



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:23 AM GMT

PDB ID : 2WXO
Title : THE CRYSTAL STRUCTURE OF THE MURINE CLASS IA PI 3-KINASE P110DELTA IN COMPLEX WITH AS5.
Authors : Berndt, A.; Miller, S.; Williams, O.; Lee, D.D.; Houseman, B.T.; Pacold, J.I.; Gorrec, F.; Hon, W.-C.; Liu, Y.; Rommel, C.; Gaillard, P.; Ruckle, T.; Schwarz, M.K.; Shokat, K.M.; Shaw, J.P.; Williams, R.L.
Deposited on : 2009-11-09
Resolution : 2.49 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

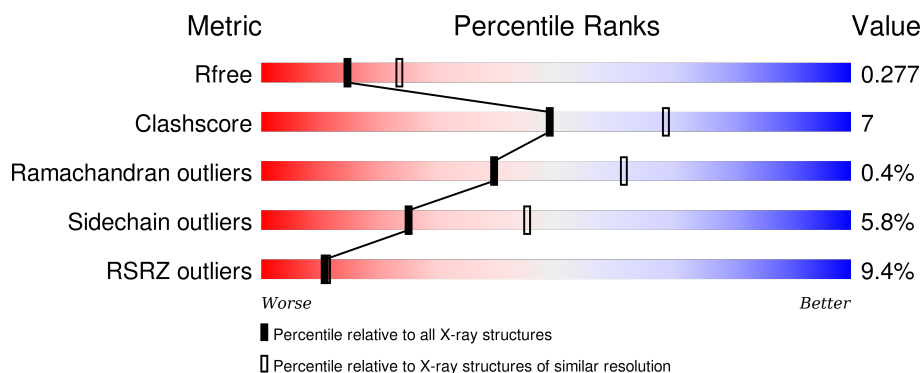
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	940	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6706 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.

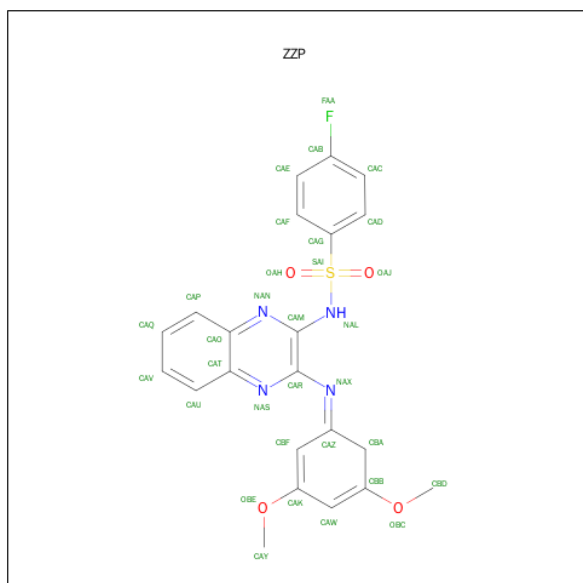
- Molecule 1 is a protein called PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT DELTA ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	822	Total	C	N	O	S	0	2	0
			6641	4259	1127	1200	55			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	GLY	-	EXPRESSION TAG	UNP Q3UDT3

- Molecule 2 is N-(3-([(1Z)-3,5-DIMETHOXYCYCLOHEXA-2,4-DIEN-1-YLIDENE]AMINO}QUINOXALIN-2-YL)-4-FLUOROBENZENESULFONAMIDE (three-letter code: ZYP) (formula: C₂₂H₁₉FN₄O₄S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			32	22	1	4	4	1		

