



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:19 PM GMT

PDB ID : 1A5A  
Title : CRYO-CRYSTALLOGRAPHY OF A TRUE SUBSTRATE, INDOLE-3-GLYCEROL PHOSPHATE, BOUND TO A MUTANT (ALPHAD60N) TRYPTOPHAN SYNTHASE ALPHA2BETA2 COMPLEX REVEALS THE CORRECT ORIENTATION OF ACTIVE SITE ALPHA GLU 49  
Authors : Rhee, S.; Miles, E.W.; Davies, D.R.  
Deposited on : 1998-02-12  
Resolution : 1.90 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 (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

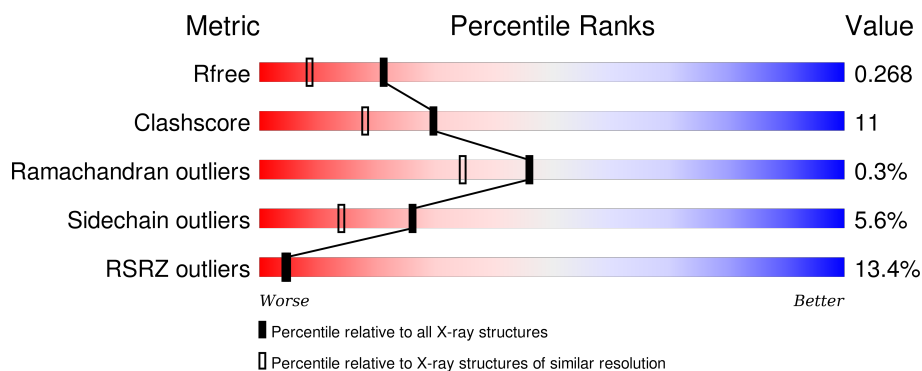
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	268	
2	B	397	

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	K	B	500	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5289 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 TRYPTOPHAN SYNTHASE (ALPHA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1929	1230	333	358	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	ASN	ASP	ENGINEERED	UNP P00929

- Molecule 2 is a protein called TRYPTOPHAN SYNTHASE (BETA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	389	Total	C	N	O	S	0	0	0
			2950	1855	518	558	19			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	396	LEU	GLU	CONFLICT	UNP P0A2K1

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C<sub>8</sub>H<sub>10</sub>NO<sub>6</sub>P).



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

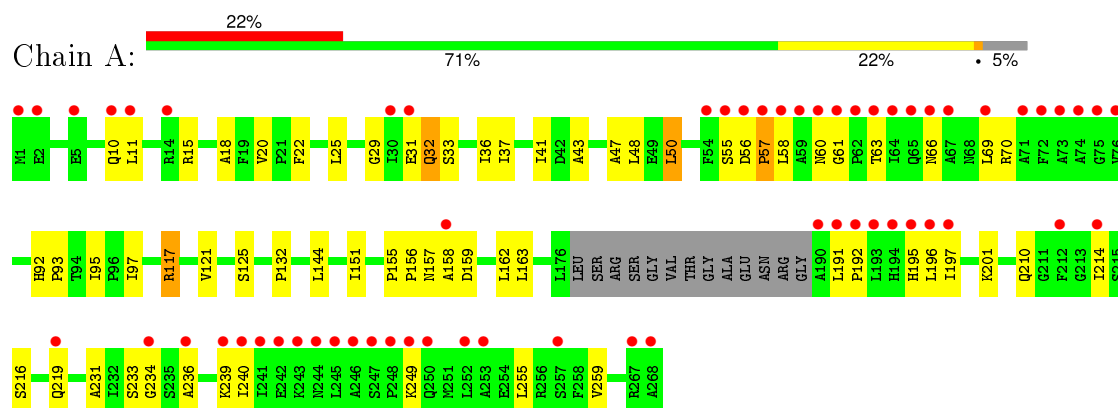
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	120	Total	O	0	0
			120	120		
5	B	274	Total	O	0	0
			274	274		

