



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:39 AM GMT

PDB ID : 3FHX
Title : Crystal structure of D235A mutant of human pyridoxal kinase
Authors : Safo, M.K.; Gandhi, A.K.; Musayev, F.N.; Ghatge, M.; Di Salvo, M.L.; Schirch, V.
Deposited on : 2008-12-10
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

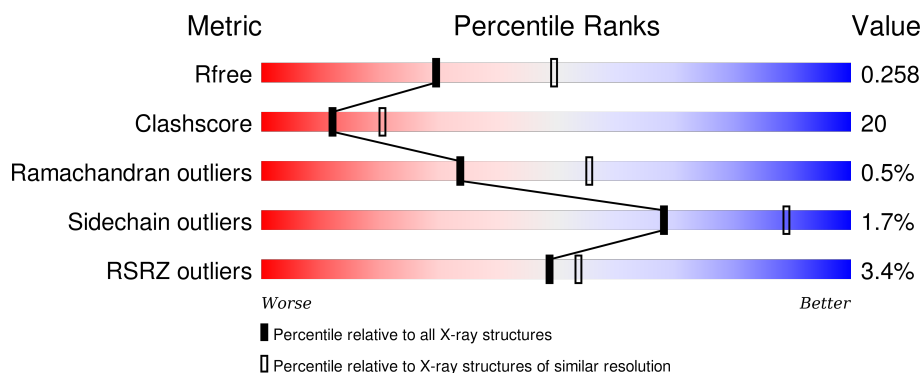
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	312	<div> <div>5%</div> <div>65%</div> <div>33%</div> <div>..</div> </div>
1	B	312	<div> <div>2%</div> <div>66%</div> <div>31%</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
5	PXL	A	313	-	-	-	X
5	PXL	B	313	-	-	X	X
6	SO4	A	316	-	-	-	X
6	SO4	A	317	-	-	-	X
7	MPD	B	319	-	-	-	X
7	MPD	B	320	-	-	-	X
8	PLP	B	314	-	-	X	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 5197 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 Pyridoxal kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	1
			2427	1529	428	455	15			
1	B	310	Total	C	N	O	S	0	0	0
			2442	1539	430	458	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	ALA	ASP	ENGINEERED	UNP O00764
B	235	ALA	ASP	ENGINEERED	UNP O00764

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

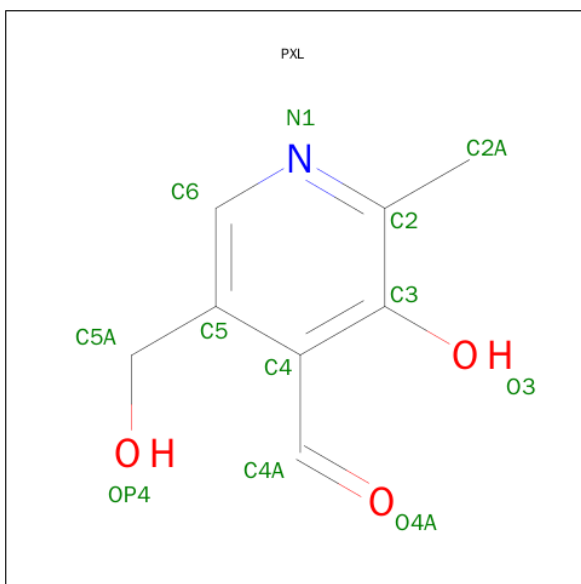
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
4	B	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 5 is 3-HYDROXY-5-(HYDROXYMETHYL)-2-METHYLISONICOTINALDEHYDE (three-letter code: PXL) (formula: $C_8H_9NO_3$).



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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			12	8	1	3		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



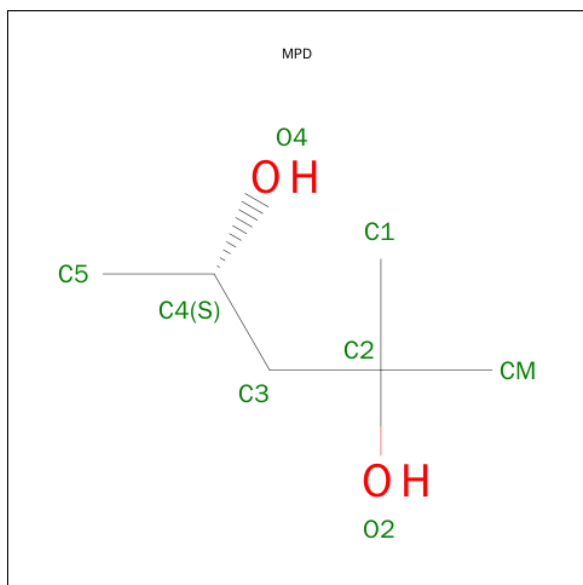
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total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

