



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2025 – 08:08 AM EDT

PDB ID : 9B47
Title : Y328F variant of P. indica phosphate transporter
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Deposited on : 2024-03-20
Resolution : 3.70 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

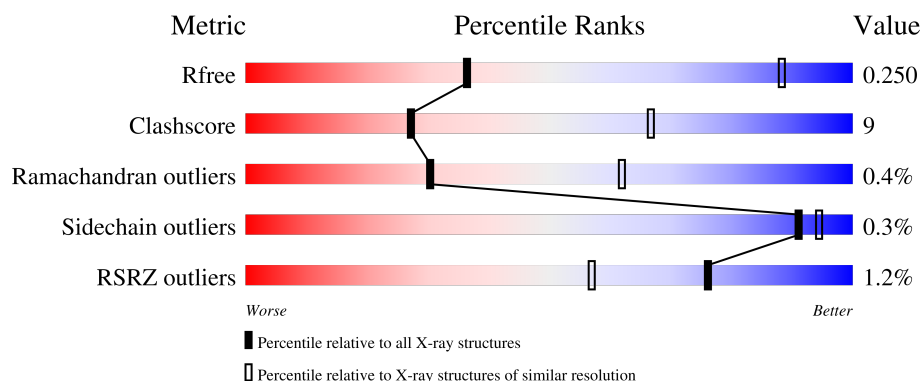
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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}	164625	1017 (3.80-3.60)
Clashscore	180529	1074 (3.80-3.60)
Ramachandran outliers	177936	1055 (3.80-3.60)
Sidechain outliers	177891	1052 (3.80-3.60)
RSRZ outliers	164620	1017 (3.80-3.60)

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	530	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 18%, green 64%, grey 18%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 64% 18% 18% </div> </div>
1	B	530	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 21%, green 59%, grey 19%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 59% 21% 19% </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6661 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 Phosphate transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	434	Total	C	N	O	S	0	0	0
			3348	2208	555	569	16			
1	B	428	Total	C	N	O	S	0	0	0
			3308	2182	548	562	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A8N031
A	0	PRO	-	expression tag	UNP A8N031
A	328	PHE	TYR	engineered mutation	UNP A8N031
A	523	GLY	-	expression tag	UNP A8N031
A	524	GLY	-	expression tag	UNP A8N031
A	525	LEU	-	expression tag	UNP A8N031
A	526	VAL	-	expression tag	UNP A8N031
A	527	PRO	-	expression tag	UNP A8N031
A	528	ARG	-	expression tag	UNP A8N031
B	-1	GLY	-	expression tag	UNP A8N031
B	0	PRO	-	expression tag	UNP A8N031
B	328	PHE	TYR	engineered mutation	UNP A8N031
B	523	GLY	-	expression tag	UNP A8N031
B	524	GLY	-	expression tag	UNP A8N031
B	525	LEU	-	expression tag	UNP A8N031
B	526	VAL	-	expression tag	UNP A8N031
B	527	PRO	-	expression tag	UNP A8N031
B	528	ARG	-	expression tag	UNP A8N031

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).

