



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:59 am GMT

PDB ID : 4QYS
Title : TrpB2 enzymes
Authors : Busch, F.; Rajendran, C.; Loeffler, P.; Merkl, R.; Sterner, R.
Deposited on : 2014-07-25
Resolution : 1.94 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 : 1.7.2 (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

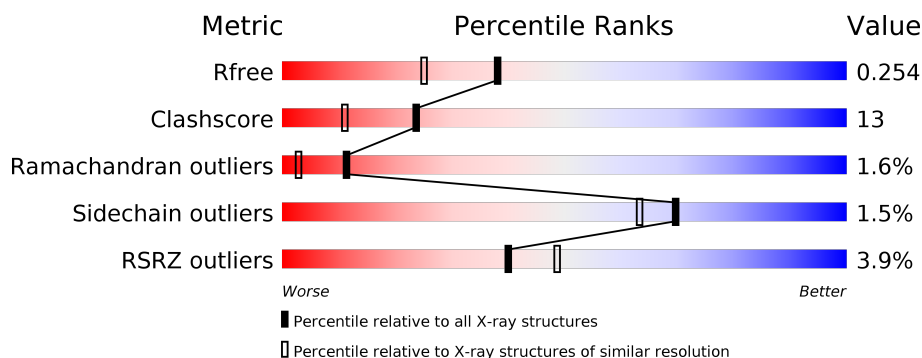
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	3233 (1.96-1.92)
Clashscore	112137	3430 (1.96-1.92)
Ramachandran outliers	110173	3395 (1.96-1.92)
Sidechain outliers	110143	3395 (1.96-1.92)
RSRZ outliers	101464	3250 (1.96-1.92)

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	442	<div> <div>5%</div> <div> <div></div> <div>67%</div> <div>23%</div> <div>• 8%</div> </div> </div>
1	B	442	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>19%</div> <div>• 5%</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	PLR	B	501	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6720 atoms, of which 12 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 beta chain 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	418	Total	C	N	O	S	0	0	0
			3279	2120	540	607	12			
1	A	408	Total	C	N	O	S	0	0	0
			3172	2053	519	588	12			

There are 26 discrepancies between the modelled and reference sequences:

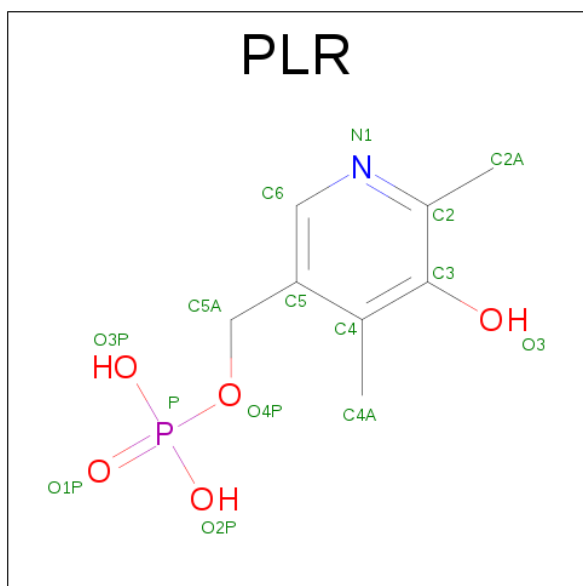
Chain	Residue	Modelled	Actual	Comment	Reference
B	430	LYS	-	EXPRESSION TAG	UNP Q97TX6
B	431	LEU	-	EXPRESSION TAG	UNP Q97TX6
B	432	ALA	-	EXPRESSION TAG	UNP Q97TX6
B	433	ALA	-	EXPRESSION TAG	UNP Q97TX6
B	434	ALA	-	EXPRESSION TAG	UNP Q97TX6
B	435	LEU	-	EXPRESSION TAG	UNP Q97TX6
B	436	GLU	-	EXPRESSION TAG	UNP Q97TX6
B	437	HIS	-	EXPRESSION TAG	UNP Q97TX6
B	438	HIS	-	EXPRESSION TAG	UNP Q97TX6
B	439	HIS	-	EXPRESSION TAG	UNP Q97TX6
B	440	HIS	-	EXPRESSION TAG	UNP Q97TX6
B	441	HIS	-	EXPRESSION TAG	UNP Q97TX6
B	442	HIS	-	EXPRESSION TAG	UNP Q97TX6
A	430	LYS	-	EXPRESSION TAG	UNP Q97TX6
A	431	LEU	-	EXPRESSION TAG	UNP Q97TX6
A	432	ALA	-	EXPRESSION TAG	UNP Q97TX6
A	433	ALA	-	EXPRESSION TAG	UNP Q97TX6
A	434	ALA	-	EXPRESSION TAG	UNP Q97TX6
A	435	LEU	-	EXPRESSION TAG	UNP Q97TX6
A	436	GLU	-	EXPRESSION TAG	UNP Q97TX6
A	437	HIS	-	EXPRESSION TAG	UNP Q97TX6
A	438	HIS	-	EXPRESSION TAG	UNP Q97TX6
A	439	HIS	-	EXPRESSION TAG	UNP Q97TX6
A	440	HIS	-	EXPRESSION TAG	UNP Q97TX6
A	441	HIS	-	EXPRESSION TAG	UNP Q97TX6