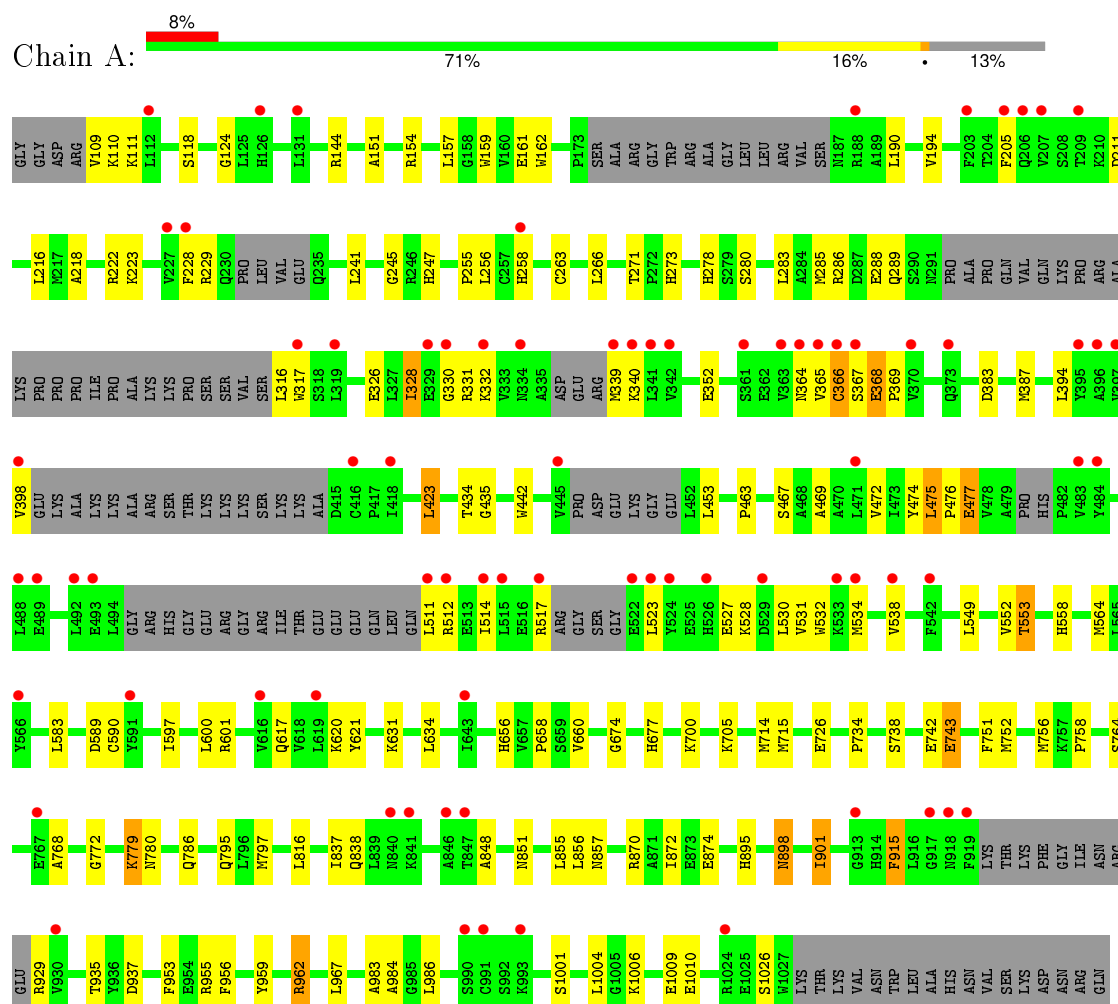
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total	O	0	0
			33	33		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT DELTA ISOFORM



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.89Å 64.17Å 117.00Å 90.00° 103.33° 90.00°	Depositor
Resolution (Å)	38.90 – 2.49 38.88 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.5 (38.90-2.49) 98.6 (38.88-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.5.0046	Depositor
R, R_{free}	0.213 , 0.277 0.216 , 0.277	Depositor DCC
R_{free} test set	1121 reflections (3.22%)	DCC
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 35959 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6706	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZYP

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	0.51	0/6790	0.61	1/9161 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	423	LEU	CA-CB-CG	6.28	129.75	115.30

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	6641	0	6626	95	4
2	A	32	0	19	1	0
3	A	33	0	0	3	0
All	All	6706	0	6645	96	4

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 7.

