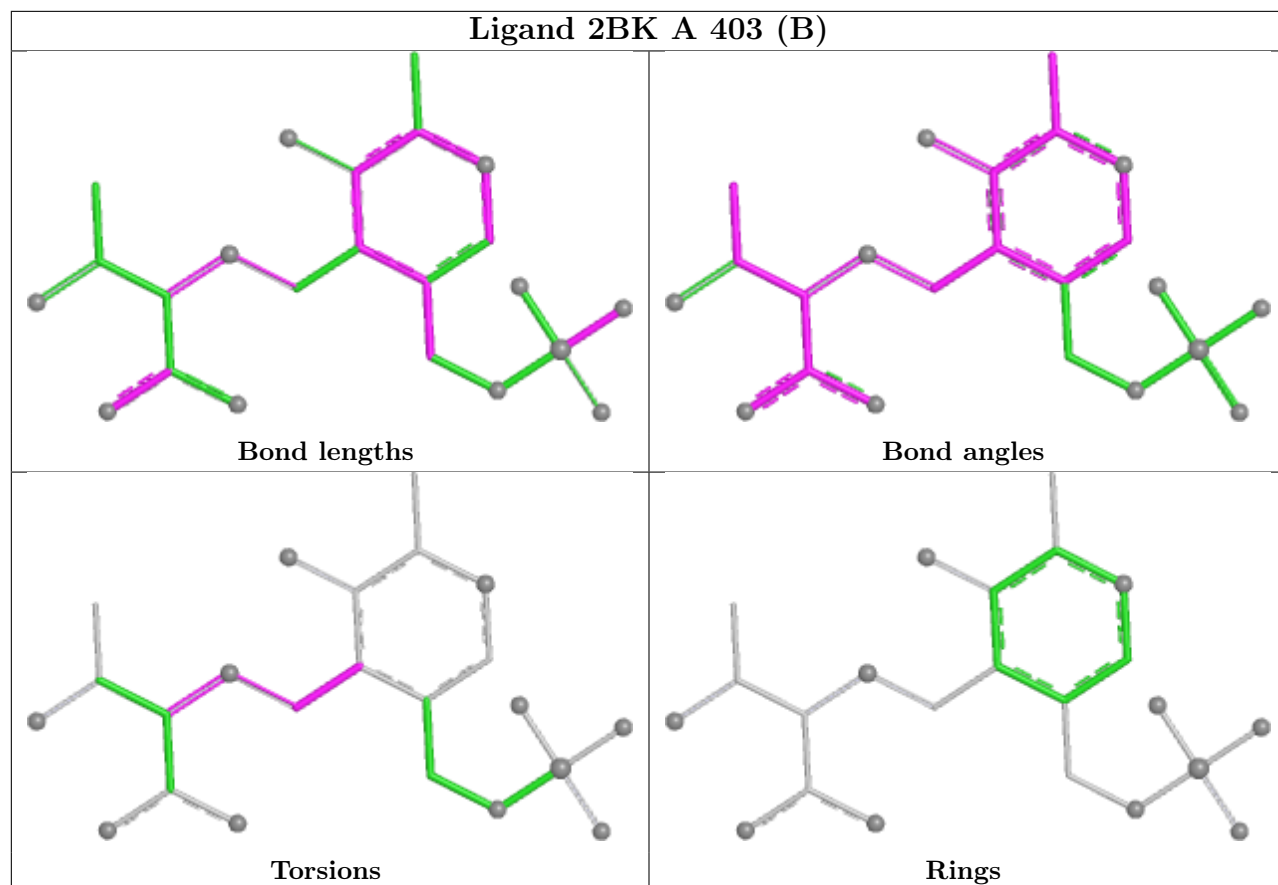
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	403	PLG	2	0
5	A	404	EPE	2	0
3	A	402[A]	2BO	2	0
4	A	403[B]	2BK	2	0
5	B	404	EPE	1	0

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.



Ligand 2BO A 402 (A)





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	332/333 (99%)	-0.43	2 (0%) 85 87	9, 19, 38, 53	1 (0%)
1	B	332/333 (99%)	-0.28	6 (1%) 67 70	8, 19, 49, 72	0
All	All	664/666 (99%)	-0.35	8 (1%) 76 78	8, 19, 43, 72	1 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	330	PHE	4.2
1	A	332	ALA	3.1
1	B	332	ALA	3.0
1	B	293	TYR	2.7
1	B	331	LEU	2.5
1	B	285	GLU	2.3
1	A	296	ALA	2.1
1	B	287	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