Continued on next page...

Continued from previous page...

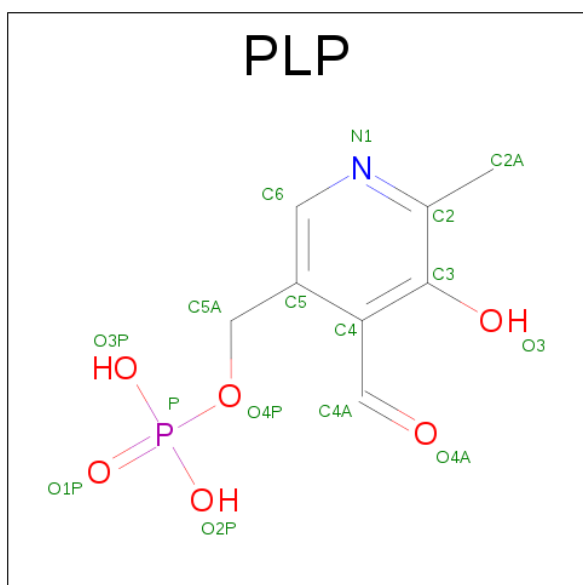
Chain	Residue	Modelled	Actual	Comment	Reference
A	442	HIS	-	EXPRESSION TAG	UNP Q97TX6

- Molecule 2 is (5-HYDROXY-4,6-DIMETHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (three-letter code: PLR) (formula: $C_8H_{12}NO_5P$).



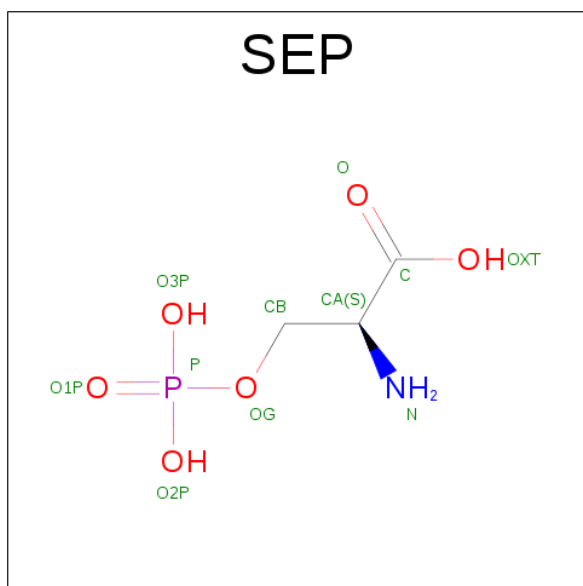
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	
			23	8	8	1	5	1	