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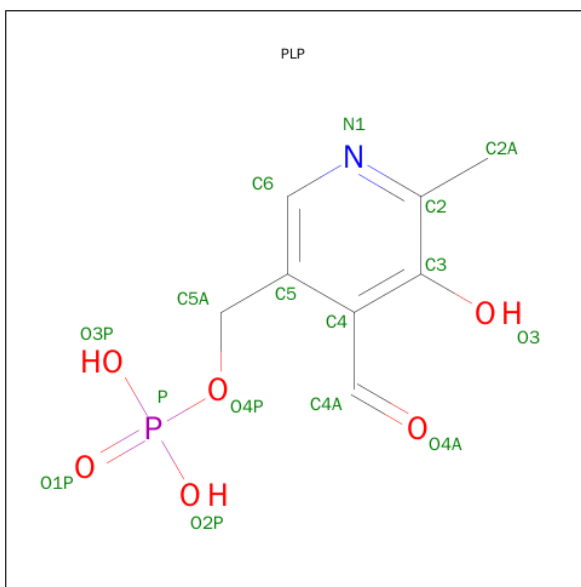
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			8	6	2		
7	B	1	Total	C	O	0	0
			8	6	2		
7	B	1	Total	C	O	0	0
			8	6	2		
7	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 8 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

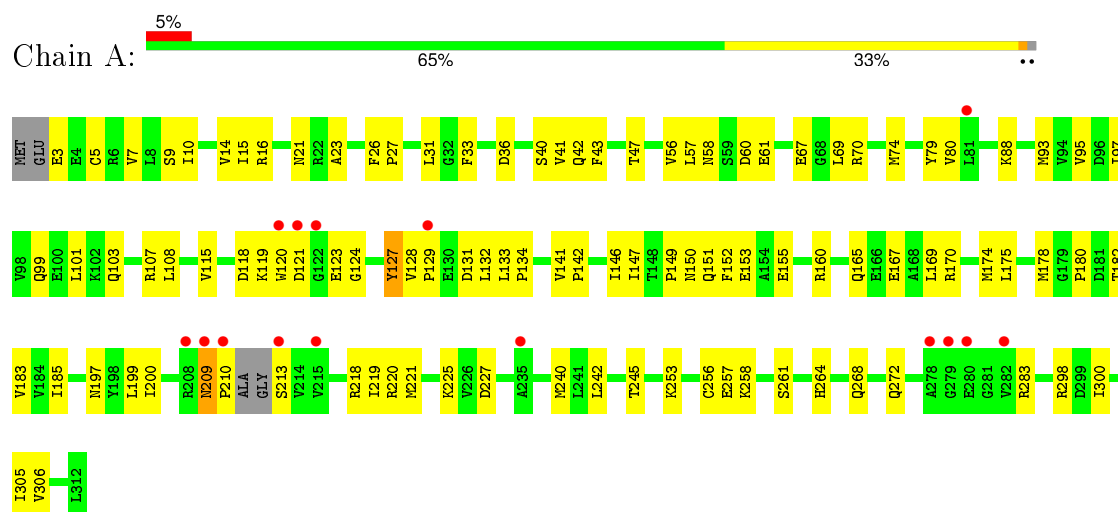
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	71	Total	O	0	0
			71	71		
9	B	64	Total	O	0	0
			64	64		

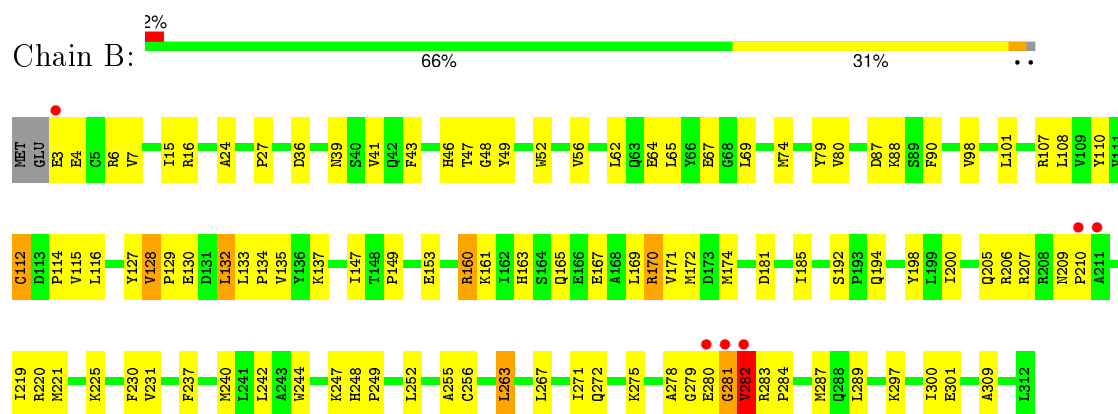
3 Residue-property plots

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



• Molecule 1: Pyridoxal kinase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	91.22Å 115.42Å 168.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.93 – 2.50 32.69 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.93-2.50) 99.7 (32.69-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.51Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.212 , 0.262 0.207 , 0.258	Depositor DCC
R_{free} test set	1568 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	36.7	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 66.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 31128 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5197	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, PLP, NA, MPD, SO4, ATP, PXL

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	0.38	0/2471	0.62	0/3348
1	B	0.42	0/2488	0.67	2/3373 (0.1%)
All	All	0.40	0/4959	0.64	2/6721 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	282	VAL	N-CA-C	-6.83	92.56	111.00
1	B	282	VAL	N-CA-CB	6.68	126.19	111.50

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	2427	0	2437	90	0
1	B	2442	0	2454	115	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	31	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	31	0	12	0	0
5	A	12	0	9	1	0
5	B	12	0	9	9	0
6	A	35	0	0	0	0
6	B	20	0	0	0	0
7	A	8	0	14	0	0
7	B	24	0	42	0	0
8	B	16	0	8	7	0
9	A	71	0	0	2	0
9	B	64	0	0	1	0
All	All	5197	0	4997	200	1

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 20.

