



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:34 PM UTC

PDB ID : 4FYF / pdb_00004fyf
Title : Structural basis for substrate recognition by a novel Legionella phosphoinositide phosphatase
Authors : Hsu, F.S.; Zhu, W.; Brennan, L.; Tao, L.; Luo, Z.Q.; Mao, Y.
Deposited on : 2012-07-04
Resolution : 2.42 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

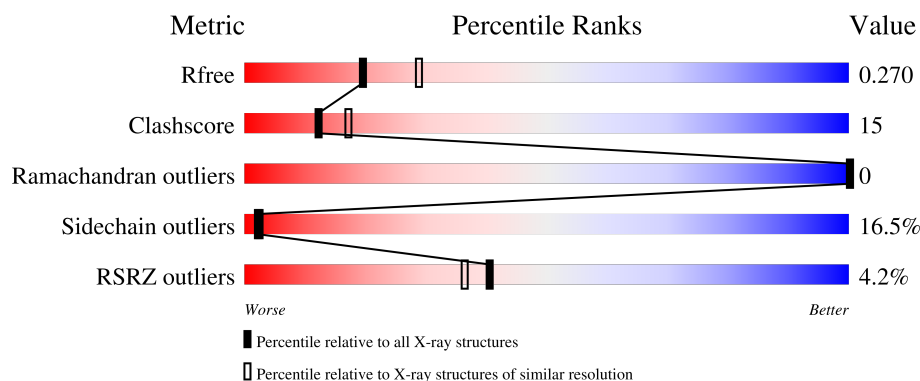
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	761	 4% 67% 23% 7% . .

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	PO4	A	801	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5984 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 SidF, inhibitor of growth family, member 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	739	5907	3671	1057	1161	18	0	3	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q5ZSD5
A	645	SER	CYS	engineered mutation	UNP Q5ZSD5

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 3 is MERCURY (II) ION (CCD ID: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Hg	0	0
			3	3		

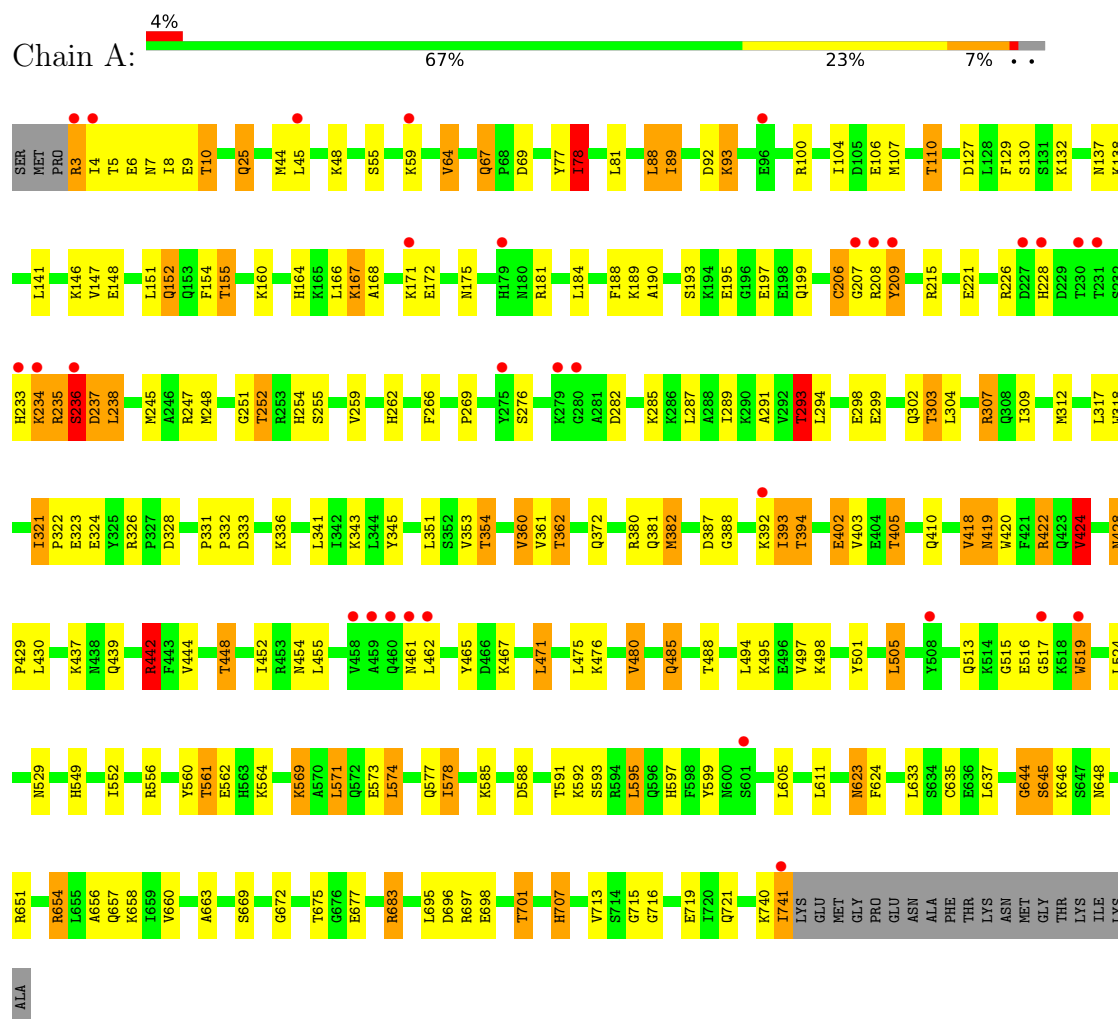
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		