- Molecule 4 is PHOSPHOSERINE (three-letter code: SEP) (formula: $C_3H_8NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	P	
			15	3	4	1	6	1	

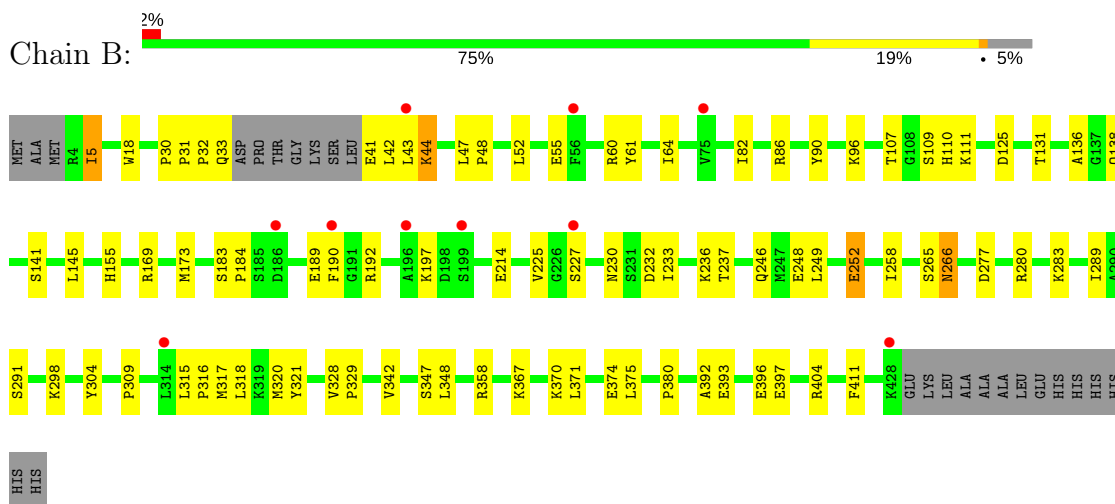
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	124	Total	O		
			124	124	0	0
5	A	92	Total	O		
			92	92	0	0

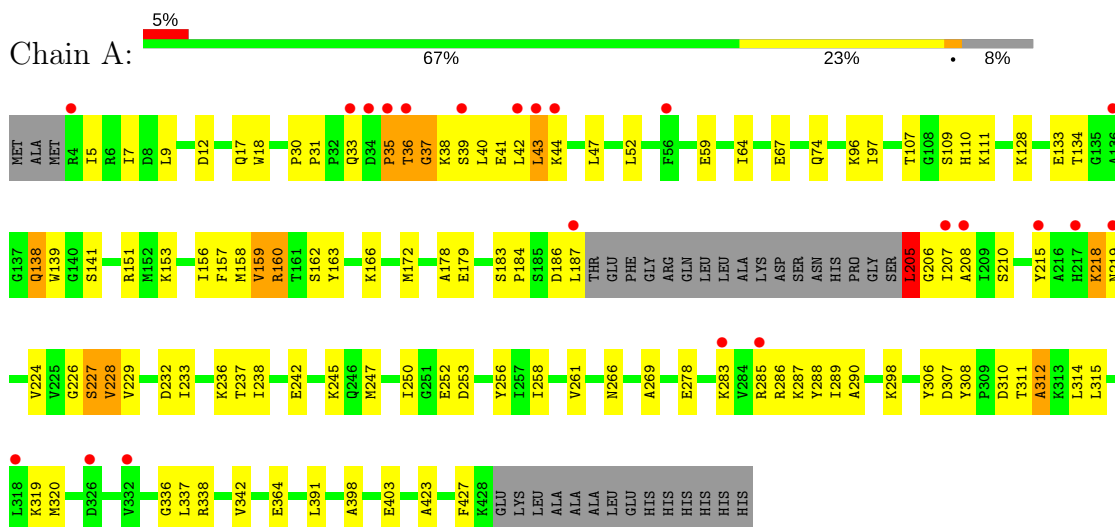
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Tryptophan synthase beta chain 2