All (200) 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:3:GLU:HB2	1:B:4:GLU:HA	1.29	1.08
1:B:231:VAL:HG13	8:B:314:PLP:H4A	1.33	1.05
1:B:278:ALA:HB1	1:B:282:VAL:CG2	1.95	0.97
1:B:3:GLU:CB	1:B:4:GLU:HA	1.92	0.96
1:A:200:ILE:HD13	1:A:220:ARG:NH2	1.87	0.88
1:B:46:HIS:CD2	1:B:48:GLY:H	1.91	0.88
1:B:192:SER:HB2	1:B:200:ILE:HD11	1.56	0.88
1:B:3:GLU:CB	1:B:4:GLU:CA	2.53	0.87
1:B:205:GLN:HE21	1:B:207:ARG:HH11	1.21	0.84
1:A:123:GLU:HG2	1:A:124:GLY:H	1.41	0.84
1:B:281:GLY:O	1:B:282:VAL:HG13	1.77	0.83
1:B:3:GLU:HB2	1:B:4:GLU:CA	2.09	0.82
1:B:278:ALA:HB1	1:B:282:VAL:HG22	1.59	0.82
1:B:47:THR:HG23	5:B:313:PXL:O3	1.80	0.82
1:B:221:MET:CE	1:B:256:CYS:HB3	2.10	0.81
1:B:46:HIS:HD2	1:B:48:GLY:H	1.27	0.80
1:B:46:HIS:HD2	1:B:48:GLY:N	1.83	0.76
1:B:231:VAL:HG13	8:B:314:PLP:C4A	2.14	0.76
1:B:221:MET:HE2	1:B:256:CYS:HB3	1.67	0.76
1:B:160:ARG:HH11	1:B:160:ARG:HG2	1.51	0.74
1:A:123:GLU:HG2	1:A:124:GLY:N	2.03	0.73
1:B:205:GLN:HE21	1:B:207:ARG:NH1	1.86	0.73
1:A:200:ILE:CD1	1:A:220:ARG:NH2	2.52	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:ASN:HB2	1:B:210:PRO:HD2	1.71	0.72
1:A:80:VAL:HG23	1:A:108:LEU:HD21	1.71	0.72
1:B:116:LEU:HB2	1:B:153:GLU:HG2	1.72	0.71
1:B:69:LEU:HD23	1:B:74:MET:HE3	1.73	0.70
1:A:99:GLN:O	1:A:103:GLN:HG3	1.92	0.69
1:B:47:THR:N	5:B:313:PXL:O4A	2.25	0.69
5:B:313:PXL:OP4	8:B:314:PLP:H5A1	1.93	0.68
1:A:221:MET:CE	1:A:256:CYS:HB3	2.26	0.66
1:B:46:HIS:CD2	1:B:48:GLY:N	2.61	0.65
1:A:200:ILE:CD1	1:A:220:ARG:HH22	2.09	0.65
1:A:123:GLU:CG	1:A:124:GLY:H	2.09	0.64
1:A:200:ILE:HD13	1:A:220:ARG:HH22	1.63	0.64
1:B:205:GLN:HB2	1:B:252:LEU:HD22	1.80	0.62
1:A:119:LYS:HG3	1:A:152:PHE:HB2	1.80	0.62
1:B:165:GLN:HE21	1:B:220:ARG:HH11	1.47	0.62
1:A:221:MET:HE1	1:A:256:CYS:HB3	1.82	0.61
1:A:15:ILE:HD11	1:B:65:LEU:HD22	1.82	0.61
1:A:42:GLN:HE22	1:B:39:ASN:H	1.47	0.61
1:B:46:HIS:HB2	5:B:313:PXL:C4A	2.30	0.61
5:B:313:PXL:H5A1	8:B:314:PLP:C6	2.30	0.61
1:B:231:VAL:CG1	8:B:314:PLP:H4A	2.21	0.61
1:B:128:VAL:HG13	1:B:132:LEU:HD22	1.83	0.61
1:A:210:PRO:N	1:A:213:SER:HB3	2.16	0.61
1:A:26:PHE:HB3	1:A:27:PRO:HD3	1.83	0.59
1:A:119:LYS:CG	1:A:152:PHE:HB2	2.32	0.59
1:A:3:GLU:CB	9:A:383:HOH:O	2.50	0.59
1:A:242:LEU:O	1:A:245:THR:HG22	2.03	0.59
1:B:209:ASN:HB2	1:B:210:PRO:CD	2.33	0.58
1:A:264:HIS:CD2	1:A:306:VAL:HG21	2.39	0.58
1:A:58:ASN:OD1	1:A:61:GLU:HG3	2.04	0.58
1:B:165:GLN:HE21	1:B:220:ARG:HD2	1.69	0.57
1:B:129:PRO:O	1:B:132:LEU:HB2	2.05	0.57
1:B:221:MET:HE1	1:B:256:CYS:HB3	1.84	0.57
1:A:3:GLU:HB2	9:A:383:HOH:O	2.05	0.57
1:B:46:HIS:HB2	5:B:313:PXL:O4A	2.05	0.57
1:B:281:GLY:O	1:B:282:VAL:CG1	2.52	0.57
1:A:133:LEU:HB3	1:A:134:PRO:HD3	1.85	0.57
1:B:69:LEU:HA	1:B:74:MET:HE2	1.87	0.57
1:B:282:VAL:HG23	1:B:283:ARG:O	2.04	0.56
1:A:147:ILE:HD11	1:A:183:VAL:HG22	1.87	0.56
1:A:95:VAL:O	1:A:99:GLN:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ILE:HG12	1:A:182:THR:HB	1.86	0.56
1:B:165:GLN:NE2	1:B:220:ARG:HH11	2.03	0.55