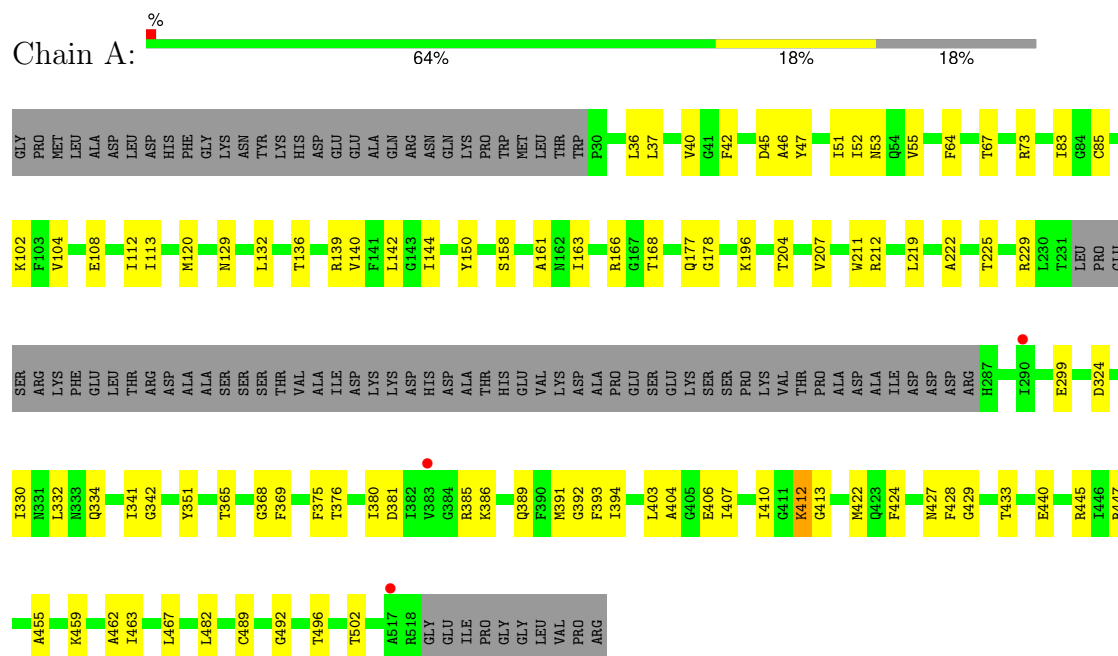


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		

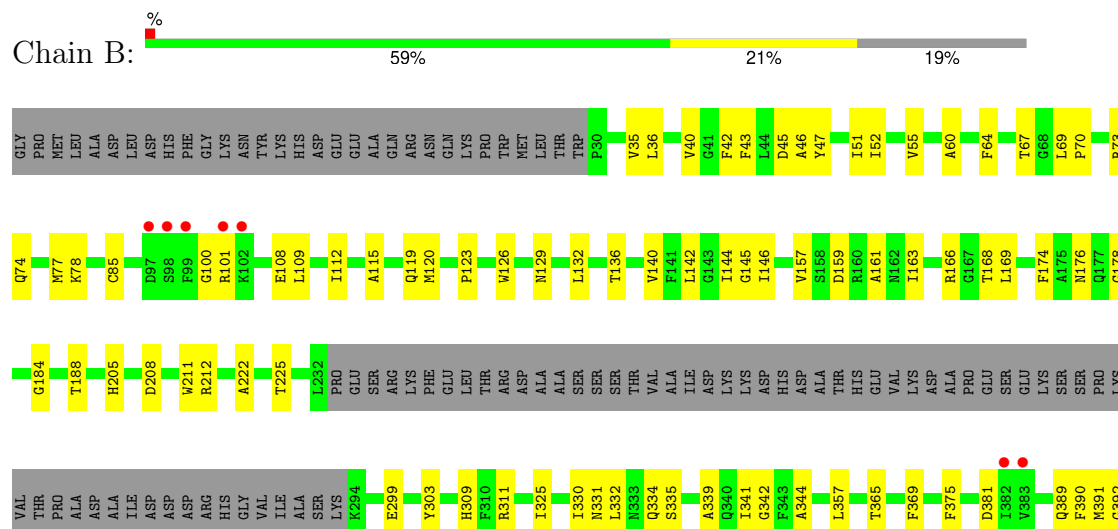
3 Residue-property plots

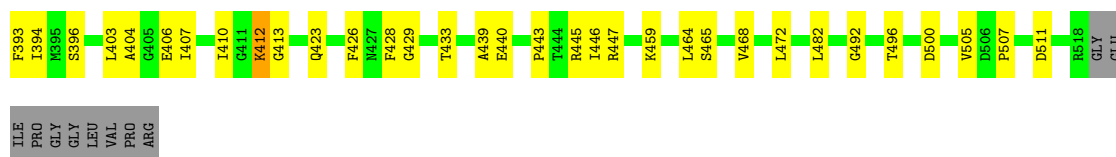
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Phosphate transporter



• Molecule 1: Phosphate transporter





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	174.23Å 174.23Å 171.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	113.29 – 3.70 113.29 – 3.70	Depositor EDS
% Data completeness (in resolution range)	98.9 (113.29-3.70) 94.4 (113.29-3.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.43 (at 3.67Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.225 , 0.257 0.224 , 0.250	Depositor DCC
R_{free} test set	1865 reflections (9.53%)	wwPDB-VP
Wilson B-factor (Å ²)	143.5	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 310.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.349 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6661	wwPDB-VP
Average B, all atoms (Å ²)	182.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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: PO4

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	0.25	0/3431	0.45	0/4647
1	B	0.25	0/3390	0.45	0/4592
All	All	0.25	0/6821	0.45	0/9239

There are no bond length outliers.