• Molecule 1: Tryptophan synthase beta chain 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.56Å 61.90Å 109.57Å 90.00° 98.23° 90.00°	Depositor
Resolution (Å)	46.44 – 1.94 46.44 – 1.94	Depositor EDS
% Data completeness (in resolution range)	96.3 (46.44-1.94) 96.3 (46.44-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 1.94Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1589)	Depositor
R, R_{free}	0.195 , 0.252 0.197 , 0.254	Depositor DCC
R_{free} test set	2639 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.5	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	0.95	EDS
Total number of atoms	6720	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PLP, PLR, SEP

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	0.45	1/3251 (0.0%)	0.56	1/4409 (0.0%)
1	B	0.41	0/3360	0.55	0/4549
All	All	0.43	1/6611 (0.0%)	0.56	1/8958 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	141	SER	CB-OG	-5.43	1.35	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	LEU	CB-CG-CD2	5.01	119.51	111.00

There are no chirality outliers.

There are no planarity outliers.

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	3172	0	3168	94	0
1	B	3279	0	3300	68	0
2	B	15	0	10	8	0
3	A	15	8	7	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	11	4	3	2	0
5	A	92	0	0	4	0
5	B	124	0	0	6	0
All	All	6708	12	6488	163	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 13.

All (163) 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:311:THR:O	1:A:312:ALA:HB3	1.46	1.15
1:A:42:LEU:O	1:A:42:LEU:HD13	1.54	1.05
1:A:42:LEU:HD13	1:A:42:LEU:C	1.82	0.99
1:A:311:THR:O	1:A:312:ALA:CB	2.10	0.94
1:B:111:LYS:CE	2:B:501:PLR:H4A2	1.99	0.91
1:A:205:LEU:HA	1:A:207:ILE:H	1.41	0.86
1:B:111:LYS:NZ	2:B:501:PLR:H4A2	1.92	0.85
1:A:215:TYR:O	1:A:218:LYS:O	1.95	0.84
1:A:184:PRO:HG3	1:A:207:ILE:HG21	1.59	0.84
1:A:111:LYS:HZ1	3:A:501:PLP:C4A	1.94	0.79
1:A:133:GLU:HB2	1:A:208:ALA:HB1	1.63	0.78
1:A:205:LEU:HA	1:A:207:ILE:N	1.98	0.77
1:B:304:TYR:OH	5:B:713:HOH:O	2.03	0.76
1:A:42:LEU:CD1	1:A:42:LEU:C	2.53	0.76
1:B:189:GLU:OE2	1:B:192:ARG:NH2	2.14	0.74
1:B:111:LYS:NZ	2:B:501:PLR:O3	2.20	0.74