1:A:150:ASN:OD1	1:A:153:GLU:HG3	2.07	0.55
1:B:160:ARG:CG	1:B:160:ARG:HH11	2.19	0.55
1:B:49:TYR:HE2	1:B:287:MET:HB2	1.72	0.55
1:A:23:ALA:O	1:A:27:PRO:HG2	2.07	0.55
1:A:69:LEU:HD23	1:A:74:MET:HE1	1.88	0.54
1:B:149:PRO:O	1:B:185:ILE:HA	2.08	0.54
1:A:253:LYS:O	1:A:257:GLU:HG3	2.07	0.54
1:A:41:VAL:HG12	1:A:56:VAL:HG13	1.89	0.54
1:A:298:ARG:HH11	1:A:298:ARG:HG3	1.71	0.54
1:B:24:ALA:O	1:B:27:PRO:HD2	2.08	0.54
1:B:283:ARG:NH1	9:B:378:HOH:O	2.41	0.54
1:B:107:ARG:HB2	1:B:107:ARG:NH1	2.23	0.53
1:B:110:TYR:CZ	1:B:112:CYS:HB2	2.44	0.53
1:A:47:THR:HG23	5:A:313:PXL:O3	2.09	0.53
1:A:42:GLN:NE2	1:B:39:ASN:H	2.06	0.52
1:B:247:LYS:HG3	1:B:248:HIS:CE1	2.44	0.52
1:A:169:LEU:HD22	1:A:218:ARG:HD3	1.91	0.52
1:B:181:ASP:HB3	1:B:206:ARG:O	2.09	0.52
1:B:69:LEU:HD23	1:B:74:MET:CE	2.37	0.52
1:A:120:TRP:O	1:A:121:ASP:HB2	2.09	0.52
1:A:175:LEU:O	1:A:178:MET:HB2	2.10	0.52
1:A:197:ASN:HA	1:A:225:LYS:HE2	1.90	0.52
1:B:3:GLU:HB3	1:B:4:GLU:CA	2.39	0.52
1:A:200:ILE:HD13	1:A:220:ARG:CZ	2.38	0.52
1:A:119:LYS:HE3	1:A:123:GLU:HG3	1.91	0.52
1:B:284:PRO:HB2	1:B:289:LEU:HG	1.90	0.52
1:B:41:VAL:HG12	1:B:56:VAL:HB	1.91	0.52
1:B:80:VAL:HG11	1:B:98:VAL:HG22	1.91	0.52
1:A:298:ARG:HG3	1:A:298:ARG:NH1	2.25	0.52
1:A:31:LEU:HD11	1:A:240:MET:HE1	1.92	0.51
1:A:128:VAL:HG11	1:A:132:LEU:HD23	1.92	0.51
1:B:230:PHE:CE1	1:B:289:LEU:HD22	2.45	0.51
1:A:240:MET:CE	1:A:300:ILE:HG23	2.40	0.51
1:A:219:ILE:C	1:A:219:ILE:HD12	2.30	0.51
1:B:163:HIS:HB2	1:B:167:GLU:OE2	2.11	0.51
1:B:171:VAL:HA	1:B:174:MET:CE	2.41	0.51
1:A:119:LYS:HE2	1:A:123:GLU:HA	1.93	0.51
1:B:3:GLU:HB3	1:B:4:GLU:C	2.31	0.50
1:A:16:ARG:HD3	1:B:36:ASP:OD2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:GLU:N	1:B:4:GLU:OE1	2.45	0.50
1:B:192:SER:C	1:B:194:GLN:H	2.16	0.49
1:B:165:GLN:NE2	1:B:220:ARG:HD2	2.27	0.49
1:B:247:LYS:C	1:B:249:PRO:HD3	2.32	0.49
1:B:247:LYS:O	1:B:249:PRO:HD3	2.11	0.49
1:A:149:PRO:O	1:A:185:ILE:HA	2.12	0.49
1:A:67:GLU:OE2	1:A:70:ARG:NH2	2.45	0.49
1:B:133:LEU:HG	1:B:137:LYS:HE3	1.94	0.49
1:A:123:GLU:CG	1:A:124:GLY:N	2.68	0.49
1:A:240:MET:HE1	1:A:300:ILE:HG23	1.94	0.48
1:B:7:VAL:HG22	1:B:79:TYR:HB2	1.96	0.48
1:A:42:GLN:HE22	1:B:39:ASN:N	2.11	0.48
1:B:240:MET:HE2	1:B:300:ILE:HG23	1.96	0.47
1:B:128:VAL:HG13	1:B:132:LEU:CD2	2.44	0.47
1:A:127:TYR:O	1:A:128:VAL:HG23	2.14	0.47
1:A:107:ARG:HG2	1:A:107:ARG:HH11	1.78	0.47
1:A:268:GLN:O	1:A:272:GLN:HG3	2.14	0.47
5:B:313:PXL:OP4	8:B:314:PLP:C5A	2.62	0.47
1:A:93:MET:HE3	1:A:93:MET:O	2.15	0.47
1:B:242:LEU:HD23	1:B:242:LEU:C	2.35	0.47
1:B:205:GLN:CB	1:B:252:LEU:HD22	2.45	0.47
1:B:198:TYR:N	1:B:225:LYS:HE3	2.30	0.46
1:A:221:MET:HE2	1:A:256:CYS:HB3	1.94	0.46
1:B:64:GLU:O	1:B:67:GLU:HB3	2.15	0.46
1:B:112:CYS:O	1:B:147:ILE:HA	2.15	0.46
1:A:88:LYS:HA	1:A:132:LEU:CD1	2.45	0.46
1:B:87:ASP:HB3	1:B:90:PHE:H	1.80	0.46
1:B:47:THR:N	5:B:313:PXL:O3	2.49	0.46
1:B:263:LEU:O	1:B:267:LEU:HG	2.15	0.46