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: SidF, inhibitor of growth family, member 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.83Å 115.71Å 125.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.18 – 2.42 47.18 – 2.42	Depositor EDS
% Data completeness (in resolution range)	98.3 (47.18-2.42) 98.3 (47.18-2.42)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.211 , 0.270 0.212 , 0.270	Depositor DCC
R_{free} test set	1992 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.522	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5984	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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: HG, 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	1.10	7/6020 (0.1%)	1.29	32/8111 (0.4%)

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
1	A	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	624	PHE	N-CA	8.23	1.56	1.46
1	A	635	CYS	C-N	-7.77	1.23	1.34
1	A	707	HIS	CE1-NE2	5.77	1.38	1.32
1	A	597	HIS	CG-CD2	5.52	1.42	1.35
1	A	64	VAL	C-O	-5.26	1.19	1.24
1	A	303	THR	CA-CB	5.20	1.61	1.53
1	A	318	TRP	N-CA	-5.15	1.40	1.46

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	623	ASN	CA-C-N	-11.71	104.34	122.60
1	A	623	ASN	C-N-CA	-11.71	104.34	122.60
1	A	422	ARG	NE-CZ-NH2	-8.39	111.65	119.20
1	A	207	GLY	N-CA-C	-7.25	96.00	113.18
1	A	236	SER	N-CA-C	-7.22	101.00	110.53
1	A	623	ASN	N-CA-C	7.04	122.99	111.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	307	ARG	CG-CD-NE	-6.54	97.62	112.00
1	A	623	ASN	O-C-N	-6.51	114.62	122.11
1	A	422	ARG	CG-CD-NE	-6.45	97.82	112.00
1	A	663	ALA	N-CA-C	-6.30	104.50	111.36
1	A	529	ASN	N-CA-C	6.25	118.09	111.28
1	A	654	ARG	CB-CG-CD	6.23	125.62	111.30
1	A	293	THR	CB-CA-C	6.17	121.35	110.85
1	A	405	THR	CB-CA-C	-6.13	97.22	109.79
1	A	644	GLY	N-CA-C	6.09	122.10	111.14
1	A	424	VAL	N-CA-CB	-5.97	101.47	111.38
1	A	67	GLN	CA-CB-CG	5.85	125.80	114.10
1	A	64	VAL	CB-CA-C	5.83	116.19	111.06
1	A	67	GLN	CB-CG-CD	5.77	122.41	112.60
1	A	635	CYS	O-C-N	-5.75	115.20	122.27
1	A	418	VAL	N-CA-CB	-5.70	101.82	111.23
1	A	442	ARG	N-CA-C	-5.64	105.03	111.07
1	A	360	VAL	CB-CA-C	5.53	120.36	111.29
1	A	637	LEU	N-CA-C	-5.53	106.30	113.16
1	A	64	VAL	N-CA-C	-5.51	107.45	112.96
1	A	422	ARG	CD-NE-CZ	5.38	131.94	124.40
1	A	321	ILE	CA-C-N	-5.35	114.44	119.90
1	A	321	ILE	C-N-CA	-5.35	114.44	119.90
1	A	569	LYS	N-CA-C	-5.32	105.38	111.07
1	A	424	VAL	CG1-CB-CG2	5.18	122.19	110.80
1	A	78	ILE	N-CA-CB	5.03	116.09	110.51
1	A	132	LYS	N-CA-C	-5.02	106.25	112.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	715	GLY	Peptide