There are no bond angle outliers.

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	3348	0	3373	55	0
1	B	3308	0	3339	65	0
2	A	5	0	0	1	0
All	All	6661	0	6712	120	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 9.

All (120) 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:166:ARG:NH2	1:B:505:VAL:O	2.13	0.77
1:B:85:CYS:SG	1:B:459:LYS:NZ	2.57	0.75
1:A:85:CYS:SG	1:A:459:LYS:NZ	2.59	0.71
1:B:119:GLN:HE22	1:B:142:LEU:HD22	1.58	0.69
1:B:168:THR:OG1	1:B:381:ASP:OD2	2.11	0.68
1:B:339:ALA:HA	1:B:344:ALA:HB2	1.79	0.64
1:B:52:ILE:HD11	1:B:332:LEU:HD22	1.79	0.64
1:B:123:PRO:HB2	1:B:126:TRP:CE3	2.33	0.64
1:B:299:GLU:OE2	1:B:445:ARG:NH1	2.31	0.62
1:A:166:ARG:HE	1:A:440:GLU:HG2	1.64	0.61
1:A:120:MET:O	1:A:212:ARG:NH1	2.33	0.61
1:A:168:THR:OG1	1:A:381:ASP:OD2	2.17	0.59
1:B:447:ARG:HH22	1:B:507:PRO:HG2	1.67	0.59
1:A:73:ARG:HH12	1:A:129:ASN:HB3	1.67	0.59
1:A:369:PHE:O	1:A:427:ASN:ND2	2.35	0.59
1:B:112:ILE:HB	1:B:142:LEU:HD12	1.84	0.59
1:A:392:GLY:HA3	1:A:429:GLY:HA3	1.87	0.57
1:B:77:MET:HA	1:B:136:THR:HG22	1.85	0.57
1:A:53:ASN:OD1	1:A:334:GLN:N	2.38	0.57
1:B:120:MET:O	1:B:212:ARG:NH1	2.33	0.57
1:A:376:THR:OG1	1:A:428:PHE:HA	2.05	0.56
1:B:330:ILE:O	1:B:334:GLN:N	2.38	0.56
1:A:299:GLU:OE2	1:A:445:ARG:NH1	2.34	0.56
1:B:132:LEU:O	1:B:136:THR:HG23	2.08	0.54
1:B:161:ALA:HB1	1:B:163:ILE:HG22	1.90	0.54
1:A:112:ILE:HB	1:A:142:LEU:HD12	1.91	0.53
1:B:70:PRO:HG2	1:B:73:ARG:HB2	1.90	0.53
1:B:335:SER:HB3	1:B:357:LEU:HD21	1.90	0.53
1:B:468:VAL:HG22	1:B:472:LEU:HG	1.91	0.52
1:A:365:THR:HA	1:A:369:PHE:HB3	1.91	0.52
1:A:391:MET:HA	1:A:394:ILE:HG22	1.92	0.52
1:B:43:PHE:HB2	1:B:176:ASN:HB3	1.90	0.52
1:B:392:GLY:HA3	1:B:429:GLY:HA3	1.92	0.51
1:A:52:ILE:HD11	1:A:332:LEU:HD22	1.91	0.51
1:B:439:ALA:O	1:B:447:ARG:NH1	2.43	0.51
1:A:132:LEU:O	1:A:136:THR:HG23	2.11	0.51
1:A:196:LYS:HG3	1:A:351:TYR:CE2	2.46	0.51
1:A:459:LYS:O	1:A:463:ILE:HG23	2.10	0.50
1:A:150:TYR:OH	2:A:601:PO4:O2	2.29	0.49
1:B:443:PRO:HD2	1:B:446:ILE:HD11	1.94	0.49
1:A:222:ALA:O	1:A:225:THR:OG1	2.28	0.49
1:A:55:VAL:HG13	1:A:211:TRP:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ILE:HG22	1:A:342:GLY:H	1.78	0.48
1:B:60:ALA:HB2	1:B:69:LEU:HG	1.94	0.48
1:A:42:PHE:HE1	1:A:177:GLN:HB2	1.79	0.47
1:A:64:PHE:HB3	1:A:67:THR:O	2.14	0.47
1:A:330:ILE:O	1:A:334:GLN:N	2.47	0.47