1:A:115:VAL:HA	1:A:153:GLU:OE2	2.16	0.46
1:A:93:MET:HE2	1:A:97:ILE:HG13	1.96	0.46
1:A:69:LEU:HD23	1:A:74:MET:CE	2.46	0.45
1:A:88:LYS:HD3	1:A:131:ASP:OD2	2.16	0.45
1:B:169:LEU:HD23	1:B:172:MET:CE	2.46	0.45
1:A:149:PRO:HB2	1:A:153:GLU:HB2	1.99	0.45
1:B:278:ALA:HB1	1:B:282:VAL:HG21	1.90	0.45
1:A:9:SER:OG	1:A:21:ASN:ND2	2.48	0.45
1:B:242:LEU:HD23	1:B:242:LEU:O	2.17	0.45
1:A:167:GLU:HG2	1:A:170:ARG:HH21	1.82	0.44
1:A:128:VAL:HG13	1:A:129:PRO:HD2	1.98	0.44
1:B:271:ILE:HG23	1:B:272:GLN:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:VAL:HA	1:B:174:MET:HE2	1.98	0.44
1:A:160:ARG:HG3	1:A:174:MET:SD	2.57	0.44
1:A:36:ASP:HB3	1:B:15:ILE:HG22	1.99	0.44
1:B:114:PRO:CG	1:B:149:PRO:HB3	2.47	0.44
1:B:275:LYS:O	1:B:279:GLY:N	2.50	0.44
1:A:258:LYS:HG2	1:A:305:ILE:HD11	2.00	0.44
1:A:74:MET:HE3	1:A:74:MET:HB2	1.75	0.44
1:A:56:VAL:HG12	1:A:57:LEU:N	2.32	0.44
1:B:46:HIS:HA	5:B:313:PXL:O3	2.17	0.44
1:B:181:ASP:O	1:B:205:GLN:HA	2.18	0.44
1:B:160:ARG:HG2	1:B:160:ARG:NH1	2.26	0.44
1:B:24:ALA:C	1:B:27:PRO:HD2	2.38	0.44
1:B:88:LYS:HG3	1:B:135:VAL:HG21	1.99	0.43
1:B:6:ARG:HG2	1:B:6:ARG:NH1	2.34	0.43
1:A:74:MET:SD	1:B:16:ARG:HG2	2.59	0.43
1:B:161:LYS:HD3	1:B:163:HIS:CE1	2.54	0.43
1:A:118:ASP:O	1:A:124:GLY:HA3	2.19	0.43
1:B:130:GLU:C	1:B:132:LEU:H	2.21	0.43
1:A:141:VAL:HB	1:A:142:PRO:HD3	2.01	0.43
1:B:219:ILE:C	1:B:219:ILE:HD12	2.39	0.43
1:B:221:MET:HG2	1:B:309:ALA:HA	2.01	0.42
1:B:107:ARG:HB2	1:B:107:ARG:CZ	2.49	0.42
1:B:160:ARG:CG	1:B:160:ARG:NH1	2.78	0.42
1:A:15:ILE:HD11	1:B:65:LEU:HB3	2.01	0.42
1:B:237:PHE:HB2	1:B:263:LEU:HD11	2.00	0.42
1:B:3:GLU:CB	1:B:4:GLU:C	2.87	0.42
1:B:133:LEU:HB3	1:B:134:PRO:HD3	2.02	0.42
1:B:67:GLU:HA	1:B:67:GLU:OE2	2.20	0.42
1:B:244:TRP:HB3	1:B:255:ALA:HA	2.01	0.42
1:B:43:PHE:HE2	1:B:52:TRP:CZ3	2.38	0.42
1:A:101:LEU:HB3	1:A:108:LEU:HD13	2.02	0.42
1:B:115:VAL:HA	1:B:153:GLU:OE2	2.20	0.42
1:A:219:ILE:O	1:A:219:ILE:HD12	2.20	0.42
1:A:209:ASN:C	1:A:213:SER:HB3	2.40	0.41
1:A:58:ASN:OD1	1:A:60:ASP:HB2	2.19	0.41
1:B:101:LEU:HB3	1:B:108:LEU:HD13	2.03	0.41
1:A:151:GLN:O	1:A:155:GLU:HG3	2.20	0.41
1:A:5:CYS:HG	1:A:33:PHE:HE2	1.67	0.41
1:A:40:SER:O	1:A:41:VAL:CG1	2.69	0.41
1:B:6:ARG:HH11	1:B:6:ARG:HG2	1.85	0.41
1:B:114:PRO:HG2	1:B:149:PRO:HB3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297:LYS:O	1:B:301:GLU:HG3	2.20	0.41
1:A:261:SER:O	1:A:264:HIS:HB3	2.20	0.41
1:B:110:TYR:CE2	1:B:112:CYS:HB2	2.55	0.41
1:B:62:LEU:HD22	1:B:90:PHE:CZ	2.56	0.41
1:A:227:ASP:OD2	1:A:283:ARG:NH2	2.53	0.41
1:A:10:ILE:HG22	1:A:10:ILE:O	2.21	0.41
1:B:4:GLU:H	1:B:4:GLU:CD	2.24	0.41
1:A:165:GLN:OE1	1:A:220:ARG:NH1	2.53	0.41
1:A:199:LEU:C	1:A:199:LEU:HD12	2.41	0.41
1:A:147:ILE:HD13	1:A:180:PRO:HG2	2.03	0.40
1:A:7:VAL:HG22	1:A:79:TYR:HB2	2.03	0.40
1:B:231:VAL:CG1	8:B:314:PLP:C4A	2.91	0.40
1:A:14:VAL:HA	1:A:43:PHE:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:ARG:NH1	1:B:170:ARG:NH1[3_555]	2.11	0.09