All (96) 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:837:ILE:CD1	1:A:901:ILE:HD11	1.85	1.06
1:A:367:SER:HB3	1:A:368:GLU:C	1.79	1.04
1:A:962:ARG:HH11	1:A:962:ARG:HG2	1.33	0.93
1:A:837:ILE:HD12	1:A:901:ILE:HD11	1.49	0.90
1:A:837:ILE:CD1	1:A:901:ILE:CD1	2.57	0.82
1:A:367:SER:HB3	1:A:368:GLU:CA	2.11	0.80
1:A:245:GLY:HA3	1:A:768:ALA:HB2	1.67	0.76
1:A:962:ARG:NH1	1:A:962:ARG:HG2	2.00	0.71
1:A:837:ILE:HD13	1:A:901:ILE:HD11	1.72	0.70
1:A:553:THR:HG21	1:A:564:MET:HG2	1.77	0.67
1:A:895:HIS:H	1:A:898:ASN:HD21	1.40	0.66
1:A:621:TYR:CZ	1:A:983:ALA:HB2	2.30	0.65
1:A:715:MET:HE1	1:A:751:PHE:HD1	1.62	0.65
1:A:534:MET:O	1:A:538:VAL:HG23	1.97	0.63
1:A:837:ILE:HD13	1:A:901:ILE:CD1	2.28	0.62
1:A:110:LYS:NZ	1:A:144:ARG:HH12	1.98	0.62
1:A:955:ARG:NH2	1:A:959:TYR:OH	2.32	0.62
1:A:984:ALA:CB	1:A:986:LEU:HD13	2.33	0.59
1:A:617:GLN:HE21	1:A:984:ALA:HA	1.68	0.59
1:A:435:GLY:HA2	1:A:475:LEU:O	2.03	0.58
2:A:1500:ZZP:NAS	2:A:1500:ZZP:HBF	2.19	0.58
1:A:838:GLN:NE2	1:A:937:ASP:OD2	2.38	0.56
1:A:154:ARG:NH2	1:A:674:GLY:O	2.37	0.56
1:A:984:ALA:HB1	1:A:986:LEU:HD13	1.86	0.56
1:A:527:GLU:O	1:A:531:VAL:HG23	2.07	0.55
1:A:617:GLN:NE2	1:A:984:ALA:HA	2.23	0.54
1:A:278:HIS:HD2	1:A:280:SER:OG	1.90	0.54
1:A:110:LYS:HZ1	1:A:144:ARG:HH12	1.55	0.54
1:A:617:GLN:HE22	1:A:620:LYS:NZ	2.08	0.52
1:A:583:LEU:HD11	1:A:600:LEU:HD11	1.90	0.52
1:A:205:PHE:CE1	1:A:223:LYS:HG3	2.44	0.52
1:A:247:HIS:HB2	1:A:738:SER:HA	1.90	0.52
1:A:118:SER:HB3	1:A:124:GLY:HA2	1.91	0.52
1:A:962:ARG:CG	1:A:962:ARG:HH11	2.14	0.52
1:A:255:PRO:HG2	1:A:258:HIS:CD2	2.45	0.51
1:A:157:LEU:HD22	1:A:161:GLU:HB3	1.91	0.51
1:A:953:PHE:O	1:A:956:PHE:HB3	2.11	0.51
1:A:216:LEU:HD22	1:A:241:LEU:HD11	1.93	0.50
1:A:734:PRO:O	1:A:816:LEU:HD22	2.11	0.50
1:A:387:MET:CE	1:A:590:CYS:SG	2.99	0.50
1:A:367:SER:CB	1:A:368:GLU:HB3	2.42	0.49
1:A:656:HIS:O	1:A:658:PRO:HD3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:TRP:CE3	1:A:286:ARG:HG3	2.47	0.49
1:A:915:PHE:CD1	1:A:915:PHE:C	2.87	0.48
1:A:387:MET:HE2	1:A:590:CYS:SG	2.53	0.48
1:A:367:SER:HB3	1:A:368:GLU:CB	2.43	0.48
1:A:434:THR:HG21	1:A:477:GLU:HA	1.96	0.47
1:A:271:THR:O	1:A:273:HIS:HD2	1.97	0.47
1:A:218:ALA:O	1:A:222:ARG:HG3	2.14	0.47
1:A:620:LYS:HE2	1:A:660:VAL:HG11	1.96	0.46
1:A:442:TRP:CH2	1:A:463:PRO:HD2	2.50	0.46
1:A:387:MET:HG3	1:A:589:ASP:HA	1.97	0.46
1:A:367:SER:HB3	1:A:368:GLU:HB3	1.96	0.46
1:A:364:ASN:C	1:A:366:CYS:H	2.19	0.46
1:A:194:VAL:HG21	1:A:216:LEU:HD21	1.98	0.45
1:A:848:ALA:HB2	1:A:857:ASN:ND2	2.31	0.45
1:A:532:TRP:HZ3	1:A:564:MET:HE2	1.81	0.45
1:A:330:GLY:O	1:A:368:GLU:HA	2.16	0.45
1:A:151:ALA:HB2	1:A:674:GLY:O	2.16	0.45
1:A:211:ASP:O	1:A:256:LEU:HG	2.17	0.45
1:A:915:PHE:HD1	1:A:915:PHE:C	2.20	0.45
1:A:797:MET:HG2	1:A:967:LEU:CD2	2.46	0.45
1:A:326:GLU:HB3	1:A:474:TYR:HB3	1.99	0.45
1:A:532:TRP:CZ3	1:A:564:MET:HE2	2.51	0.45
1:A:367:SER:HB3	1:A:368:GLU:O	2.14	0.45
1:A:331:ARG:O	1:A:469:ALA:HA	2.17	0.44
1:A:700:LYS:HE3	1:A:756:MET:O	2.18	0.44
1:A:383:ASP:HA	1:A:558:HIS:HB3	1.99	0.44
1:A:109:VAL:N	3:A:2001:HOH:O	2.50	0.44
1:A:285:MET:O	1:A:288:GLU:HG2	2.18	0.43
1:A:549:LEU:HD21	1:A:564:MET:HE1	2.00	0.43
1:A:870:ARG:NH2	1:A:874:GLU:OE2	2.44	0.43
1:A:159:TRP:HB3	1:A:283:LEU:HG	2.01	0.43
1:A:289:GLN:HG2	1:A:677:HIS:CD2	2.53	0.43
1:A:962:ARG:HD3	3:A:2033:HOH:O	2.19	0.43
1:A:368:GLU:O	1:A:368:GLU:HG3	2.19	0.43
1:A:229:ARG:HD3	1:A:229:ARG:HA	1.82	0.43
1:A:768:ALA:HB3	1:A:772:GLY:HA3	2.00	0.42
1:A:278:HIS:CD2	1:A:280:SER:H	2.37	0.42
1:A:263:CYS:HA	1:A:266:LEU:HD12	2.01	0.42
1:A:742:GLU:HB2	1:A:764:SER:O	2.19	0.42
1:A:597:ILE:O	1:A:601:ARG:HG3	2.19	0.42
1:A:758:PRO:HA	3:A:2018:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1006:LYS:HB3	1:A:1010:GLU:HB2	2.02	0.41
1:A:743:GLU:HG2	1:A:764:SER:O	2.21	0.41
1:A:328:ILE:HB	1:A:472:VAL:HG23	2.02	0.41
1:A:368:GLU:N	1:A:369:PRO:CD	2.83	0.41
1:A:512:ARG:HB3	1:A:512:ARG:CZ	2.50	0.41
1:A:528:LYS:HG2	1:A:552:VAL:HG12	2.02	0.40
1:A:435:GLY:O	1:A:475:LEU:N	2.41	0.40
1:A:758:PRO:HB3	1:A:779:LYS:HD3	2.04	0.40
1:A:929:ARG:HH22	1:A:1001:SER:HA	1.86	0.40
1:A:475:LEU:HA	1:A:476:PRO:HD3	1.90	0.40
1:A:856:LEU:HD11	1:A:872:ILE:HD11	2.04	0.40
1:A:715:MET:CE	1:A:751:PHE:HD1	2.32	0.40
1:A:700:LYS:NZ	1:A:780:ASN:O	2.47	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:714:MET:CE	1:A:714:MET:CE[2_555]	0.94	1.26
1:A:714:MET:SD	1:A:714:MET:CE[2_555]	1.15	1.05
1:A:714:MET:CG	1:A:714:MET:CE[2_555]	2.03	0.17
1:A:714:MET:SD	1:A:714:MET:SD[2_555]	2.08	0.12