1:A:440:GLU:OE1	1:A:502:THR:OG1	2.24	0.47
1:A:330:ILE:HD13	1:A:422:MET:HE1	1.97	0.47
1:B:375:PHE:HB3	1:B:428:PHE:CE1	2.50	0.47
1:B:406:GLU:HB3	1:B:410:ILE:HD12	1.96	0.47
1:B:157:VAL:HG13	1:B:169:LEU:HD23	1.96	0.47
1:B:303:TYR:CE1	1:B:309:HIS:HB3	2.49	0.47
1:B:311:ARG:NH1	1:B:500:ASP:OD1	2.46	0.47
1:B:365:THR:HA	1:B:369:PHE:HB3	1.96	0.47
1:B:393:PHE:CE1	1:B:492:GLY:HA3	2.50	0.47
1:B:178:GLY:HA2	1:B:369:PHE:CE2	2.50	0.46
1:A:139:ARG:HA	1:A:142:LEU:HB3	1.97	0.46
1:A:404:ALA:HB2	1:A:482:LEU:HB2	1.96	0.46
1:A:36:LEU:O	1:A:40:VAL:HG23	2.16	0.46
1:B:341:ILE:HG22	1:B:342:GLY:H	1.81	0.46
1:B:142:LEU:O	1:B:146:ILE:HG13	2.16	0.46
1:B:222:ALA:O	1:B:225:THR:OG1	2.34	0.46
1:B:445:ARG:NE	1:B:511:ASP:OD2	2.34	0.45
1:A:108:GLU:OE1	1:A:108:GLU:N	2.46	0.45
1:A:324:ASP:HB3	1:A:462:ALA:HB2	1.99	0.45
1:A:393:PHE:HD1	1:A:489:CYS:HA	1.81	0.45
1:A:403:LEU:HB3	1:A:482:LEU:HD13	1.99	0.45
1:A:403:LEU:O	1:A:407:ILE:N	2.49	0.45
1:B:64:PHE:HB3	1:B:67:THR:O	2.17	0.45
1:B:73:ARG:HH12	1:B:129:ASN:HB3	1.80	0.45
1:B:42:PHE:HE2	1:B:174:PHE:HA	1.81	0.44
1:B:47:TYR:O	1:B:51:ILE:HG12	2.17	0.44
1:A:389:GLN:HB2	1:A:433:THR:HG21	1.98	0.44
1:B:159:ASP:OD2	1:B:447:ARG:NE	2.51	0.44
1:B:404:ALA:HB2	1:B:482:LEU:HB2	2.00	0.44
1:A:161:ALA:HB1	1:A:163:ILE:HG22	2.00	0.44
1:B:331:ASN:OD1	1:B:423:GLN:NE2	2.51	0.43
1:A:47:TYR:O	1:A:51:ILE:HG12	2.18	0.43
1:B:55:VAL:HG22	1:B:211:TRP:HB2	2.01	0.43
1:B:108:GLU:HB2	1:B:145:GLY:HA2	2.00	0.43
1:A:178:GLY:HA2	1:A:369:PHE:CE2	2.53	0.43
1:A:406:GLU:HB3	1:A:410:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:389:GLN:HB2	1:B:433:THR:HG21	2.00	0.43
1:A:83:ILE:HD11	1:A:467:LEU:HD11	2.01	0.42
1:A:385:ARG:HB3	1:A:433:THR:HG23	2.01	0.42
1:A:412:LYS:HD2	1:A:413:GLY:N	2.34	0.42
1:B:115:ALA:O	1:B:119:GLN:HG3	2.19	0.42
1:A:375:PHE:HB3	1:A:428:PHE:CE1	2.54	0.42
1:B:464:LEU:O	1:B:468:VAL:HG12	2.19	0.42
1:A:380:ILE:HB	1:A:385:ARG:HH11	1.85	0.42
1:B:100:GLY:O	1:B:101:ARG:HD2	2.20	0.42
1:B:184:GLY:O	1:B:188:THR:OG1	2.24	0.42
1:A:37:LEU:HD11	1:A:229:ARG:NH1	2.35	0.42
1:B:36:LEU:O	1:B:40:VAL:HG23	2.20	0.42
1:B:391:MET:HA	1:B:394:ILE:HG22	2.01	0.42
1:A:204:THR:O	1:A:207:VAL:HG12	2.19	0.41
1:A:386:LYS:HE3	1:A:496:THR:O	2.20	0.41
1:B:74:GLN:O	1:B:78:LYS:HG3	2.19	0.41
1:B:403:LEU:HB3	1:B:482:LEU:HD13	2.02	0.41
1:B:35:VAL:HG11	1:B:169:LEU:HD21	2.02	0.41