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	304/312 (97%)	282 (93%)	21 (7%)	1 (0%)	46	68
1	B	308/312 (99%)	289 (94%)	17 (6%)	2 (1%)	30	50
All	All	612/624 (98%)	571 (93%)	38 (6%)	3 (0%)	34	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	282	VAL
1	A	209	ASN
1	B	281	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	271/274 (99%)	270 (100%)	1 (0%)	93	98
1	B	272/274 (99%)	264 (97%)	8 (3%)	50	77
All	All	543/548 (99%)	534 (98%)	9 (2%)	68	89

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	TYR
1	B	112	CYS
1	B	127	TYR
1	B	128	VAL
1	B	132	LEU
1	B	160	ARG
1	B	170	ARG
1	B	263	LEU
1	B	280	GLU

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

Mol	Chain	Res	Type
1	A	11	GLN
1	A	21	ASN
1	A	42	GLN
1	A	45	ASN
1	A	205	GLN
1	A	209	ASN
1	A	264	HIS

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Mol	Chain	Res	Type
1	B	45	ASN
1	B	46	HIS
1	B	163	HIS
1	B	165	GLN
1	B	205	GLN
1	B	268	GLN
1	B	272	GLN
1	B	308	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 4 are monoatomic - leaving 20 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
5	PXL	A	313	-	12,12,12	3.58	7 (58%)	15,16,16	1.35	2 (13%)
6	SO4	A	314	-	4,4,4	0.19	0	6,6,6	0.15	0
6	SO4	A	315	-	4,4,4	0.24	0	6,6,6	0.05	0
6	SO4	A	316	-	4,4,4	0.24	0	6,6,6	0.09	0
6	SO4	A	317	-	4,4,4	0.21	0	6,6,6	0.10	0
6	SO4	A	318	-	4,4,4	0.21	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SO4	A	319	-	4,4,4	0.20	0	6,6,6	0.10	0
6	SO4	A	320	-	4,4,4	0.25	0	6,6,6	0.09	0
7	MPD	A	321	-	6,7,7	1.48	1 (16%)	7,10,10	0.43	0
4	ATP	A	407	3,2	24,33,33	1.28	2 (8%)	31,52,52	2.56	11 (35%)
5	PXL	B	313	-	12,12,12	3.05	7 (58%)	15,16,16	1.08	2 (13%)
8	PLP	B	314	-	16,16,16	1.65	3 (18%)	21,23,23	2.14	4 (19%)
6	SO4	B	315	-	4,4,4	0.19	0	6,6,6	0.11	0
6	SO4	B	316	-	4,4,4	0.21	0	6,6,6	0.10	0
6	SO4	B	317	-	4,4,4	0.24	0	6,6,6	0.09	0
6	SO4	B	318	-	4,4,4	0.19	0	6,6,6	0.10	0
7	MPD	B	319	-	6,7,7	1.47	1 (16%)	7,10,10	0.45	0
7	MPD	B	320	-	6,7,7	1.44	1 (16%)	7,10,10	0.50	0
7	MPD	B	321	-	6,7,7	1.56	1 (16%)	7,10,10	0.54	0
4	ATP	B	409	3,2	24,33,33	1.30	2 (8%)	31,52,52	2.39	11 (35%)