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	802/940 (85%)	775 (97%)	24 (3%)	3 (0%)	39 61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	365	VAL
1	A	328	ILE
1	A	368	GLU

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	730/827 (88%)	688 (94%)	42 (6%)	25	45

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	LYS
1	A	190	LEU
1	A	228	PHE
1	A	316	LEU
1	A	317	TRP
1	A	332	LYS
1	A	339	MET
1	A	340	LYS
1	A	352	GLU
1	A	366	CYS
1	A	394	LEU
1	A	398	VAL
1	A	423	LEU
1	A	453	LEU
1	A	467	SER
1	A	475	LEU
1	A	477	GLU
1	A	511	LEU
1	A	514	ILE
1	A	517	ARG
1	A	523	LEU
1	A	530	LEU
1	A	553	THR
1	A	631	LYS

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Mol	Chain	Res	Type
1	A	634	LEU
1	A	705	LYS
1	A	726	GLU
1	A	743	GLU
1	A	752	MET
1	A	779	LYS
1	A	786	GLN
1	A	795	GLN
1	A	851	ASN
1	A	855	LEU
1	A	898	ASN
1	A	901	ILE
1	A	915	PHE
1	A	935	THR
1	A	962	ARG
1	A	1004	LEU
1	A	1009	GLU
1	A	1026	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	156	GLN
1	A	273	HIS
1	A	278	HIS
1	A	291	ASN
1	A	344	GLN
1	A	536	HIS
1	A	539	GLN
1	A	617	GLN
1	A	748	GLN
1	A	780	ASN
1	A	851	ASN
1	A	895	HIS
1	A	898	ASN