1:A:210:SER:OG	1:A:311:THR:O	2.06	0.74
1:A:36:THR:O	1:A:38:LYS:N	2.19	0.72
1:A:41:GLU:HA	1:A:44:LYS:HD2	1.72	0.71
1:B:111:LYS:HE3	2:B:501:PLR:H4A2	1.70	0.71
1:B:55:GLU:OE2	1:B:230:ASN:N	2.23	0.71
1:B:42:LEU:HD13	1:B:42:LEU:C	2.12	0.70
1:A:278:GLU:OE2	1:A:288:TYR:OH	2.08	0.69
1:B:248:GLU:HG3	5:B:646:HOH:O	1.92	0.69
1:B:5:ILE:HD12	1:B:82:ILE:HG23	1.76	0.68
1:A:9:LEU:HD11	1:A:245:LYS:HD2	1.76	0.68
1:B:86:ARG:NE	1:B:375:LEU:O	2.28	0.67
1:A:151:ARG:NH1	5:A:692:HOH:O	2.25	0.66
1:A:35:PRO:O	1:A:37:GLY:N	2.28	0.66
1:B:367:LYS:HD2	5:B:661:HOH:O	1.96	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:ASP:OD1	5:A:640:HOH:O	2.15	0.64
1:A:336:GLY:O	1:A:338:ARG:HG3	1.99	0.63
1:B:318:LEU:HB2	1:B:320:MET:CE	2.27	0.63
1:B:41:GLU:HA	1:B:43:LEU:H	1.64	0.63
1:A:336:GLY:O	1:A:338:ARG:N	2.31	0.62
1:A:205:LEU:N	1:A:206:GLY:HA3	2.15	0.62
1:B:33:GLN:HE22	1:B:317:MET:HE3	1.63	0.62
1:B:90:TYR:CE2	1:B:371:LEU:HD21	2.35	0.62
1:A:43:LEU:HD11	1:A:47:LEU:CD1	2.30	0.61
1:A:43:LEU:HD12	1:A:43:LEU:O	2.01	0.61
1:B:320:MET:HB2	1:B:342:VAL:O	1.99	0.61
1:A:39:SER:HB2	1:A:314:LEU:O	2.01	0.60
1:A:364:GLU:OE1	5:A:635:HOH:O	2.15	0.60
1:B:42:LEU:HD13	1:B:43:LEU:N	2.17	0.59
1:A:186:ASP:O	1:A:187:LEU:HB2	2.02	0.59
1:A:43:LEU:CD1	1:A:47:LEU:HG	2.32	0.59
1:A:139:TRP:HZ2	1:A:224:VAL:HG12	1.67	0.59
1:A:133:GLU:HB2	1:A:208:ALA:CB	2.33	0.58
1:A:43:LEU:HD11	1:A:47:LEU:HG	1.84	0.58
1:B:393:GLU:O	1:B:397:GLU:HG2	2.02	0.58
1:B:348:LEU:HB2	5:B:713:HOH:O	2.04	0.57
1:B:41:GLU:HA	1:B:43:LEU:N	2.19	0.57
1:A:310:ASP:HB3	1:A:315:LEU:HD12	1.87	0.57
1:A:283:LYS:HE2	1:A:285:ARG:HB3	1.87	0.57
1:B:392:ALA:O	1:B:396:GLU:HG2	2.05	0.56
1:B:96:LYS:NZ	1:B:252:GLU:OE2	2.25	0.56
1:B:43:LEU:HD22	1:B:47:LEU:CD1	2.35	0.56
1:A:110:HIS:NE2	1:A:266:ASN:HB3	2.21	0.55
1:B:111:LYS:NZ	2:B:501:PLR:C4A	2.66	0.55
1:B:318:LEU:HB2	1:B:320:MET:HE2	1.88	0.55
1:B:86:ARG:HD3	1:A:74:GLN:NE2	2.20	0.55
1:B:44:LYS:HA	1:B:52:LEU:HD11	1.89	0.55
1:A:109:SER:HB3	1:A:138:GLN:HG2	1.89	0.54
1:A:162:SER:O	1:A:166:LYS:HB2	2.07	0.54
1:B:321:TYR:HD1	1:B:347:SER:HB3	1.71	0.54
1:A:153:LYS:NZ	1:A:179:GLU:HG3	2.23	0.54
1:A:134:THR:HG23	1:A:158:MET:HG3	1.91	0.53