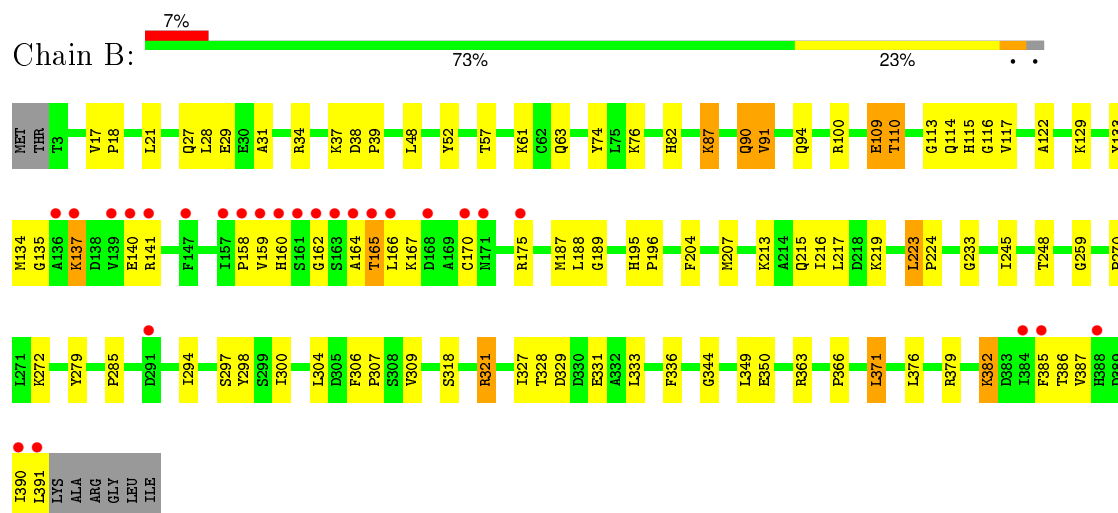
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: TRYPTOPHAN SYNTHASE (ALPHA CHAIN)



#### • Molecule 2: TRYPTOPHAN SYNTHASE (BETA CHAIN)



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	183.50 Å   59.40 Å   67.30 Å 90.00°   94.60°   90.00°	Depositor
Resolution (Å)	8.00 – 1.90 8.00 – 1.90	Depositor EDS
% Data completeness (in resolution range)	77.7 (8.00-1.90) 83.6 (8.00-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.13 (at 1.90 Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.238   ,   0.298 0.221   ,   0.268	Depositor DCC
$R_{free}$ test set	4719 reflections (10.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.6	Xtriage
Anisotropy	0.736	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.50 , 104.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 48728 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5289	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: K, PLP

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	0.36	0/1968	0.61	0/2673
2	B	0.42	1/3008 (0.0%)	0.68	0/4064
All	All	0.40	1/4976 (0.0%)	0.65	0/6737

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
2	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	87	LYS	CB-CG	6.14	1.69	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	298	TYR	Sidechain

### 5.2 Too-close contacts [i](#)

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



the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1929	0	1940	38	0
2	B	2950	0	2924	75	0
3	B	1	0	0	0	0
4	B	15	0	7	0	0
5	A	120	0	0	1	0
5	B	274	0	0	17	0
All	All	5289	0	4871	109	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 11.