5.3.3 RNA ⓘ

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](#)

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	ZZP	A	1500	-	32,35,35	2.34	7 (21%)	39,50,50	1.79	7 (17%)

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
2	ZZP	A	1500	-	-	1/17/31/31	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1500	ZZP	CAM-NAL	-3.85	1.34	1.40
2	A	1500	ZZP	CAM-CAR	-2.05	1.40	1.45
2	A	1500	ZZP	SAI-NAL	2.05	1.67	1.63
2	A	1500	ZZP	CBF-CAK	2.22	1.40	1.36
2	A	1500	ZZP	CAW-CBB	2.46	1.40	1.34
2	A	1500	ZZP	OAJ-SAI	4.96	1.48	1.43
2	A	1500	ZZP	OAH-SAI	9.05	1.53	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	ZZP	OAH-SAI-OAJ	-6.41	111.03	119.54
2	A	1500	ZZP	CAK-CBF-CAZ	-4.02	119.42	124.66
2	A	1500	ZZP	CBD-OBC-CBB	-2.94	113.07	117.39
2	A	1500	ZZP	CBA-CBB-CAW	-2.06	119.40	122.41
2	A	1500	ZZP	OBE-CAK-CAW	2.14	116.55	113.08
2	A	1500	ZZP	CAM-NAN-CAO	2.65	122.08	116.84
2	A	1500	ZZP	OBC-CBB-CBA	4.63	120.01	110.63

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1500	ZZP	CBD-OBC-CBB-CAW

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1500	ZZP	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 ⓘ

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	822/940 (87%)	0.58	77 (9%) 11 11	8, 19, 35, 54	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	341	LEU	6.8
1	A	317	TRP	6.4
1	A	366	CYS	5.8
1	A	334	ASN	5.5
1	A	919	PHE	5.4
1	A	492	LEU	4.9
1	A	488	LEU	4.6
1	A	514	ILE	4.5
1	A	591	TYR	4.4
1	A	395	TYR	4.3
1	A	330	GLY	4.1
1	A	846	ALA	4.0
1	A	340	LYS	3.8
1	A	205	PHE	3.8
1	A	228	PHE	3.8
1	A	522	GLU	3.5
1	A	227	VAL	3.3
1	A	511	LEU	3.2
1	A	367	SER	3.2
1	A	396	ALA	3.2
1	A	416	CYS	3.2
1	A	332	LYS	3.1
1	A	512	ARG	3.1
1	A	339	MET	3.1
1	A	517	ARG	3.1
1	A	493	GLU	3.0
1	A	542	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	206	GLN	3.0
1	A	1024	ARG	3.0
1	A	329	GLU	2.9
1	A	529	ASP	2.9
1	A	370	VAL	2.9
1	A	207	VAL	2.9
1	A	993	LYS	2.9
1	A	841	LYS	2.8
1	A	847	THR	2.8
1	A	538	VAL	2.8
1	A	342	VAL	2.8
1	A	990	SER	2.8
1	A	484	TYR	2.7
1	A	524	TYR	2.7
1	A	913	GLY	2.7
1	A	515	LEU	2.6
1	A	533	LYS	2.6
1	A	365	VAL	2.6
1	A	363	VAL	2.5
1	A	991	CYS	2.5
1	A	209	THR	2.5
1	A	418	ILE	2.5
1	A	361	SER	2.5
1	A	398	VAL	2.5
1	A	523	LEU	2.5
1	A	188	ARG	2.4
1	A	203	PHE	2.4
1	A	364	ASN	2.4
1	A	373	GLN	2.4
1	A	471	LEU	2.4
1	A	397	VAL	2.3
1	A	616	VAL	2.3
1	A	619	LEU	2.3
1	A	918	ASN	2.3
1	A	445	VAL	2.2
1	A	534	MET	2.2
1	A	566	TYR	2.2
1	A	258	HIS	2.2
1	A	112	LEU	2.2
1	A	526	HIS	2.1
1	A	319	LEU	2.1
1	A	840	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	126	HIS	2.1
1	A	930	VAL	2.1
1	A	767	GLU	2.1
1	A	917	GLY	2.1
1	A	489	GLU	2.1
1	A	483	VAL	2.0
1	A	643	ILE	2.0
1	A	131	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZZP	A	1500	32/32	0.97	0.15	-0.59	20,25,33,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.