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
5	PXL	A	313	-	-	0/4/4/4	0/1/1/1
6	SO4	A	314	-	-	0/0/0/0	0/0/0/0
6	SO4	A	315	-	-	0/0/0/0	0/0/0/0
6	SO4	A	316	-	-	0/0/0/0	0/0/0/0
6	SO4	A	317	-	-	0/0/0/0	0/0/0/0
6	SO4	A	318	-	-	0/0/0/0	0/0/0/0
6	SO4	A	319	-	-	0/0/0/0	0/0/0/0
6	SO4	A	320	-	-	0/0/0/0	0/0/0/0
7	MPD	A	321	-	-	0/5/5/5	0/0/0/0
4	ATP	A	407	3,2	-	0/18/38/38	0/3/3/3
5	PXL	B	313	-	-	0/4/4/4	0/1/1/1
8	PLP	B	314	-	-	0/8/8/8	0/1/1/1
6	SO4	B	315	-	-	0/0/0/0	0/0/0/0
6	SO4	B	316	-	-	0/0/0/0	0/0/0/0
6	SO4	B	317	-	-	0/0/0/0	0/0/0/0
6	SO4	B	318	-	-	0/0/0/0	0/0/0/0
7	MPD	B	319	-	-	0/5/5/5	0/0/0/0
7	MPD	B	320	-	-	0/5/5/5	0/0/0/0
7	MPD	B	321	-	-	0/5/5/5	0/0/0/0
4	ATP	B	409	3,2	-	0/18/38/38	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	321	MPD	CM-C2	-3.73	1.39	1.52
7	A	321	MPD	CM-C2	-3.53	1.40	1.52
7	B	319	MPD	CM-C2	-3.50	1.40	1.52
7	B	320	MPD	CM-C2	-3.41	1.40	1.52
8	B	314	PLP	C2A-C2	2.08	1.54	1.50
8	B	314	PLP	O4A-C4A	2.35	1.28	1.21
5	B	313	PXL	C6-C5	2.54	1.43	1.37
4	B	409	ATP	O4'-C1'	2.89	1.44	1.41
5	A	313	PXL	C6-C5	2.90	1.44	1.37
4	A	407	ATP	O4'-C1'	3.02	1.45	1.41
4	A	407	ATP	PG-O1G	3.17	1.61	1.51
4	B	409	ATP	PG-O1G	3.28	1.62	1.51
5	A	313	PXL	C4-C5	3.36	1.46	1.42
5	B	313	PXL	C6-N1	3.52	1.42	1.34
5	B	313	PXL	C4-C3	3.76	1.45	1.40
5	A	313	PXL	C6-N1	3.96	1.42	1.34
5	B	313	PXL	C4-C4A	4.15	1.56	1.46
8	B	314	PLP	C4-C4A	4.21	1.56	1.46
5	B	313	PXL	C3-C2	4.27	1.43	1.40
5	A	313	PXL	C2-N1	4.31	1.43	1.34
5	B	313	PXL	C2-N1	4.37	1.43	1.34
5	A	313	PXL	C4-C4A	4.50	1.57	1.46
5	B	313	PXL	C4-C5	4.56	1.48	1.42
5	A	313	PXL	C4-C3	5.36	1.47	1.40
5	A	313	PXL	C3-C2	6.62	1.45	1.40