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	5907	0	5795	181	0
2	A	5	0	0	2	0
3	A	3	0	0	0	0
4	A	69	0	0	4	0
All	All	5984	0	5795	181	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 15.

All (181) 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:208:ARG:NH2	1:A:394:THR:HG22	1.45	1.29
1:A:235:ARG:HD2	1:A:235:ARG:C	1.71	1.10
1:A:235:ARG:HD2	1:A:235:ARG:O	1.55	1.03
1:A:208:ARG:NH2	1:A:394:THR:CG2	2.26	0.98
1:A:208:ARG:HH22	1:A:394:THR:CG2	1.77	0.97
1:A:394:THR:HG23	1:A:402:GLU:HG3	1.46	0.97
1:A:516:GLU:HA	1:A:519:TRP:HE3	1.31	0.95
1:A:382:MET:HA	1:A:382:MET:HE2	1.46	0.95
1:A:516:GLU:HA	1:A:519:TRP:CE3	2.03	0.93
1:A:208:ARG:HH22	1:A:394:THR:HG22	1.18	0.91
1:A:235:ARG:C	1:A:235:ARG:CD	2.42	0.91
1:A:252:THR:CG2	1:A:262:HIS:NE2	2.34	0.91
1:A:252:THR:HG23	1:A:262:HIS:NE2	1.86	0.90
1:A:151:LEU:O	1:A:155:THR:HG23	1.71	0.88
1:A:238:LEU:HD22	1:A:238:LEU:H	1.38	0.88
1:A:208:ARG:HH21	1:A:394:THR:HG22	1.37	0.88
1:A:362:THR:HG21	1:A:419:ASN:HD21	1.40	0.84
1:A:208:ARG:O	1:A:299:GLU:OE1	1.95	0.83
1:A:424:VAL:HG13	1:A:428:ASN:HB3	1.59	0.82
1:A:362:THR:HG21	1:A:419:ASN:ND2	1.95	0.82
1:A:394:THR:CG2	1:A:402:GLU:HG3	2.09	0.81
1:A:302:GLN:HE21	1:A:394:THR:H	1.29	0.81
1:A:574:LEU:O	1:A:578:ILE:HB	1.81	0.81
1:A:312:MET:HE1	1:A:345:TYR:CE2	2.17	0.80
1:A:77:TYR:OH	1:A:155:THR:HG21	1.81	0.80
1:A:428:ASN:HD22	1:A:430:LEU:H	1.30	0.80
1:A:428:ASN:ND2	1:A:430:LEU:H	1.81	0.78
1:A:444:VAL:O	1:A:448:THR:CG2	2.32	0.78
1:A:7:ASN:HD22	1:A:10:THR:HG23	1.50	0.76
1:A:561:THR:HA	1:A:564:LYS:HE2	1.68	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ASP:H	1:A:137:ASN:HD21	1.33	0.74
1:A:444:VAL:O	1:A:448:THR:HG22	1.89	0.72
1:A:235:ARG:HD3	1:A:236:SER:O	1.89	0.72
1:A:93:LYS:HD2	1:A:93:LYS:C	2.14	0.72
1:A:235:ARG:CD	1:A:236:SER:O	2.38	0.71
1:A:188:PHE:CD2	1:A:698:GLU:HG2	2.26	0.71
1:A:494:LEU:HD13	1:A:498:LYS:HE3	1.73	0.71
1:A:291:ALA:HB2	1:A:505:LEU:CD2	2.20	0.71
1:A:93:LYS:HD2	1:A:93:LYS:O	1.89	0.71
1:A:354:THR:HB	1:A:410:GLN:HB3	1.73	0.71
1:A:106:GLU:O	1:A:110:THR:HG22	1.91	0.70
1:A:237:ASP:OD2	1:A:285:LYS:HE2	1.91	0.70
1:A:591:THR:O	1:A:595:LEU:HD22	1.92	0.69
1:A:428:ASN:HD22	1:A:428:ASN:C	2.01	0.69
1:A:419:ASN:HD22	1:A:419:ASN:C	2.01	0.69
1:A:25:GLN:HE21	1:A:25:GLN:H	1.41	0.69
1:A:197:GLU:HG2	1:A:254:HIS:HA	1.74	0.68
1:A:656:ALA:O	1:A:660:VAL:HG23	1.94	0.68
1:A:291:ALA:HB2	1:A:505:LEU:HD22	1.73	0.68
1:A:234:LYS:HD2	1:A:234:LYS:H	1.59	0.67
1:A:372:GLN:NE2	1:A:651:ARG:HH12	1.93	0.67
1:A:465:TYR:HD1	1:A:577:GLN:NE2	1.94	0.66
1:A:7:ASN:HD22	1:A:10:THR:H	1.44	0.66
1:A:465:TYR:HD1	1:A:577:GLN:HE21	1.45	0.65
1:A:516:GLU:HG2	1:A:517:GLY:H	1.62	0.65
1:A:235:ARG:CZ	1:A:237:ASP:HA	2.27	0.65
1:A:93:LYS:C	1:A:93:LYS:CD	2.69	0.65
1:A:190:ALA:H	1:A:199:GLN:HE21	1.45	0.63
