



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:11 AM GMT

PDB ID : 3DPD  
Title : Achieving multi-isoform PI3K inhibition in a series of substituted 3,4-Dihydro-2H-benzo[1,4]oxazines  
Authors : Ceska, T.A.  
Deposited on : 2008-07-08  
Resolution : 2.85 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](mailto: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.

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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

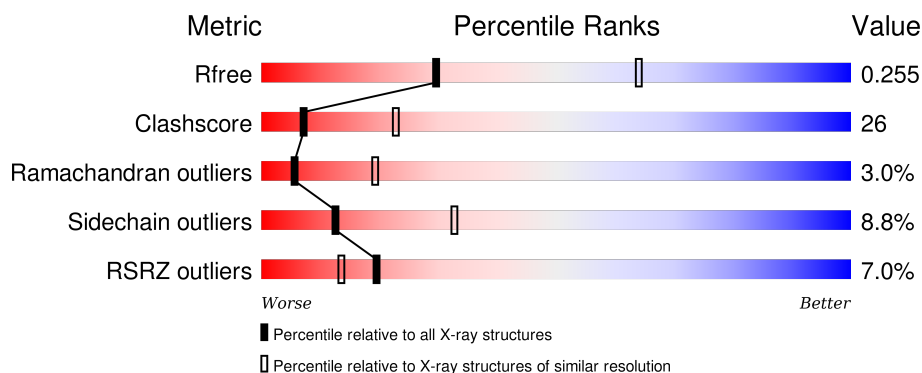
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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  $\geq 3$ , 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	966	<div> <div>6%</div> <div>42%</div> <div>40%</div> <div>6%</div> <div>12%</div> </div>

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6879 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.

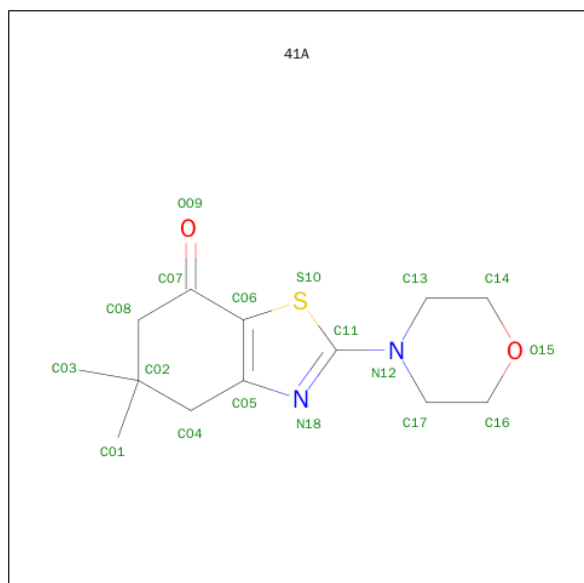
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	846	Total	C	N	O	S	0	0	0
			6861	4412	1168	1245	36			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	INITIATING METHIONINE	UNP P48736
A	1103	HIS	-	EXPRESSION TAG	UNP P48736
A	1104	HIS	-	EXPRESSION TAG	UNP P48736
A	1105	HIS	-	EXPRESSION TAG	UNP P48736
A	1106	HIS	-	EXPRESSION TAG	UNP P48736
A	1107	HIS	-	EXPRESSION TAG	UNP P48736
A	1108	HIS	-	EXPRESSION TAG	UNP P48736

- Molecule 2 is 5,5-DIMETHYL-2-MORPHOLIN-4-YL-5,6-DIHYDRO-1,3-BENZOTHAZOL-7(4H)-ONE (three-letter code: 41A) (formula: C<sub>13</sub>H<sub>18</sub>N<sub>2</sub>O<sub>2</sub>S).

