



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 9, 2017 – 09:42 AM EST

PDB ID : 5SXD
Title : Crystal Structure of PI3Kalpha in complex with fragment 22
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Deposited on : 2016-08-09
Resolution : 3.50 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

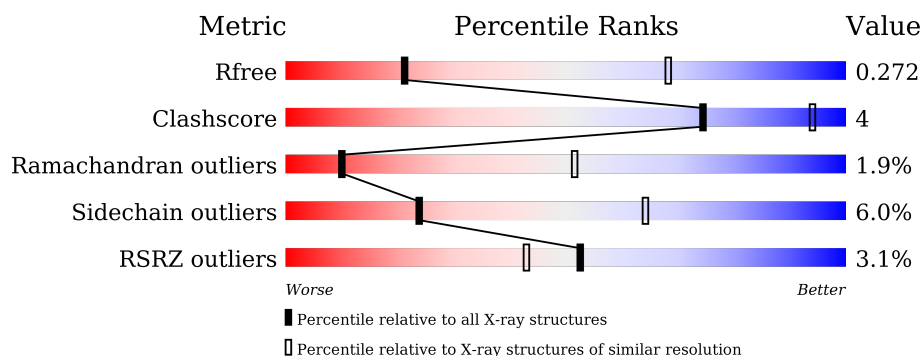
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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 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	1096	<div> <div>2%</div> <div>78%</div> <div>17%</div> <div>...</div> </div>
2	B	279	<div> <div>6%</div> <div>75%</div> <div>12%</div> <div>13%</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
3	71F	B	701	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10694 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 sub-unit alpha isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1051	Total	C	N	O	P	S	0	0	0
			8593	5486	1475	1561	2	69			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP P42336
A	-26	SER	-	expression tag	UNP P42336
A	-25	TYR	-	expression tag	UNP P42336
A	-24	TYR	-	expression tag	UNP P42336
A	-23	HIS	-	expression tag	UNP P42336
A	-22	HIS	-	expression tag	UNP P42336
A	-21	HIS	-	expression tag	UNP P42336
A	-20	HIS	-	expression tag	UNP P42336
A	-19	HIS	-	expression tag	UNP P42336
A	-18	HIS	-	expression tag	UNP P42336
A	-17	ASP	-	expression tag	UNP P42336
A	-16	TYR	-	expression tag	UNP P42336
A	-15	ASP	-	expression tag	UNP P42336
A	-14	ILE	-	expression tag	UNP P42336
A	-13	PRO	-	expression tag	UNP P42336
A	-12	THR	-	expression tag	UNP P42336
A	-11	THR	-	expression tag	UNP P42336
A	-10	GLU	-	expression tag	UNP P42336
A	-9	ASN	-	expression tag	UNP P42336
A	-8	LEU	-	expression tag	UNP P42336
A	-7	TYR	-	expression tag	UNP P42336
A	-6	PHE	-	expression tag	UNP P42336
A	-5	GLN	-	expression tag	UNP P42336
A	-4	GLY	-	expression tag	UNP P42336
A	-3	ALA	-	expression tag	UNP P42336
A	-2	MET	-	expression tag	UNP P42336

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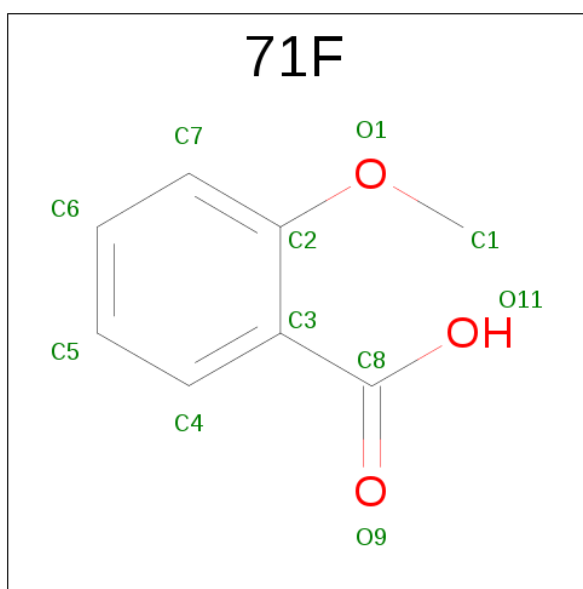
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P42336
A	0	SER	-	expression tag	UNP P42336