1:A:578:ILE:CD1	1:A:595:LEU:HG	2.28	0.63
1:A:7:ASN:HD21	1:A:9:GLU:HB3	1.63	0.62
1:A:302:GLN:NE2	1:A:394:THR:H	1.95	0.62
1:A:238:LEU:HD22	1:A:238:LEU:N	2.12	0.62
1:A:442:ARG:HG2	1:A:549:HIS:CD2	2.35	0.62
1:A:59[B]:LYS:CB	1:A:59[B]:LYS:NZ	2.63	0.62
1:A:428:ASN:HD22	1:A:429:PRO:N	1.98	0.62
1:A:571:LEU:HD22	1:A:599:TYR:CE2	2.35	0.62
1:A:362:THR:CG2	1:A:419:ASN:ND2	2.63	0.61
1:A:167:LYS:HZ2	1:A:167:LYS:HB2	1.65	0.61
1:A:93:LYS:O	1:A:93:LYS:CD	2.48	0.61
1:A:444:VAL:O	1:A:448:THR:HG23	2.00	0.61
1:A:226:ARG:HH22	1:A:394:THR:HG21	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:THR:HG22	4:A:925:HOH:O	2.00	0.61
1:A:683:ARG:HD3	1:A:696:ASP:OD2	2.01	0.60
1:A:152:GLN:HE22	1:A:741:ILE:HB	1.65	0.60
1:A:428:ASN:HD21	1:A:430:LEU:HG	1.66	0.60
1:A:560:TYR:CE2	1:A:564:LYS:HD3	2.37	0.59
1:A:578:ILE:HD12	1:A:595:LEU:HG	1.85	0.58
1:A:152:GLN:NE2	1:A:741:ILE:HB	2.19	0.58
1:A:382:MET:HA	1:A:382:MET:CE	2.29	0.58
1:A:382:MET:HE2	1:A:382:MET:CA	2.26	0.57
1:A:234:LYS:HD2	1:A:234:LYS:N	2.18	0.57
1:A:235:ARG:NE	1:A:237:ASP:HA	2.20	0.57
1:A:248:MET:HE3	1:A:660:VAL:HG22	1.87	0.57
1:A:3:ARG:HH11	1:A:3:ARG:HB3	1.68	0.57
1:A:461:ASN:O	1:A:462:LEU:HD22	2.05	0.57
1:A:485:GLN:HE21	1:A:485:GLN:HA	1.69	0.57
1:A:233:HIS:CE1	1:A:234:LYS:O	2.57	0.56
1:A:209:TYR:O	1:A:226:ARG:NH1	2.36	0.56
1:A:669:SER:HB2	1:A:672:GLY:H	1.70	0.56
1:A:238:LEU:H	1:A:238:LEU:CD2	2.15	0.55
1:A:252:THR:HG22	1:A:262:HIS:NE2	2.20	0.55
1:A:237:ASP:OD1	1:A:237:ASP:N	2.38	0.55
1:A:362:THR:H	1:A:372:GLN:NE2	2.05	0.55
1:A:516:GLU:CA	1:A:519:TRP:CE3	2.86	0.54
1:A:167:LYS:HG3	1:A:168:ALA:N	2.23	0.54
1:A:291:ALA:CB	1:A:505:LEU:HD22	2.38	0.53
1:A:701:THR:HG21	4:A:920:HOH:O	2.08	0.53
1:A:317:LEU:O	1:A:321:ILE:HG13	2.09	0.52
1:A:59[B]:LYS:CB	1:A:59[B]:LYS:HZ2	2.22	0.52
1:A:234:LYS:H	1:A:234:LYS:CD	2.22	0.52
1:A:394:THR:HG23	1:A:402:GLU:CG	2.31	0.52
1:A:78:ILE:HD12	1:A:154:PHE:CD2	2.44	0.51
1:A:382:MET:HE1	1:A:501:TYR:HE2	1.75	0.51
1:A:92:ASP:OD2	1:A:164:HIS:HE1	1.94	0.51
1:A:480:VAL:CG2	1:A:552:ILE:HG12	2.42	0.50
1:A:382:MET:CE	1:A:382:MET:CA	2.90	0.50
1:A:6:GLU:CB	1:A:44:MET:HE1	2.42	0.49
1:A:106:GLU:O	1:A:110:THR:CG2	2.58	0.49
1:A:129:PHE:CD1	1:A:697:ARG:HG2	2.47	0.49
1:A:89:ILE:HG22	1:A:100:ARG:NH1	2.27	0.49
1:A:402:GLU:HG2	1:A:403:VAL:N	2.27	0.49
1:A:3:ARG:HH21	1:A:206:CYS:HB3	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:GLY:HA2	1:A:262:HIS:CD2	2.48	0.48
1:A:6:GLU:HB2	1:A:44:MET:HE1	1.96	0.48
1:A:208:ARG:HH22	1:A:394:THR:HG21	1.71	0.48
1:A:7:ASN:ND2	1:A:10:THR:H	2.08	0.48
1:A:7:ASN:HD22	1:A:10:THR:CG2	2.23	0.47
1:A:25:GLN:H	1:A:25:GLN:NE2	2.08	0.47
1:A:107:MET:HA	1:A:110:THR:HG23	1.95	0.47
1:A:380:ARG:HG3	1:A:439:GLN:HG2	1.96	0.47
1:A:7:ASN:ND2	1:A:10:THR:HG23	2.25	0.47