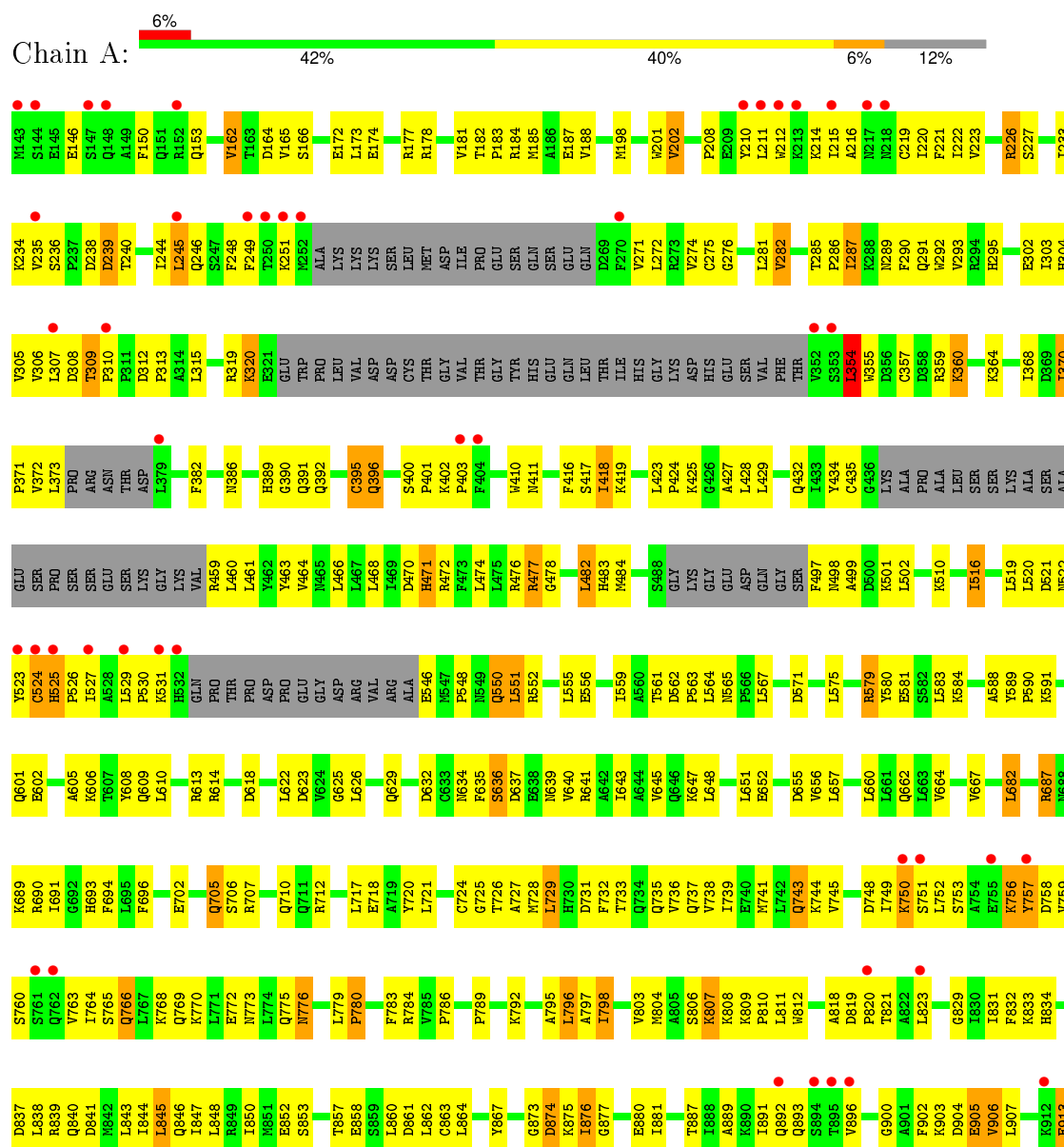


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			18	13	2	2	1		

### 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 ( $\text{RSRZ} > 2$ ). 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 gamma isoform



D1053	K914	R982	K915
V1057	S915	V983	P916
	P917	P984	T917
	E918	F985	E919
E1061	V986	L987	K920
E1062	N1060	T988	F921
D1063	P989	P989	Q922
A1064	D990	F991	
K1065	K1065		V925
K1066	K1066		E926
Y1067	M995	M995	R927
F1068	G996	G996	
L1069	T997	T997	A933
D1070	S998	S998	G934
Q1071	G999	K1000	Y935
	K1001	T1002	C936
V1074	K1001	S1003	V937
C1075	T1002	P1004	A938
R1076	S1003	H1005	T939
D1077	H1005		
K1078	K1008		I944
G1079	G1009		G945
W1080	Q1010		D946
T1081	C1013		R947
V1082	V1014		H948
Q1083	Y1017		N949
F1084	R1021		D950
N1085	T1024		N951
W1086	N1025		T952
F1087	L1026		M953
L1088	L1027		I954
H1089	I1028		T955
L1090	I1029		E956
V1091	L1030		T957
L1092	F1031		G958
G1093	S1032		N959
I1094	L1035		L960
LYS	M1036		F961
GLN	T1037		H962
GLY	G1038		I963
GLY	H1039		D964
LYS	M1039		F965
LYS	P1040		G966
HIS	Q1041		HIS
SER	L1042		ILE
ALA	T1043		ILE
HIS	S1044		LEU
HIS	K1045		GLY
HIS	T1048		ASN
HIS	E1049		TYR
HIS	R1052		LYS
			SER
			PHE
			LEU
			GLY
			ILE
			M979
			K980
			E981

## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.23Å 67.77Å 105.87Å 90.00° 95.96° 90.00°	Depositor
Resolution (Å)	30.00 – 2.85 30.56 – 2.84	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.85) 96.4 (30.56-2.84)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.85Å)	Xtriage
Refinement program	CNX 2002	Depositor
R, $R_{free}$	0.242 , 0.318 0.245 , 0.255	Depositor DCC
$R_{free}$ test set	1172 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	64.7	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 71.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 22970 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6879	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 41A

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	0.40	0/7010	0.58	0/9483

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 [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	6861	0	6909	362	0
2	A	18	0	18	0	0
All	All	6879	0	6927	362	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 26.

All (362) 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:629:GLN:HG2	1:A:1029:ILE:HG13	1.46	0.98
1:A:497:PHE:HB2	1:A:1042:LEU:HD22	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1039:MET:HB3	1:A:1041:GLN:HE22	1.26	0.95
1:A:418:ILE:HG12	1:A:419:LYS:H	1.34	0.93
1:A:1045:LYS:HD2	1:A:1045:LYS:H	1.35	0.90
1:A:221:PHE:HE1	1:A:234:LYS:HG2	1.36	0.90
1:A:689:LYS:HD2	1:A:728:MET:SD	2.17	0.83
1:A:949:ASN:HB2	1:A:1083:GLN:NE2	1.93	0.83
1:A:798:ILE:HD12	1:A:798:ILE:H	1.44	0.81
1:A:629:GLN:HG2	1:A:1029:ILE:CG1	2.13	0.79
1:A:497:PHE:HD1	1:A:1042:LEU:HB3	1.47	0.79
1:A:477:ARG:NE	1:A:522:ASN:HA	1.98	0.78
1:A:302:GLU:HB2	1:A:304:HIS:CE1	2.18	0.77
1:A:477:ARG:HE	1:A:522:ASN:HA	1.48	0.76
1:A:838:LEU:HD12	1:A:877:GLY:HA3	1.68	0.75
1:A:949:ASN:HB2	1:A:1083:GLN:HE22	1.48	0.74
1:A:222:ILE:HG22	1:A:303:ILE:HB	1.69	0.73
1:A:837:ASP:HB3	1:A:840:GLN:HE21	1.51	0.73
1:A:1014:VAL:HG11	1:A:1065:LYS:HG3	1.70	0.73
1:A:482:LEU:H	1:A:482:LEU:HD12	1.55	0.72
1:A:172:GLU:HG3	1:A:471:HIS:ND1	2.04	0.72
1:A:921:PHE:O	1:A:925:VAL:HG23	1.90	0.72
1:A:948:HIS:ND1	1:A:1086:TRP:HB3	2.07	0.70
1:A:202:VAL:HG12	1:A:290:PHE:HA	1.72	0.70
1:A:951:ASN:HA	1:A:963:ILE:HD11	1.73	0.70
1:A:531:LYS:HD2	1:A:608:TYR:HD1	1.57	0.70
1:A:579:ARG:HG2	1:A:610:LEU:HD11	1.73	0.69
1:A:499:ALA:HA	1:A:502:LEU:HD12	1.74	0.69
1:A:173:LEU:O	1:A:177:ARG:HG3	1.92	0.69
1:A:561:THR:HG21	1:A:565:ASN:ND2	2.07	0.68
1:A:1076:ARG:HH11	1:A:1076:ARG:HB3	1.57	0.68
1:A:772:GLU:HG2	1:A:798:ILE:HG12	1.75	0.68
1:A:198:MET:SD	1:A:282:VAL:HG21	2.34	0.68