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			2090	1315	371	398	6			

- Molecule 3 is 2-methoxybenzoic acid (three-letter code: 71F) (formula: C₈H₈O₃).

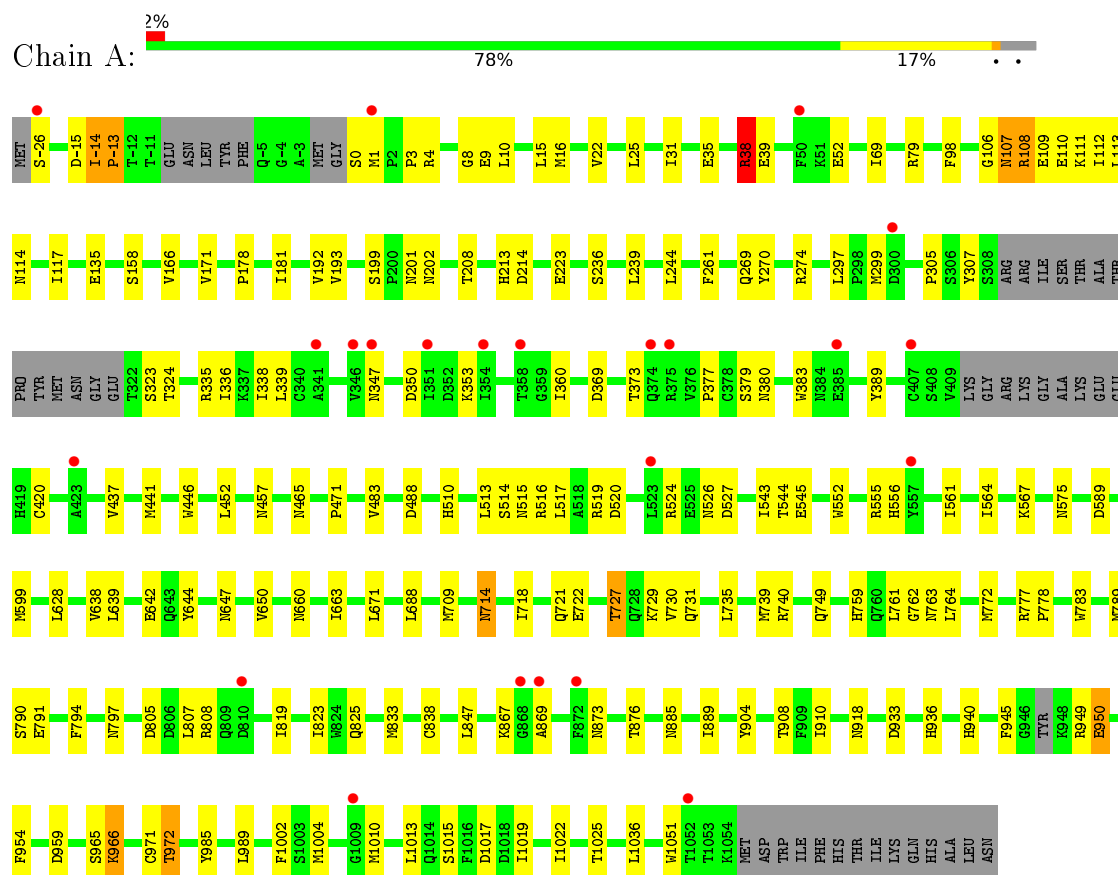


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			11	8	3		

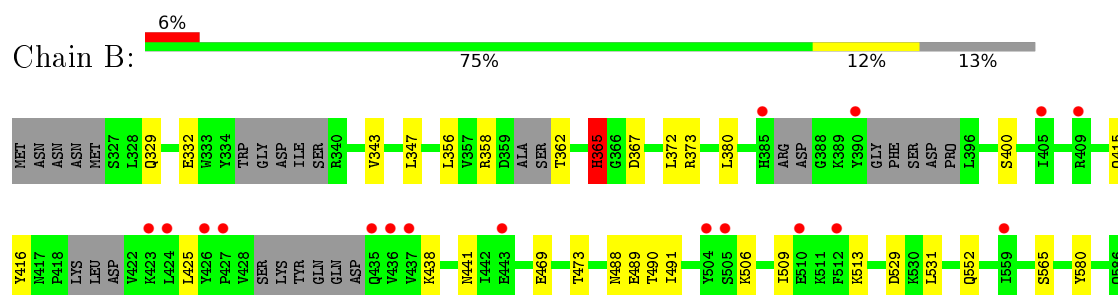
3 Residue-property plots

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 alpha isoform



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha



LYS	GLY	VAL	ARG	GLN	K592	K593	L594	N595	L598	GLY	ASN
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.87Å 116.44Å 149.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.97 – 3.50 49.07 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (91.97-3.50) 99.7 (49.07-3.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.194 , 0.276 0.195 , 0.272	Depositor DCC
R_{free} test set	1331 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	113.3	Xtriage
Anisotropy	0.230	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 95.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10694	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: 71F, 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	0.54	0/8769	0.77	0/11849
2	B	0.50	0/2118	0.71	0/2826
All	All	0.53	0/10887	0.76	0/14675

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	LEU	Peptide

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	8593	0	8572	79	0
2	B	2090	0	2078	13	0
3	B	11	0	0	0	0
All	All	10694	0	10650	86	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 4.