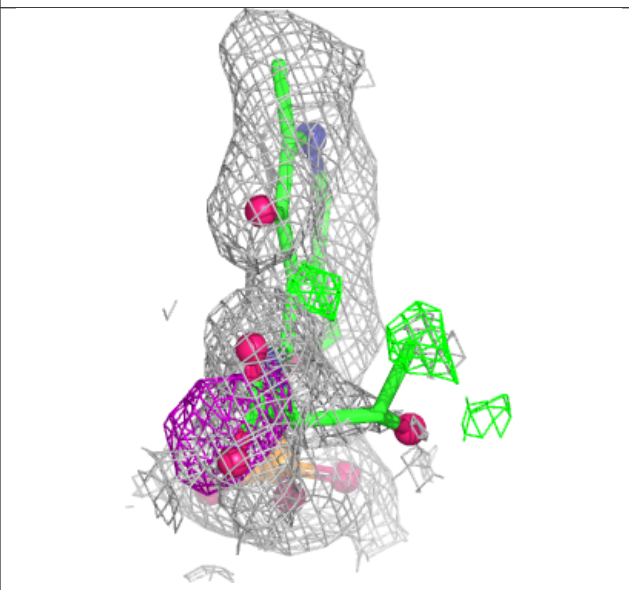
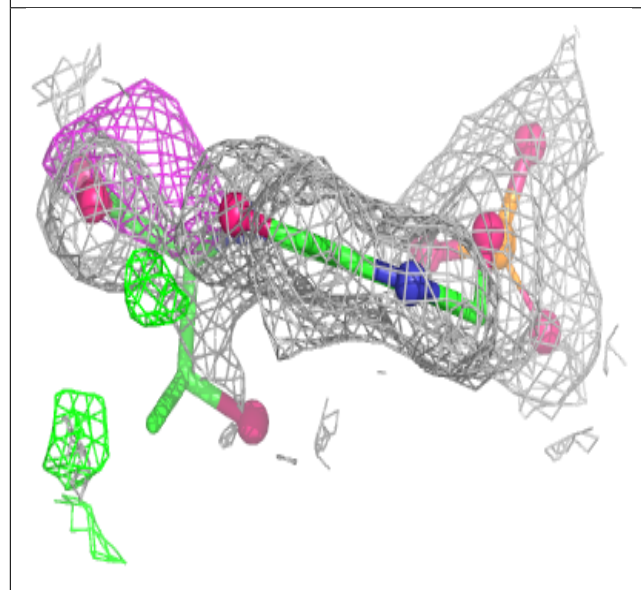
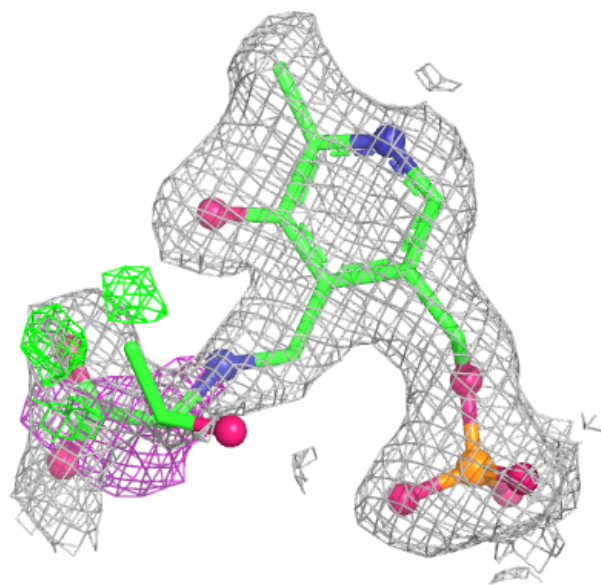
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EPE	B	404	15/15	0.86	0.19	66,67,70,71	0
4	2BK	A	403[B]	23/23	0.91	0.11	13,22,26,30	23
5	EPE	A	404	15/15	0.94	0.09	27,30,36,38	0
3	2BO	A	402[A]	23/23	0.94	0.10	13,22,26,27	23
7	PLG	B	403	20/20	0.94	0.09	15,25,40,41	0
2	MG	B	402	1/1	0.96	0.08	27,27,27,27	0
6	CL	A	405	1/1	0.98	0.34	20,20,20,20	1
2	MG	B	401	1/1	0.99	0.02	8,8,8,8	0
2	MG	A	401	1/1	0.99	0.03	8,8,8,8	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.