1:B:33:GLN:NE2	1:B:317:MET:HE3	2.23	0.53
1:A:320:MET:HB2	1:A:342:VAL:O	2.09	0.52
1:A:285:ARG:HG3	1:A:286:ARG:N	2.24	0.52
1:B:190:PHE:HB3	1:B:214:GLU:OE1	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:SER:O	1:A:228:VAL:HG22	2.10	0.52
1:B:43:LEU:HD22	1:B:47:LEU:HD11	1.91	0.51
1:A:156:ILE:HD12	1:A:156:ILE:N	2.26	0.51
1:A:111:LYS:HZ1	4:A:502:SEP:CA	2.24	0.50
1:A:97:ILE:HD13	1:A:391:LEU:HD13	1.92	0.50
1:B:197:LYS:HE2	5:B:645:HOH:O	2.11	0.50
1:A:96:LYS:NZ	1:A:252:GLU:OE2	2.38	0.50
1:B:96:LYS:HE2	1:B:404:ARG:HH21	1.77	0.50
1:A:250:ILE:HG13	1:A:252:GLU:HB2	1.94	0.50
1:A:43:LEU:HD11	1:A:47:LEU:CG	2.42	0.50
3:A:501:PLP:O3	4:A:502:SEP:N	2.45	0.50
1:B:18:TRP:CE2	1:B:64:ILE:HG12	2.47	0.50
1:A:398:ALA:HB1	1:A:403:GLU:O	2.12	0.49
1:A:33:GLN:HG3	1:A:306:TYR:CE1	2.47	0.49
1:B:318:LEU:HB2	1:B:320:MET:HE1	1.94	0.49
1:A:256:TYR:CD1	1:A:287:LYS:HB2	2.48	0.49
1:A:307:ASP:OD1	1:A:308:TYR:N	2.42	0.49
1:A:7:ILE:HD12	1:A:7:ILE:N	2.28	0.49
1:A:59:GLU:N	1:A:59:GLU:OE1	2.46	0.49
1:A:238:ILE:O	1:A:242:GLU:HG3	2.14	0.48
1:B:41:GLU:CA	1:B:43:LEU:H	2.27	0.48
1:B:32:PRO:HB3	1:B:318:LEU:HD23	1.94	0.48
1:A:210:SER:OG	1:A:312:ALA:HB3	2.14	0.48
1:A:44:LYS:HG2	1:A:52:LEU:HD21	1.96	0.48
1:B:183:SER:HA	1:B:184:PRO:C	2.34	0.48
1:B:41:GLU:N	1:B:42:LEU:HB3	2.28	0.48
1:A:253:ASP:OD1	1:A:286:ARG:NH2	2.37	0.47
1:A:228:VAL:HG23	1:A:229:VAL:N	2.29	0.47
1:A:183:SER:HA	1:A:184:PRO:C	2.34	0.47
1:A:160:ARG:HA	1:A:163:TYR:HB3	1.97	0.46
1:B:136:ALA:HB3	1:B:138:GLN:OE1	2.16	0.46
1:B:291:SER:HA	1:B:358:ARG:O	2.16	0.46
1:A:156:ILE:HD13	1:A:178:ALA:HB1	1.97	0.46
1:A:227:SER:HA	1:A:232:ASP:OD2	2.16	0.46
1:A:39:SER:CB	1:A:314:LEU:O	2.64	0.46
1:B:232:ASP:OD2	1:B:236:LYS:NZ	2.32	0.46
1:B:380:PRO:HB3	1:B:411:PHE:CZ	2.51	0.46
1:A:17:GLN:HG2	5:A:647:HOH:O	2.16	0.45
1:A:159:VAL:O	1:A:160:ARG:CB	2.63	0.45
1:B:111:LYS:HZ1	2:B:501:PLR:H4A2	1.80	0.45
1:B:309:PRO:HG2	1:B:315:LEU:HB2	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LYS:HZ1	2:B:501:PLR:C4A	2.29	0.45
1:A:128:LYS:HA	1:A:128:LYS:HD3	1.66	0.45
1:A:320:MET:CB	1:A:342:VAL:O	2.65	0.44
1:B:233:ILE:O	1:B:237:THR:HG23	2.18	0.44
1:A:258:ILE:HA	1:A:289:ILE:O	2.17	0.44