All (109) 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:A:57:PRO:HB2	1:A:60:ASN:HB2	1.37	1.03
1:A:56:ASP:HB2	2:B:167:LYS:HE2	1.59	0.84
2:B:90:GLN:HE22	2:B:94:GLN:HE21	1.25	0.82
2:B:135:GLY:HA2	2:B:159:VAL:HG12	1.66	0.78
2:B:166:LEU:HA	5:B:777:HOH:O	1.86	0.75
1:A:69:LEU:HD21	2:B:162:GLY:HA2	1.69	0.75
2:B:82:HIS:HA	5:B:754:HOH:O	1.88	0.72
2:B:87:LYS:HD2	2:B:114:GLN:HG3	1.73	0.70
2:B:233:GLY:HA2	2:B:306:PHE:HD2	1.58	0.68
2:B:34:ARG:HG3	2:B:100:ARG:HH11	1.60	0.67
1:A:36:ILE:HG23	1:A:255:LEU:HD13	1.77	0.67
2:B:110:THR:HG21	2:B:116:GLY:H	1.62	0.65
2:B:216:ILE:HG21	2:B:224:PRO:HD3	1.79	0.64
2:B:195:HIS:CD2	2:B:196:PRO:HA	2.33	0.64
2:B:90:GLN:NE2	2:B:94:GLN:HE21	1.95	0.64
2:B:279:TYR:CD2	2:B:294:ILE:HG13	2.33	0.64
2:B:129:LYS:HA	5:B:686:HOH:O	1.98	0.63
2:B:195:HIS:HD2	5:B:726:HOH:O	1.82	0.63
2:B:170:CYS:HB2	5:B:745:HOH:O	1.98	0.62
1:A:22:PHE:HB3	1:A:234:GLY:HA2	1.82	0.61
2:B:63:GLN:HG2	5:B:736:HOH:O	1.99	0.61
2:B:318:SER:HB3	5:B:549:HOH:O	2.01	0.61
2:B:165:THR:HB	5:B:860:HOH:O	2.01	0.61
2:B:18:PRO:HD2	2:B:21:LEU:HD12	1.83	0.61
2:B:382:LYS:HG3	5:B:771:HOH:O	2.00	0.60
2:B:297:SER:OG	2:B:307:PRO:HA	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:GLY:HA3	5:A:746:HOH:O	2.02	0.60
2:B:109:GLU:HA	2:B:133:TYR:O	2.02	0.59
1:A:37:ILE:HG23	1:A:48:LEU:HD21	1.84	0.58
1:A:216:SER:O	1:A:219:GLN:HB2	2.04	0.58
1:A:163:LEU:HD21	1:A:196:LEU:HD12	1.85	0.58
2:B:115:HIS:CE1	2:B:189:GLY:HA2	2.40	0.57
2:B:385:PHE:HB3	5:B:712:HOH:O	2.04	0.56
2:B:248:THR:HA	2:B:321:ARG:HH12	1.69	0.56
1:A:20:VAL:HG22	1:A:47:ALA:HB3	1.86	0.56
2:B:224:PRO:HA	2:B:371:LEU:HD13	1.88	0.56
2:B:344:GLY:N	5:B:627:HOH:O	2.38	0.55
1:A:197:ILE:O	1:A:201:LYS:HG3	2.07	0.55
2:B:215:GLN:O	2:B:219:LYS:HG2	2.07	0.55
2:B:213:LYS:O	2:B:217:LEU:HB2	2.08	0.53
2:B:91:VAL:HG13	2:B:122:ALA:HB2	1.91	0.53
2:B:379:ARG:HD3	5:B:785:HOH:O	2.10	0.52
2:B:160:HIS:HA	2:B:164:ALA:HB2	1.91	0.52
2:B:137:LYS:HD3	2:B:164:ALA:HB3	1.92	0.52
1:A:95:ILE:HG13	1:A:95:ILE:O	2.10	0.52
1:A:57:PRO:CB	1:A:60:ASN:HB2	2.26	0.51
1:A:158:ALA:CB	1:A:162:LEU:HD23	2.41	0.51
2:B:135:GLY:HA2	2:B:159:VAL:CG1	2.38	0.50
2:B:285:PRO:HG2	2:B:309:VAL:HG22	1.93	0.50
1:A:66:ASN:O	1:A:70:ARG:HG3	2.12	0.50
1:A:11:LEU:CD1	1:A:18:ALA:HB2	2.42	0.49
1:A:192:PRO:O	1:A:195:HIS:HB3	2.13	0.49
2:B:90:GLN:HA	2:B:204:PHE:HB3	1.94	0.49
1:A:214:ILE:HG13	1:A:231:ALA:HB1	1.95	0.48
1:A:233:SER:OG	1:A:236:ALA:HB3	2.12	0.48
1:A:240:ILE:HD12	1:A:255:LEU:HD23	1.95	0.47
2:B:304:LEU:HG	2:B:350:GLU:HG3	1.95	0.47