1:A:113:ILE:HG23	1:A:219:LEU:HD22	2.02	0.41
1:B:325:ILE:HG23	1:B:465:SER:HB3	2.02	0.41
1:B:412:LYS:HD2	1:B:413:GLY:N	2.35	0.41
1:A:393:PHE:CE1	1:A:492:GLY:HA3	2.55	0.41
1:A:455:ALA:O	1:A:459:LYS:HG2	2.21	0.41
1:B:396:SER:HB2	1:B:426:PHE:CE1	2.56	0.41
1:B:403:LEU:O	1:B:407:ILE:N	2.52	0.41
1:A:140:VAL:O	1:A:144:ILE:HG13	2.21	0.41
1:B:109:LEU:O	1:B:112:ILE:HG12	2.20	0.41
1:B:390:PHE:CE1	1:B:496:THR:HB	2.56	0.41
1:A:158:SER:OG	1:A:447:ARG:NH1	2.54	0.41
1:B:45:ASP:OD1	1:B:46:ALA:N	2.54	0.41
1:B:208:ASP:O	1:B:212:ARG:HG3	2.21	0.41
1:A:393:PHE:CZ	1:A:492:GLY:HA3	2.56	0.41
1:B:365:THR:HA	1:B:369:PHE:CB	2.51	0.40
1:A:368:GLY:O	1:A:424:PHE:HA	2.21	0.40
1:A:45:ASP:OD1	1:A:46:ALA:N	2.54	0.40
1:B:140:VAL:O	1:B:144:ILE:HG13	2.21	0.40
1:B:166:ARG:HE	1:B:440:GLU:HG2	1.87	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	430/530 (81%)	405 (94%)	23 (5%)	2 (0%)	25	57
1	B	424/530 (80%)	397 (94%)	26 (6%)	1 (0%)	44	72
All	All	854/1060 (81%)	802 (94%)	49 (6%)	3 (0%)	30	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	LYS
1	B	205	HIS
1	A	104	VAL

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	342/433 (79%)	341 (100%)	1 (0%)	91	94
1	B	340/433 (78%)	339 (100%)	1 (0%)	91	94
All	All	682/866 (79%)	680 (100%)	2 (0%)	91	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	412	LYS
1	B	412	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	119	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	A	601	-	4,4,4	0.96	0	6,6,6	0.53	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	PO4	1	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 [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	434/530 (81%)	-0.79	3 (0%) 84 68	88, 176, 257, 289	0
1	B	428/530 (80%)	-0.77	7 (1%) 70 51	110, 177, 260, 311	0
All	All	862/1060 (81%)	-0.78	10 (1%) 76 57	88, 177, 258, 311	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	99	PHE	6.3
1	B	97	ASP	4.3
1	B	382	ILE	4.1
1	B	98	SER	3.8
1	B	383	VAL	3.3
1	B	102	LYS	2.8
1	B	101	ARG	2.4
1	A	517	ALA	2.3
1	A	290	ILE	2.2
1	A	383	VAL	2.2

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 monosaccharides in this entry.

6.4 Ligands

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(\AA^2)	Q<0.9
2	PO4	A	601	5/5	0.99	0.10	181,191,218,239	0

6.5 Other polymers

There are no such residues in this entry.