1:B:42:LEU:CD1	1:B:42:LEU:C	2.83	0.44
1:A:153:LYS:HZ2	1:A:179:GLU:HG3	1.82	0.44
1:A:210:SER:HG	1:A:312:ALA:HB3	1.82	0.44
1:A:187:LEU:HD22	1:A:215:TYR:CD1	2.53	0.43
1:A:18:TRP:CE2	1:A:64:ILE:HG12	2.53	0.43
1:A:247:MET:HB3	1:A:252:GLU:O	2.19	0.43
1:A:43:LEU:O	1:A:47:LEU:HB2	2.19	0.43
1:B:225:VAL:O	1:B:225:VAL:HG13	2.19	0.43
1:B:42:LEU:CD1	1:B:43:LEU:N	2.82	0.43
1:A:160:ARG:HA	1:A:163:TYR:CB	2.48	0.43
1:B:258:ILE:HA	1:B:289:ILE:O	2.19	0.42
1:A:261:VAL:HG23	1:A:290:ALA:HB1	2.00	0.42
1:A:310:ASP:OD1	1:A:315:LEU:HB2	2.18	0.42
1:B:277:ASP:OD1	1:B:280:ARG:NH2	2.52	0.42
1:B:30:PRO:HA	1:B:31:PRO:HD2	1.85	0.42
1:A:205:LEU:CA	1:A:207:ILE:H	2.20	0.42
1:A:30:PRO:HG2	1:A:319:LYS:HD3	2.01	0.42
1:A:423:ALA:HA	1:A:427:PHE:CD2	2.54	0.42
1:B:96:LYS:HD2	1:B:252:GLU:OE2	2.19	0.42
1:B:131:THR:HG22	1:B:155:HIS:HB2	2.02	0.42
1:A:133:GLU:HA	1:A:157:PHE:O	2.20	0.42
1:A:236:LYS:O	1:A:269:ALA:HB1	2.20	0.42
1:A:33:GLN:HG3	1:A:306:TYR:CZ	2.54	0.42
1:B:370:LYS:O	1:B:374:GLU:HG3	2.20	0.42
2:B:501:PLR:H4A1	2:B:501:PLR:O4P	2.19	0.42
1:B:141:SER:HA	1:B:173:MET:HG2	2.01	0.41
1:B:315:LEU:HB3	1:B:316:PRO:HD2	2.01	0.41
5:B:705:HOH:O	1:A:5:ILE:HD11	2.19	0.41
1:B:107:THR:HG23	1:B:145:LEU:HD22	2.02	0.41
1:B:283:LYS:HG3	1:B:283:LYS:O	2.20	0.41
1:A:187:LEU:HD23	1:A:215:TYR:HA	2.02	0.41
1:A:283:LYS:HE3	1:A:283:LYS:HB2	1.89	0.41
1:A:67:GLU:N	1:A:67:GLU:OE1	2.54	0.41
1:A:133:GLU:O	1:A:139:TRP:HD1	2.03	0.41
1:A:107:THR:HG22	1:A:172:MET:HE2	2.03	0.41
1:A:139:TRP:CH2	1:A:226:GLY:HA2	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:ARG:HG2	1:B:61:TYR:CE2	2.56	0.41
1:A:43:LEU:HD11	1:A:47:LEU:HD12	2.03	0.41
1:B:110:HIS:NE2	1:B:266:ASN:HB3	2.35	0.40
1:A:31:PRO:O	1:A:306:TYR:OH	2.33	0.40
1:B:169:ARG:O	1:B:173:MET:HG3	2.21	0.40
1:B:233:ILE:HG12	1:B:265:SER:HA	2.03	0.40
1:B:48:PRO:HA	1:B:125:ASP:OD2	2.21	0.40
1:A:233:ILE:O	1:A:237:THR:HG23	2.21	0.40
1:B:246:GLN:O	1:B:249:LEU:HB3	2.20	0.40
1:B:328:VAL:HA	1:B:329:PRO:HD3	1.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	404/442 (91%)	378 (94%)	14 (4%)	12 (3%)	5	0
1	B	414/442 (94%)	403 (97%)	10 (2%)	1 (0%)	51	40
All	All	818/884 (92%)	781 (96%)	24 (3%)	13 (2%)	11	3