All (86) 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:108:ARG:HH12	1:A:111:LYS:HD2	1.51	0.75
1:A:166:VAL:HG21	1:A:297:LEU:HD22	1.74	0.70
1:A:761:LEU:HD22	1:A:783:TRP:CD2	2.26	0.69
1:A:15:LEU:HD13	1:A:718:ILE:HD11	1.75	0.69
2:B:343:VAL:HG13	2:B:356:LEU:HD11	1.78	0.66
1:A:749:GLN:O	1:A:762:GLY:HA2	1.97	0.65
1:A:761:LEU:HD22	1:A:783:TRP:CE3	2.32	0.64
1:A:261:PHE:HA	1:A:270:TYR:CE2	2.35	0.61
1:A:513:LEU:O	1:A:515:ASN:N	2.35	0.60
1:A:561:ILE:O	1:A:564:ILE:HG22	2.01	0.60
1:A:336:ILE:HD12	1:A:389:TYR:CE2	2.37	0.60
1:A:772:MET:HB2	1:A:778:PRO:HG2	1.82	0.59
1:A:8:GLY:HA2	1:A:714:ASN:HD21	1.67	0.59
1:A:106:GLY:O	1:A:108:ARG:N	2.34	0.59
1:A:8:GLY:CA	1:A:714:ASN:HD21	2.16	0.59
1:A:642:GLU:HG2	1:A:647:ASN:CG	2.23	0.58
1:A:873:ASN:HB3	1:A:876:THR:HG23	1.85	0.58
1:A:452:LEU:HD21	1:A:457:ASN:HD21	1.69	0.58
1:A:543:ILE:HD11	1:A:567:LYS:HD3	1.85	0.58
1:A:111:LYS:O	1:A:114:ASN:ND2	2.38	0.56
1:A:324:THR:HG22	1:A:483:VAL:HG23	1.86	0.56
1:A:31:ILE:HD11	2:B:531:LEU:HD13	1.88	0.56
1:A:98:PHE:CE2	2:B:490:THR:HG23	2.41	0.56
2:B:347:LEU:HD22	2:B:373:ARG:HB2	1.89	0.55
1:A:9:GLU:OE1	1:A:38:ARG:NH1	2.41	0.53
1:A:989:LEU:HD11	1:A:1036:LEU:HD11	1.91	0.53
1:A:178:PRO:HD2	1:A:181:ILE:HD12	1.90	0.53
1:A:671:LEU:HB2	1:A:688:LEU:HD21	1.90	0.53
1:A:0:SER:O	1:A:1:MET:HG2	2.09	0.52
1:A:552:TRP:CZ3	1:A:555:ARG:HD3	2.45	0.52
1:A:10:LEU:HD13	1:A:16:MET:HE1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:709:MET:HE1	1:A:847:LEU:HD21	1.93	0.51
1:A:446:TRP:CZ2	1:A:465:ASN:HA	2.46	0.51
1:A:452:LEU:CD2	1:A:457:ASN:HD21	2.23	0.50
1:A:135:GLU:OE2	1:A:644:TYR:HB3	2.12	0.50
1:A:1022:ILE:HA	1:A:1025:THR:HG22	1.94	0.49
2:B:343:VAL:HG21	2:B:358:ARG:HD3	1.94	0.49
1:A:759:HIS:HB3	1:A:797:ASN:HD21	1.78	0.48
1:A:524:ARG:HD2	1:A:526:ASN:HD22	1.79	0.47
2:B:488:ASN:HA	2:B:491:ILE:HD12	1.96	0.47
2:B:469:GLU:O	2:B:473:THR:OG1	2.26	0.47
1:A:833:MET:HE1	1:A:904:TYR:HA	1.97	0.47
1:A:910:ILE:O	1:A:1025:THR:HG21	2.14	0.47
1:A:789:MET:O	1:A:790:SEP:C	2.63	0.47
1:A:513:LEU:O	1:A:516:ARG:N	2.42	0.47