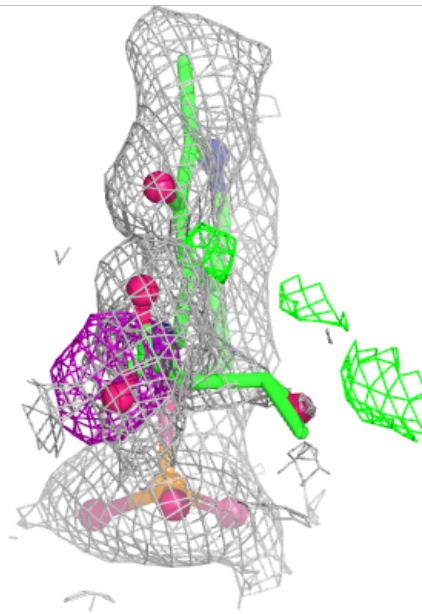
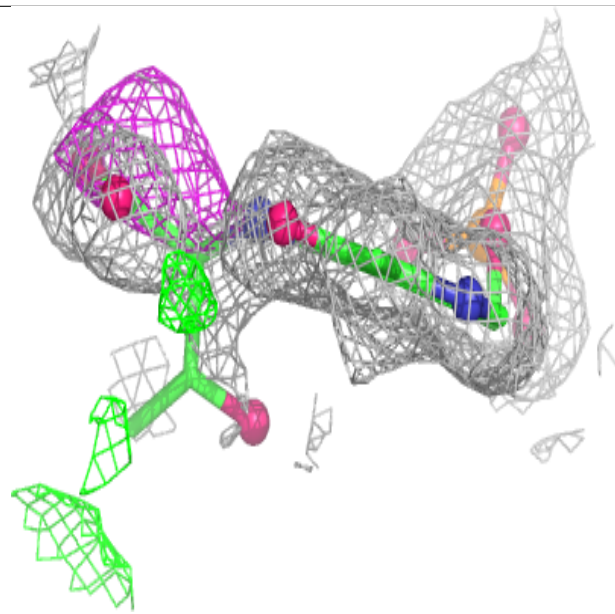
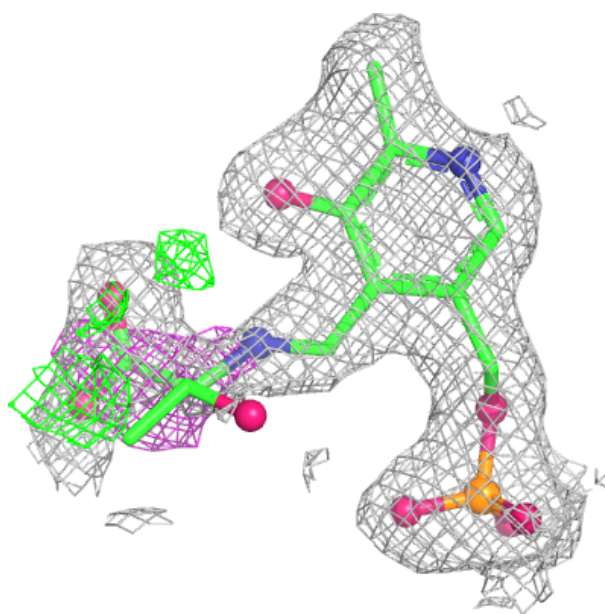
Electron density around 2BK A 403 (B):

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



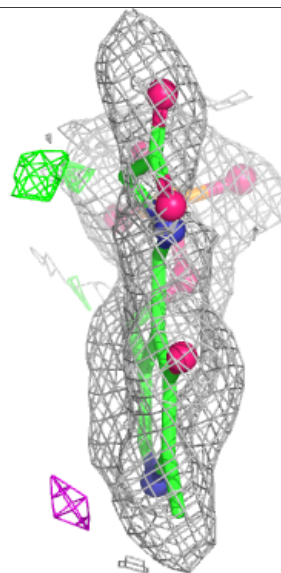
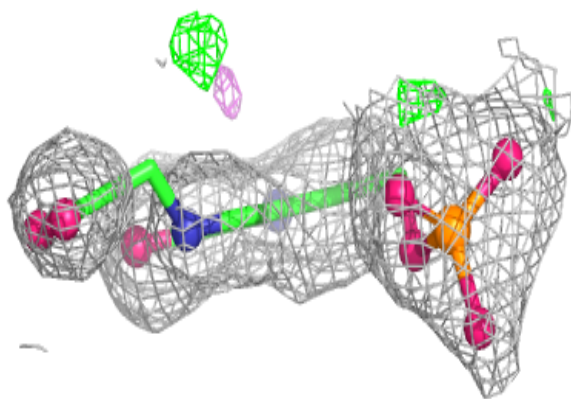
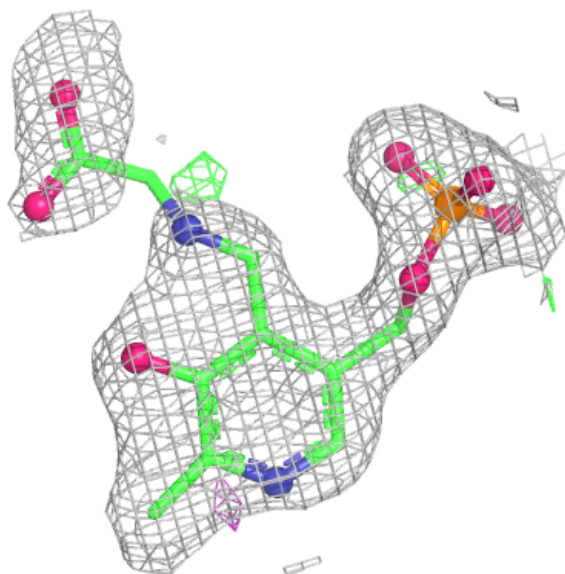
Electron density around 2BO A 402 (A):

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



Electron density around PLG B 403:

$2mF_o-DF_c$ (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.