2:B:27:GLN:HG3	2:B:28:LEU:N	2.30	0.47
2:B:336:PHE:CE2	2:B:387:VAL:HG21	2.50	0.47
2:B:328:THR:HG22	2:B:329:ASP:N	2.29	0.46
2:B:27:GLN:HB3	5:B:534:HOH:O	2.15	0.46
2:B:245:ILE:O	2:B:321:ARG:NH1	2.49	0.46
1:A:236:ALA:HA	1:A:239:LYS:HD2	1.97	0.46
1:A:132:PRO:HD3	2:B:17:VAL:O	2.15	0.46
1:A:32:GLN:O	1:A:36:ILE:HG13	2.16	0.46
2:B:160:HIS:HB2	5:B:862:HOH:O	2.16	0.46
2:B:285:PRO:HG2	2:B:309:VAL:CG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:PRO:HB2	1:A:157:ASN:OD1	2.16	0.46
1:A:43:ALA:HB1	1:A:259:VAL:HB	1.98	0.46
2:B:34:ARG:HE	2:B:100:ARG:HD3	1.81	0.45
2:B:31:ALA:O	2:B:34:ARG:HG2	2.17	0.45
2:B:38:ASP:OD2	2:B:100:ARG:NH2	2.49	0.45
2:B:259:GLY:O	2:B:328:THR:HG23	2.17	0.45
2:B:38:ASP:HA	2:B:39:PRO:HD2	1.87	0.45
2:B:270:PRO:HG2	2:B:309:VAL:HG13	1.98	0.45
2:B:57:THR:OG1	2:B:76:LYS:HE3	2.17	0.45
2:B:61:LYS:HB2	2:B:74:TYR:CE2	2.52	0.45
2:B:327:ILE:HG23	2:B:331:GLU:HB2	1.99	0.45
1:A:219:GLN:HA	1:A:219:GLN:OE1	2.16	0.44
2:B:91:VAL:HG22	2:B:187:MET:SD	2.57	0.44
1:A:50:LEU:HD22	1:A:97:ILE:HG23	1.99	0.44
1:A:56:ASP:O	1:A:58:LEU:N	2.50	0.44
2:B:34:ARG:HH21	2:B:100:ARG:HG2	1.82	0.44
1:A:29:GLY:O	1:A:33:SER:HB2	2.18	0.44
2:B:135:GLY:CA	2:B:159:VAL:HG12	2.41	0.44
1:A:125:SER:HB2	1:A:151:ILE:HG12	1.99	0.44
1:A:158:ALA:HB1	1:A:162:LEU:HD23	2.00	0.43
2:B:110:THR:CG2	2:B:116:GLY:H	2.29	0.43
1:A:61:GLY:HA2	2:B:175:ARG:HE	1.83	0.43
2:B:29:GLU:OE2	2:B:195:HIS:HE1	2.02	0.43
1:A:156:PRO:O	1:A:191:LEU:HD13	2.18	0.43
1:A:249:LYS:HA	1:A:249:LYS:HD2	1.88	0.43
2:B:217:LEU:HD13	2:B:223:LEU:CD1	2.49	0.42
2:B:48:LEU:O	2:B:52:TYR:HB3	2.19	0.42
1:A:92:HIS:HA	1:A:93:PRO:HD2	1.85	0.42
1:A:43:ALA:CB	1:A:259:VAL:HB	2.49	0.42
2:B:110:THR:HG23	2:B:115:HIS:HB3	2.00	0.42
2:B:113:GLY:O	2:B:117:VAL:HG23	2.19	0.42
2:B:134:MET:O	2:B:158:PRO:HA	2.20	0.42
2:B:141:ARG:HG3	2:B:141:ARG:HH11	1.84	0.41
2:B:300:ILE:HB	2:B:329:ASP:CG	2.40	0.41
2:B:363:ARG:O	2:B:366:PRO:HD3	2.20	0.41
2:B:321:ARG:HG3	5:B:766:HOH:O	2.20	0.41
1:A:117:ARG:O	1:A:121:VAL:HG22	2.20	0.41
2:B:386:THR:O	2:B:390:ILE:HG12	2.20	0.41
2:B:114:GLN:NE2	5:B:808:HOH:O	2.53	0.40
2:B:349:LEU:HD23	2:B:349:LEU:HA	1.95	0.40
1:A:41:ILE:HD13	1:A:95:ILE:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:272:LYS:HE3	5:B:740: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	251/268 (94%)	242 (96%)	7 (3%)	2 (1%)	24	11
2	B	387/397 (98%)	371 (96%)	16 (4%)	0	100	100
All	All	638/665 (96%)	613 (96%)	23 (4%)	2 (0%)	46	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	SER
1	A	57	PRO