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	407	ATP	N3-C2-N1	-9.88	121.33	128.89
4	B	409	ATP	N3-C2-N1	-8.92	122.06	128.89
4	A	407	ATP	PA-O3A-PB	-3.89	121.80	132.73
4	B	409	ATP	PA-O3A-PB	-3.69	122.37	132.73
4	A	407	ATP	O3A-PA-O5'	-3.52	93.60	102.94
4	A	407	ATP	O5'-PA-O1A	-3.22	97.11	109.62
4	B	409	ATP	O3A-PA-O5'	-3.17	94.51	102.94
4	B	409	ATP	O5'-PA-O1A	-3.09	97.61	109.62
8	B	314	PLP	C5A-C5-C6	-2.84	113.91	119.28
4	B	409	ATP	PB-O3B-PG	-2.72	123.53	132.67
4	A	407	ATP	PB-O3B-PG	-2.70	123.60	132.67
5	A	313	PXL	O4A-C4A-C4	-2.68	119.71	125.11
4	B	409	ATP	O2A-PA-O5'	-2.67	95.00	108.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	313	PXL	C5-C6-N1	-2.53	119.47	123.86
4	A	407	ATP	O2A-PA-O5'	-2.53	95.72	108.46
5	A	313	PXL	C5-C6-N1	-2.45	119.60	123.86
4	A	407	ATP	C4-C5-N7	-2.45	107.23	109.48
8	B	314	PLP	O2P-P-O4P	-2.36	99.77	106.56
4	B	409	ATP	C4-C5-N7	-2.16	107.50	109.48
5	B	313	PXL	O4A-C4A-C4	-2.03	121.01	125.11
4	B	409	ATP	O2B-PB-O1B	2.24	124.65	112.53
4	A	407	ATP	O2A-PA-O1A	2.31	125.06	112.53
4	A	407	ATP	O2B-PB-O1B	2.31	125.06	112.53
4	B	409	ATP	O2A-PA-O1A	2.32	125.09	112.53
4	A	407	ATP	O2B-PB-O3B	2.77	117.66	105.09
4	A	407	ATP	O2A-PA-O3A	2.81	117.83	105.09
4	B	409	ATP	O2B-PB-O3B	2.82	117.90	105.09
4	B	409	ATP	O2A-PA-O3A	2.85	118.02	105.09
8	B	314	PLP	C5A-C5-C4	3.29	127.01	121.47
8	B	314	PLP	O4P-C5A-C5	7.21	120.90	108.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	313	PXL	1	0
5	B	313	PXL	9	0
8	B	314	PLP	7	0

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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	308/312 (98%)	-0.01	15 (4%) 33 38	24, 42, 75, 100	0
1	B	310/312 (99%)	-0.20	6 (1%) 70 73	19, 37, 66, 91	0
All	All	618/624 (99%)	-0.11	21 (3%) 49 54	19, 40, 72, 100	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	282	VAL	5.3
1	B	281	GLY	5.3
1	A	120	TRP	4.5
1	A	210	PRO	4.0
1	A	282	VAL	3.7
1	A	209	ASN	3.7
1	B	3	GLU	3.5
1	A	279	GLY	3.2
1	A	208	ARG	3.0
1	A	122	GLY	2.9
1	A	215	VAL	2.8
1	A	280	GLU	2.8
1	B	211	ALA	2.8
1	B	280	GLU	2.7
1	A	121	ASP	2.6
1	A	235	ALA	2.6
1	A	213	SER	2.6
1	A	81	LEU	2.5
1	A	129	PRO	2.4
1	B	210	PRO	2.1
1	A	278	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, 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	LLDF	B-factors(Å ²)	Q<0.9
7	MPD	B	319	8/8	0.75	0.34	12.89	82,85,91,96	0
5	PXL	B	313	12/12	0.75	0.49	10.46	80,83,91,100	0
5	PXL	A	313	12/12	0.72	0.47	9.35	83,95,100,100	0
8	PLP	B	314	16/16	0.78	0.38	5.23	58,74,84,85	0
7	MPD	B	320	8/8	0.89	0.24	4.41	55,58,64,67	0
6	SO4	A	316	5/5	0.93	0.26	3.81	79,80,81,84	5
6	SO4	A	317	5/5	0.86	0.46	3.67	98,100,100,100	5
6	SO4	B	317	5/5	0.95	0.15	1.48	72,72,74,77	5
3	NA	B	406	1/1	0.98	0.21	1.32	27,27,27,27	0
6	SO4	A	318	5/5	0.96	0.13	1.29	66,67,71,72	5
6	SO4	A	314	5/5	0.93	0.26	1.02	66,69,78,78	0
6	SO4	A	320	5/5	0.85	0.20	0.58	96,98,100,100	5
6	SO4	B	316	5/5	0.92	0.14	0.54	80,81,81,85	5
3	NA	A	402	1/1	0.94	0.21	0.52	40,40,40,40	0
4	ATP	A	407	31/31	0.97	0.14	-0.11	23,37,72,72	0
4	ATP	B	409	31/31	0.97	0.12	-0.70	27,35,58,61	0
2	MG	A	400	1/1	0.87	0.13	-	43,43,43,43	0
7	MPD	A	321	8/8	0.87	0.26	-	92,94,96,96	0
6	SO4	A	319	5/5	0.93	0.14	-	97,98,99,100	5
7	MPD	B	321	8/8	0.93	0.19	-	51,59,66,68	0
2	MG	B	404	1/1	0.92	0.15	-	30,30,30,30	0
6	SO4	B	315	5/5	0.88	0.20	-	80,81,83,85	5
6	SO4	B	318	5/5	0.87	0.38	-	95,96,96,97	5
6	SO4	A	315	5/5	0.90	0.20	-	73,78,79,83	5

6.5 Other polymers ⓘ

There are no such residues in this entry.