1:A:100:ARG:O	1:A:104:ILE:HG12	2.14	0.47
1:A:215:ARG:HD3	1:A:221:GLU:OE2	2.14	0.47
1:A:467:LYS:HD2	1:A:573:GLU:HB3	1.97	0.47
1:A:428:ASN:ND2	1:A:428:ASN:C	2.71	0.47
1:A:235:ARG:O	1:A:235:ARG:CD	2.43	0.47
1:A:578:ILE:HD11	1:A:595:LEU:HG	1.95	0.47
1:A:151:LEU:O	1:A:155:THR:CG2	2.55	0.47
1:A:228:HIS:HE1	1:A:299:GLU:OE1	1.98	0.47
1:A:387:ASP:OD1	1:A:387:ASP:C	2.57	0.46
1:A:701:THR:HG22	4:A:948:HOH:O	2.15	0.46
1:A:55:SER:OG	1:A:698:GLU:OE2	2.32	0.46
1:A:234:LYS:O	1:A:234:LYS:HG2	2.16	0.46
1:A:707:HIS:CD2	1:A:716:GLY:H	2.34	0.46
1:A:88:LEU:HD13	1:A:172:GLU:HG2	1.98	0.46
1:A:321:ILE:O	1:A:322:PRO:C	2.58	0.45
1:A:289:ILE:O	1:A:293:THR:HG22	2.16	0.45
1:A:592:LYS:HE3	1:A:592:LYS:HB2	1.77	0.45
1:A:516:GLU:CG	1:A:517:GLY:H	2.27	0.45
1:A:516:GLU:CG	1:A:517:GLY:N	2.80	0.45
1:A:189:LYS:HE3	1:A:193:SER:OG	2.17	0.44
1:A:309:ILE:HA	1:A:312:MET:HE2	1.99	0.44
1:A:324:GLU:H	1:A:324:GLU:HG2	1.29	0.44
1:A:247:ARG:CZ	1:A:307:ARG:HG3	2.47	0.44
1:A:654:ARG:HH21	1:A:657:GLN:HE22	1.66	0.44
1:A:7:ASN:HB3	1:A:10:THR:HG23	2.00	0.44
1:A:675:THR:OG1	1:A:677:GLU:HG3	2.17	0.44
1:A:465:TYR:HA	1:A:577:GLN:HE22	1.83	0.43
1:A:362:THR:H	1:A:372:GLN:HE21	1.66	0.43
1:A:3:ARG:HB3	1:A:3:ARG:NH1	2.32	0.43
1:A:452:ILE:HD12	1:A:476:LYS:HA	2.01	0.42
1:A:471:LEU:HD22	1:A:475:LEU:HG	1.99	0.42
1:A:480:VAL:HG21	1:A:552:ILE:HG12	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:MET:HE3	1:A:317:LEU:HD21	2.01	0.42
1:A:644:GLY:HA2	1:A:648:ASN:OD1	2.18	0.42
1:A:422:ARG:HH22	1:A:721:GLN:HE21	1.67	0.42
1:A:571:LEU:CD2	1:A:599:TYR:CE2	3.01	0.42
1:A:323:GLU:HA	1:A:326:ARG:HD2	2.02	0.42
1:A:424:VAL:CG1	1:A:428:ASN:HB3	2.39	0.42
1:A:465:TYR:CD1	1:A:577:GLN:NE2	2.80	0.42
1:A:515:GLY:O	1:A:519:TRP:N	2.52	0.42
1:A:419:ASN:ND2	1:A:419:ASN:C	2.67	0.42
1:A:645:SER:HB2	2:A:801:PO4:P	2.59	0.42
1:A:645:SER:HB2	2:A:801:PO4:O2	2.20	0.42
1:A:302:GLN:HA	1:A:393:ILE:HG12	2.01	0.42
1:A:88:LEU:HD12	1:A:88:LEU:HA	1.74	0.41
1:A:69:ASP:OD1	1:A:69:ASP:C	2.62	0.41
1:A:266:PHE:CE2	1:A:304:LEU:CD2	3.04	0.41
1:A:78:ILE:HG23	1:A:154:PHE:CZ	2.56	0.41
1:A:362:THR:CG2	1:A:419:ASN:HD21	2.20	0.41
1:A:381:GLN:HB3	1:A:382:MET:HE3	2.03	0.41
1:A:388:GLY:O	1:A:495:LYS:HD3	2.21	0.41
1:A:331:PRO:HA	1:A:332:PRO:HD3	1.93	0.41
1:A:141:LEU:HD23	1:A:141:LEU:HA	1.99	0.41
1:A:420:TRP:HD1	1:A:721:GLN:HE22	1.68	0.41
1:A:654:ARG:HD3	4:A:929:HOH:O	2.20	0.41
1:A:148:GLU:O	1:A:152:GLN:HG2	2.21	0.40
1:A:333:ASP:HB3	1:A:336:LYS:HB3	2.03	0.40
1:A:387:ASP:OD1	1:A:388:GLY:N	2.54	0.40
1:A:78:ILE:HD11	1:A:151:LEU:CD2	2.51	0.40
1:A:245:MET:SD	1:A:269:PRO:HD3	2.61	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	740/761 (97%)	711 (96%)	29 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	639/654 (98%)	534 (84%)	105 (16%)	2	2