### 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	199/208 (96%)	188 (94%)	11 (6%)	27	14
2	B	305/311 (98%)	288 (94%)	17 (6%)	26	14
All	All	504/519 (97%)	476 (94%)	28 (6%)	26	14

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	15	ARG
1	A	25	LEU
1	A	31	GLU
1	A	32	GLN
1	A	50	LEU
1	A	63	THR
1	A	117	ARG
1	A	144	LEU
1	A	159	ASP
1	A	210	GLN
2	B	37	LYS
2	B	90	GLN
2	B	91	VAL
2	B	109	GLU
2	B	110	THR
2	B	137	LYS
2	B	140	GLU
2	B	165	THR
2	B	188	LEU
2	B	207	MET
2	B	223	LEU
2	B	321	ARG
2	B	333	LEU
2	B	371	LEU
2	B	376	LEU
2	B	382	LYS
2	B	391	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	ASN
1	A	60	ASN
1	A	165	GLN
1	A	210	GLN
2	B	27	GLN
2	B	90	GLN
2	B	114	GLN
2	B	145	ASN
2	B	195	HIS

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Mol	Chain	Res	Type
2	B	365	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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	PLP	B	501	2	15,15,16	3.91	9 (60%)	21,22,23	2.11	5 (23%)

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
4	PLP	B	501	2	-	0/6/6/8	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	PLP	P-O3P	-4.33	1.39	1.54
4	B	501	PLP	P-O4P	-3.40	1.48	1.60
4	B	501	PLP	C6-N1	2.74	1.40	1.34
4	B	501	PLP	C6-C5	3.49	1.45	1.37
4	B	501	PLP	C2-N1	3.74	1.42	1.34
4	B	501	PLP	C5-C4	4.69	1.46	1.40
4	B	501	PLP	C3-C2	6.03	1.44	1.40
4	B	501	PLP	C4A-C4	6.43	1.64	1.51
4	B	501	PLP	C3-C4	7.71	1.59	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	501	PLP	C3-C2-N1	-2.68	116.91	120.61
4	B	501	PLP	C6-N1-C2	3.51	126.45	119.28
4	B	501	PLP	C2A-C2-C3	4.23	126.14	121.04
4	B	501	PLP	O4P-C5A-C5	4.27	116.05	108.99
4	B	501	PLP	O3P-P-O4P	4.99	120.94	106.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 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	255/268 (95%)	1.07	60 (23%) <b>1</b> <b>1</b>	10, 29, 79, 94	4 (1%)
2	B	389/397 (97%)	0.17	26 (6%) <b>21</b> <b>23</b>	6, 17, 52, 78	3 (0%)
All	All	644/665 (96%)	0.53	86 (13%) <b>4</b> <b>5</b>	6, 21, 66, 94	7 (1%)

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	59	ALA	15.0
1	A	57	PRO	9.9
1	A	58	LEU	8.5
1	A	191	LEU	7.6
2	B	163	SER	7.5
1	A	60	ASN	7.0
1	A	56	ASP	7.0
2	B	159	VAL	6.8
1	A	268	ALA	5.8
1	A	61	GLY	5.6
1	A	257	SER	5.6
1	A	212	PHE	5.2
1	A	249	LYS	5.1
2	B	391	LEU	5.1
2	B	160	HIS	4.9
2	B	164	ALA	4.7
1	A	55	SER	4.6
1	A	250	GLN	4.3
1	A	194	HIS	4.3
2	B	165	THR	4.2
2	B	162	GLY	4.0
2	B	385	PHE	4.0
1	A	71	ALA	4.0
1	A	247	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	10	GLN	3.8
1	A	69	LEU	3.8
1	A	195	HIS	3.8
1	A	241	ILE	3.7
1	A	1	MET	3.7
1	A	72	PHE	3.7
1	A	65	GLN	3.6
2	B	161	SER	3.6
2	B	168	ASP	3.5
1	A	190	ALA	3.5
1	A	245	LEU	3.5
1	A	253	ALA	3.4
1	A	67	ALA	3.3
1	A	244	ASN	3.3
2	B	137	LYS	3.3
1	A	75	GLY	3.3
1	A	2	GLU	3.3
1	A	248	PRO	3.2
1	A	196	LEU	3.0
1	A	192	PRO	2.9
2	B	140	GLU	2.9
1	A	31	GLU	2.9
1	A	63	THR	2.8
1	A	246	ALA	2.8
2	B	136	ALA	2.8
2	B	141	ARG	2.8
2	B	388	HIS	2.8
1	A	252	LEU	2.8
1	A	62	PRO	2.7
2	B	158	PRO	2.7
1	A	239	LYS	2.7
1	A	242	GLU	2.6
2	B	390	ILE	2.6
2	B	171	ASN	2.6
1	A	76	VAL	2.6
2	B	166	LEU	2.5
1	A	234	GLY	2.5
1	A	5	GLU	2.5
2	B	175	ARG	2.5
1	A	66	ASN	2.4
2	B	139	VAL	2.4
1	A	267	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	74	ALA	2.4
1	A	54	PHE	2.3
1	A	14	ARG	2.3
1	A	219	GLN	2.3
1	A	214	ILE	2.2
1	A	193	LEU	2.2
1	A	30	ILE	2.2
1	A	197	ILE	2.2
2	B	147	PHE	2.2
1	A	64	ILE	2.2
1	A	73	ALA	2.1
2	B	157	ILE	2.1
1	A	11	LEU	2.1
2	B	291	ASP	2.1
1	A	158	ALA	2.1
1	A	243	LYS	2.0
2	B	170	CYS	2.0
1	A	236	ALA	2.0
1	A	240	ILE	2.0
2	B	384	ILE	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
3	K	B	500	1/1	0.96	0.42	7.85	8,8,8,8	0
4	PLP	B	501	15/16	0.96	0.10	0.39	10,17,23,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.