1:A:807:LEU:HD12	1:A:838:CYS:SG	2.55	0.47
1:A:718:ILE:O	1:A:721:GLN:O	2.32	0.46
1:A:457:ASN:N	1:A:457:ASN:HD22	2.13	0.46
1:A:885:ASN:HB3	1:A:889:ILE:HG22	1.96	0.46
1:A:324:THR:HG22	1:A:483:VAL:CG2	2.45	0.46
1:A:985:TYR:HH	1:A:1051:TRP:HE3	1.63	0.46
1:A:79:ARG:HD2	2:B:489:GLU:OE1	2.16	0.45
2:B:506:LYS:HA	2:B:509:ILE:HG22	1.99	0.45
1:A:519:ARG:NE	1:A:527:ASP:OD2	2.50	0.44
1:A:524:ARG:CD	1:A:526:ASN:HD22	2.31	0.43
1:A:949:ARG:O	1:A:950:GLU:C	2.56	0.43
2:B:362:THR:HB	2:B:365:HIS:HB2	1.99	0.43
1:A:1002:PHE:HB3	1:A:1019:ILE:HG12	2.01	0.43
1:A:213:HIS:CE1	1:A:214:ASP:HB3	2.54	0.43
1:A:111:LYS:HE2	1:A:305:PRO:HA	2.00	0.43
1:A:639:LEU:HD22	1:A:650:VAL:HG22	2.00	0.43
1:A:360:ILE:N	1:A:360:ILE:HD12	2.34	0.42
1:A:31:ILE:CD1	2:B:531:LEU:HD13	2.48	0.42
1:A:544:THR:HG22	2:B:380:LEU:HB3	2.02	0.42
1:A:660:ASN:OD1	1:A:660:ASN:C	2.58	0.42
1:A:192:VAL:HG12	1:A:193:VAL:H	1.84	0.42
1:A:347:ASN:ND2	2:B:565:SER:OG	2.52	0.42
1:A:114:ASN:HA	1:A:117:ILE:HD12	2.01	0.42
1:A:171:VAL:HG12	1:A:269:GLN:HG2	2.02	0.42
1:A:628:LEU:HD23	1:A:663:ILE:HD13	2.00	0.42
1:A:727:THR:O	1:A:730:VAL:N	2.53	0.41
1:A:10:LEU:HD13	1:A:16:MET:CE	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:VAL:HG12	1:A:193:VAL:N	2.34	0.41
1:A:908:THR:HG21	1:A:954:PHE:HB2	2.01	0.41
1:A:1010:MET:HE3	1:A:1013:LEU:HD12	2.03	0.41
1:A:735:LEU:O	1:A:739:MET:HG3	2.20	0.41
1:A:353:LYS:HA	1:A:377:PRO:HB2	2.02	0.41
1:A:819:ILE:HG22	1:A:823:ILE:HD12	2.03	0.41
1:A:731:GLN:OE1	1:A:777:ARG:NH2	2.49	0.41
1:A:-14:ILE:N	1:A:-13:PRO:CD	2.84	0.41
1:A:338:ILE:O	1:A:339:LEU:HD12	2.21	0.41
1:A:965:SER:OG	1:A:971:CYS:HB3	2.22	0.40
1:A:193:VAL:HG22	1:A:208:THR:HG22	2.03	0.40
1:A:936:HIS:HB3	1:A:940:HIS:HB3	2.03	0.40
1:A:599:MET:HB3	1:A:1004:MET:SD	2.62	0.40
1:A:555:ARG:HG3	1:A:556:HIS:CD2	2.56	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	1037/1096 (95%)	906 (87%)	111 (11%)	20 (2%)	10	51
2	B	228/279 (82%)	210 (92%)	14 (6%)	4 (2%)	11	53
All	All	1265/1375 (92%)	1116 (88%)	125 (10%)	24 (2%)	10	51