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	4	ILE
1	A	5	THR
1	A	8	ILE
1	A	10	THR
1	A	25	GLN
1	A	45	LEU
1	A	48	LYS
1	A	64	VAL
1	A	67	GLN
1	A	78	ILE
1	A	81	LEU
1	A	88	LEU
1	A	89	ILE
1	A	93	LYS
1	A	110	THR
1	A	130	SER
1	A	138	LYS
1	A	146	LYS
1	A	147	VAL
1	A	152	GLN
1	A	155	THR
1	A	160	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	166	LEU
1	A	167	LYS
1	A	171	LYS
1	A	175	ASN
1	A	181	ARG
1	A	184	LEU
1	A	195	GLU
1	A	206	CYS
1	A	209	TYR
1	A	234	LYS
1	A	235	ARG
1	A	236	SER
1	A	237	ASP
1	A	238	LEU
1	A	252	THR
1	A	255	SER
1	A	259	VAL
1	A	276	SER
1	A	282	ASP
1	A	287	LEU
1	A	293	THR
1	A	294	LEU
1	A	298	GLU
1	A	303	THR
1	A	328	ASP
1	A	341	LEU
1	A	343	LYS
1	A	351	LEU
1	A	353	VAL
1	A	354	THR
1	A	360	VAL
1	A	361	VAL
1	A	362	THR
1	A	382	MET
1	A	392	LYS
1	A	393	ILE
1	A	394	THR
1	A	402	GLU
1	A	405	THR
1	A	418	VAL
1	A	419	ASN
1	A	424	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	428	ASN
1	A	437	LYS
1	A	442	ARG
1	A	448	THR
1	A	454	ASN
1	A	455	LEU
1	A	471	LEU
1	A	480	VAL
1	A	485	GLN
1	A	488	THR
1	A	497	VAL
1	A	505	LEU
1	A	513	GLN
1	A	519	TRP
1	A	524	LEU
1	A	556	ARG
1	A	561	THR
1	A	562	GLU
1	A	569	LYS
1	A	571	LEU
1	A	574	LEU
1	A	578	ILE
1	A	585	LYS
1	A	588	ASP
1	A	593	SER
1	A	595	LEU
1	A	605	LEU
1	A	611	LEU
1	A	623	ASN
1	A	633	LEU
1	A	645	SER
1	A	646	LYS
1	A	658	LYS
1	A	683	ARG
1	A	695	LEU
1	A	701	THR
1	A	713	VAL
1	A	719	GLU
1	A	740	LYS
1	A	741	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	25	GLN
1	A	26	ASN
1	A	28	HIS
1	A	137	ASN
1	A	152	GLN
1	A	164	HIS
1	A	174	HIS
1	A	180	ASN
1	A	225	ASN
1	A	228	HIS
1	A	302	GLN
1	A	365	GLN
1	A	372	GLN
1	A	375	GLN
1	A	381	GLN
1	A	419	ASN
1	A	428	ASN
1	A	485	GLN
1	A	526	GLN
1	A	530	GLN
1	A	550	ASN
1	A	572	GLN
1	A	577	GLN
1	A	609	GLN
1	A	622	ASN
1	A	623	ASN
1	A	657	GLN
1	A	681	HIS
1	A	691	ASN
1	A	706	HIS
1	A	721	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are 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	$\# Z > 2$
2	PO4	A	801	-	4,4,4	2.05	1 (25%)	6,6,6	1.01	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	PO4	P-O3	-2.65	1.46	1.54