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	44	LYS
1	A	35	PRO
1	A	36	THR
1	A	37	GLY
1	A	219	ASN
1	A	337	LEU
1	A	40	LEU
1	A	159	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	160	ARG
1	A	218	LYS
1	A	227	SER
1	A	228	VAL
1	A	312	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	333/369 (90%)	329 (99%)	4 (1%)	75	71
1	B	348/369 (94%)	342 (98%)	6 (2%)	66	58
All	All	681/738 (92%)	671 (98%)	10 (2%)	70	63

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

Mol	Chain	Res	Type
1	B	5	ILE
1	B	109	SER
1	B	227	SER
1	B	252	GLU
1	B	266	ASN
1	B	298	LYS
1	A	43	LEU
1	A	138	GLN
1	A	205	LEU
1	A	298	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

3 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	$\# Z > 2$
3	PLP	A	501	4	15,15,16	1.60	2 (13%)	20,22,23	1.17	1 (5%)
4	SEP	A	502	3	6,10,10	0.98	0	8,14,14	1.67	2 (25%)
2	PLR	B	501	-	15,15,15	1.38	2 (13%)	20,22,22	1.56	5 (25%)

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
3	PLP	A	501	4	-	0/6/6/8	0/1/1/1
4	SEP	A	502	3	-	0/6/10/10	0/0/0/0
2	PLR	B	501	-	-	0/6/6/6	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	PLP	C3-C2	-3.36	1.38	1.40
3	A	501	PLP	C5-C4	-3.11	1.36	1.40
2	B	501	PLR	C5-C4	-2.69	1.37	1.40
2	B	501	PLR	C3-C2	-2.43	1.39	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	PLR	C4A-C4-C5	-2.35	118.48	120.86
2	B	501	PLR	C5-C6-N1	-2.11	120.30	123.87
2	B	501	PLR	O2P-P-O4P	2.14	112.43	106.73
2	B	501	PLR	O3P-P-O4P	2.15	112.46	106.73
3	A	501	PLP	O3P-P-O4P	2.45	113.24	106.73
4	A	502	SEP	O3P-P-OG	2.55	113.52	106.73
4	A	502	SEP	OG-P-O1P	2.84	114.44	106.47
2	B	501	PLR	O4P-P-O1P	3.65	116.71	106.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	PLP	2	0
4	A	502	SEP	2	0
2	B	501	PLR	8	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	408/442 (92%)	0.44	22 (5%)	26 34	20, 35, 57, 75	0
1	B	418/442 (94%)	0.22	10 (2%)	59 68	18, 30, 48, 62	0
All	All	826/884 (93%)	0.33	32 (3%)	40 49	18, 33, 53, 75	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	PRO	5.2
1	A	332	VAL	4.9
1	A	36	THR	4.8
1	A	56	PHE	4.2
1	A	187	LEU	4.1
1	A	39	SER	3.7
1	B	428	LYS	3.5
1	A	34	ASP	3.4
1	A	207	ILE	3.4
1	A	285	ARG	3.2
1	A	33	GLN	3.0
1	B	56	PHE	2.9
1	A	217	HIS	2.9
1	B	314	LEU	2.8
1	A	283	LYS	2.6
1	A	318	LEU	2.6
1	B	199	SER	2.6
1	A	219	ASN	2.6
1	A	43	LEU	2.5
1	A	215	TYR	2.5
1	A	44	LYS	2.4
1	B	227	SER	2.4
1	A	4	ARG	2.3
1	B	75	VAL	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	43	LEU	2.3
1	B	196	ALA	2.3
1	A	136	ALA	2.1
1	A	42	LEU	2.1
1	A	326	ASP	2.1
1	A	208	ALA	2.1
1	B	186	ASP	2.1
1	B	190	PHE	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 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
3	PLP	A	501	15/16	0.95	0.15	0.52	27,33,38,45	0
2	PLR	B	501	15/15	0.97	0.10	-0.42	21,27,33,38	0
4	SEP	A	502	11/11	0.93	0.12	-0.47	31,35,42,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.