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	ASN
1	A	514	SER
1	A	945	PHE
1	A	3	PRO

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Mol	Chain	Res	Type
1	A	38	ARG
1	A	201	ASN
1	A	379	SER
1	A	763	ASN
1	A	869	ALA
1	A	966	LYS
2	B	438	LYS
1	A	520	ASP
1	A	918	ASN
1	A	972	THR
2	B	332	GLU
2	B	365	HIS
1	A	108	ARG
1	A	471	PRO
1	A	950	GLU
1	A	-13	PRO
1	A	202	ASN
1	A	307	TYR
2	B	513	LYS
1	A	933	ASP

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	959/997 (96%)	902 (94%)	57 (6%)	24	65
2	B	229/259 (88%)	215 (94%)	14 (6%)	23	64
All	All	1188/1256 (95%)	1117 (94%)	71 (6%)	24	64

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-26	SER
1	A	-15	ASP
1	A	-14	ILE

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Mol	Chain	Res	Type
1	A	4	ARG
1	A	22	VAL
1	A	25	LEU
1	A	35	GLU
1	A	38	ARG
1	A	39	GLU
1	A	52	GLU
1	A	69	ILE
1	A	107	ASN
1	A	109	GLU
1	A	110	GLU
1	A	112	ILE
1	A	158	SER
1	A	199	SER
1	A	223	GLU
1	A	236	SER
1	A	239	LEU
1	A	244	LEU
1	A	274	ARG
1	A	299	MET
1	A	323	SER
1	A	335	ARG
1	A	350	ASP
1	A	369	ASP
1	A	373	THR
1	A	380	ASN
1	A	383	TRP
1	A	420	CYS
1	A	437	VAL
1	A	441	MET
1	A	488	ASP
1	A	510	HIS
1	A	517	LEU
1	A	545	GLU
1	A	575	ASN
1	A	589	ASP
1	A	638	VAL
1	A	714	ASN
1	A	722	GLU
1	A	727	THR
1	A	729	LYS
1	A	740	ARG