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 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	PO4	2	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	739/761 (97%)	0.15	31 (4%) 40 36	27, 53, 101, 148	3 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ARG	4.9
1	A	4	ILE	4.8
1	A	462	LEU	4.6
1	A	59[A]	LYS	4.0
1	A	741	ILE	3.8
1	A	208	ARG	3.6
1	A	458	VAL	3.5
1	A	459	ALA	3.3
1	A	508	TYR	3.2
1	A	461	ASN	3.2
1	A	280	GLY	3.2
1	A	236	SER	3.1
1	A	45	LEU	2.9
1	A	228	HIS	2.9
1	A	209	TYR	2.9
1	A	460	GLN	2.6
1	A	392	LYS	2.6
1	A	179	HIS	2.6
1	A	275	TYR	2.6
1	A	231	THR	2.6
1	A	519	TRP	2.5
1	A	601	SER	2.4
1	A	96	GLU	2.4
1	A	230	THR	2.3
1	A	234	LYS	2.3
1	A	227	ASP	2.2
1	A	207	GLY	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	233	HIS	2.1
1	A	517	GLY	2.1
1	A	279	LYS	2.0
1	A	171	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HG	A	802	1/1	0.95	0.23	132,132,132,132	0
3	HG	A	803	1/1	0.96	0.19	132,132,132,132	1
3	HG	A	804	1/1	0.96	0.25	132,132,132,132	1
2	PO4	A	801	5/5	0.97	0.06	38,48,51,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.