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Mol	Chain	Res	Type
1	A	764	LEU
1	A	791	GLU
1	A	794	PHE
1	A	805	ASP
1	A	808	ARG
1	A	825	GLN
1	A	867	LYS
1	A	959	ASP
1	A	966	LYS
1	A	972	THR
1	A	1015	SER
1	A	1017	ASP
2	B	329	GLN
2	B	365	HIS
2	B	367	ASP
2	B	372	LEU
2	B	400	SER
2	B	415	GLN
2	B	416	TYR
2	B	425	LEU
2	B	441	ASN
2	B	529	ASP
2	B	552	GLN
2	B	580	TYR
2	B	594	LEU
2	B	595	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	137	GLN
1	A	331	ASN
1	A	347	ASN
1	A	374	GLN
1	A	457	ASN
1	A	526	ASN
1	A	554	HIS
1	A	556	HIS
1	A	575	ASN
1	A	605	ASN
1	A	714	ASN

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Mol	Chain	Res	Type
1	A	749	GLN
1	A	795	GLN
1	A	797	ASN
2	B	377	ASN
2	B	378	ASN
2	B	552	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SEP	A	7	1	7,9,10	0.91	0	8,12,14	1.93	1 (12%)
1	SEP	A	790	1	7,9,10	0.63	0	8,12,14	1.88	1 (12%)

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
1	SEP	A	7	1	-	0/5/8/10	0/0/0/0
1	SEP	A	790	1	-	0/5/8/10	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	790	SEP	OG-CB-CA	3.63	111.42	108.26
1	A	7	SEP	OG-CB-CA	4.26	111.98	108.26

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
1	A	790	SEP	1	0

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	$\# Z > 2$
3	71F	B	701	-	8,11,11	0.88	0	10,14,14	1.78	3 (30%)

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	71F	B	701	-	-	0/2/6/6	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	701	71F	C4-C3-C2	2.06	120.25	117.43
3	B	701	71F	O1-C2-C3	2.16	119.58	116.29
3	B	701	71F	C1-O1-C2	4.25	123.73	117.53

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, 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	1049/1096 (95%)	-0.03	23 (2%) 65 55	69, 121, 188, 257	0
2	B	244/279 (87%)	0.43	17 (6%) 19 15	113, 188, 232, 272	0
All	All	1293/1375 (94%)	0.06	40 (3%) 52 43	69, 129, 210, 272	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	505	SER	4.1
2	B	409	ARG	4.0
1	A	869	ALA	3.7
2	B	436	VAL	3.5
2	B	424	LEU	3.3
2	B	405	ILE	3.1
2	B	437	VAL	3.1
1	A	374	GLN	3.1
1	A	358	THR	3.1
1	A	-26	SER	3.1
2	B	385	HIS	3.0
2	B	443	GLU	2.9
1	A	347	ASN	2.8
1	A	872	PHE	2.7
1	A	1	MET	2.7
1	A	557	TYR	2.7
1	A	810	ASP	2.6
2	B	504	TYR	2.5
2	B	512	PHE	2.3
1	A	300	ASP	2.3
1	A	423	ALA	2.3
2	B	426	TYR	2.3
2	B	559	ILE	2.3
1	A	523	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1009	GLY	2.2
1	A	341	ALA	2.2
2	B	435	GLN	2.2
1	A	375	ARG	2.1
2	B	510	GLU	2.1
1	A	50	PHE	2.1
2	B	423	LYS	2.1
1	A	354	ILE	2.1
1	A	385	GLU	2.1
2	B	427	PRO	2.0
1	A	1052	THR	2.0
1	A	346	VAL	2.0
1	A	351	ILE	2.0
2	B	390	TYR	2.0
1	A	407	CYS	2.0
1	A	868	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	7	10/11	0.82	0.20	-	164,181,187,203	0
1	SEP	A	790	10/11	0.93	0.17	-	92,113,186,194	0

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
3	71F	B	701	11/11	0.89	0.66	4.20	153,158,171,172	0

6.5 Other polymers [i](#)

There are no such residues in this entry.