1:A:818:ALA:O	1:A:820:PRO:HD3	1.94	0.68
1:A:364:LYS:HB3	1:A:519:LEU:HB3	1.76	0.68
1:A:645:VAL:HA	1:A:648:LEU:HD12	1.75	0.68
1:A:274:VAL:HA	1:A:305:VAL:HG12	1.76	0.67
1:A:432:GLN:HB3	1:A:460:LEU:HD11	1.75	0.67
1:A:579:ARG:HB3	1:A:610:LEU:HD21	1.76	0.67
1:A:293:VAL:HG13	1:A:303:ILE:HD13	1.76	0.66
1:A:690:ARG:HE	1:A:694:PHE:HE1	1.42	0.66
1:A:983:VAL:CG2	1:A:984:PRO:HD2	2.25	0.66
1:A:395:CYS:HB3	1:A:416:PHE:HD2	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:629:GLN:HG2	1:A:1029:ILE:CD1	2.26	0.66
1:A:757:TYR:HA	1:A:809:LYS:NZ	2.11	0.65
1:A:927:ARG:HE	1:A:959:ASN:HD22	1.42	0.65
1:A:947:ARG:HH11	1:A:947:ARG:HB3	1.62	0.65
1:A:983:VAL:HG22	1:A:984:PRO:HD2	1.76	0.65
1:A:418:ILE:HG12	1:A:419:LYS:N	2.07	0.65
1:A:201:TRP:NE1	1:A:291:GLN:HG3	2.11	0.65
1:A:354:LEU:HA	1:A:527:ILE:O	1.96	0.64
1:A:625:GLY:O	1:A:629:GLN:HG3	1.97	0.64
1:A:629:GLN:CG	1:A:1029:ILE:HG13	2.25	0.64
1:A:360:LYS:HE2	1:A:419:LYS:HG2	1.80	0.64
1:A:852:GLU:HG3	1:A:864:LEU:HD12	1.79	0.64
1:A:687:ARG:HH11	1:A:687:ARG:HG3	1.61	0.64
1:A:995:MET:O	1:A:1005:HIS:HB2	1.98	0.63
1:A:315:LEU:O	1:A:726:THR:HG22	1.97	0.63
1:A:606:LYS:O	1:A:609:GLN:HB2	1.98	0.62
1:A:1060:ASN:ND2	1:A:1063:ASP:H	1.98	0.62
1:A:660:LEU:O	1:A:664:VAL:HG23	1.99	0.62
1:A:756:LYS:HA	1:A:756:LYS:HZ2	1.64	0.62
1:A:955:THR:C	1:A:957:THR:H	2.01	0.61
1:A:880:GLU:HG2	1:A:881:ILE:N	2.14	0.61
1:A:271:VAL:HB	1:A:310:PRO:HG3	1.83	0.61
1:A:424:PRO:HD2	1:A:427:ALA:HB2	1.82	0.61
1:A:946:ASP:HB2	1:A:983:VAL:O	2.00	0.61
1:A:760:SER:O	1:A:763:VAL:HG12	2.01	0.61
1:A:531:LYS:HE2	1:A:605:ALA:HB2	1.83	0.60
1:A:775:GLN:NE2	1:A:795:ALA:HB1	2.15	0.60
1:A:370:ILE:HD13	1:A:371:PRO:N	2.15	0.60
1:A:784:ARG:HD3	1:A:789:PRO:O	2.02	0.60
1:A:806:SER:HB3	1:A:810:PRO:HD3	1.84	0.60
1:A:201:TRP:CE2	1:A:291:GLN:HG3	2.37	0.59
1:A:355:TRP:HH2	1:A:531:LYS:HG2	1.67	0.59
1:A:561:THR:O	1:A:591:LYS:NZ	2.35	0.59
1:A:1010:GLN:HB3	1:A:1069:LEU:HD21	1.84	0.59
1:A:162:VAL:HG21	1:A:718:GLU:OE2	2.03	0.59
1:A:567:LEU:HD22	1:A:571:ASP:HB3	1.85	0.59
1:A:876:ILE:N	1:A:876:ILE:HD13	2.16	0.59
1:A:287:ILE:O	1:A:287:ILE:HD13	2.03	0.59
1:A:757:TYR:HA	1:A:809:LYS:HZ1	1.68	0.59
1:A:743:GLN:HG2	1:A:876:ILE:HG21	1.85	0.59
1:A:319:ARG:HG2	1:A:320:LYS:H	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.86	0.58
1:A:784:ARG:CZ	1:A:792:LYS:HE3	2.33	0.58
1:A:905:GLU:CD	1:A:905:GLU:H	2.06	0.58
1:A:389:HIS:O	1:A:392:GLN:HB3	2.04	0.58
1:A:359:ARG:HD2	1:A:360:LYS:H	1.69	0.58
1:A:181:VAL:HG12	1:A:185:MET:CE	2.34	0.57
1:A:402:LYS:HB3	1:A:403:PRO:HD2	1.86	0.57
1:A:208:PRO:HD2	1:A:211:LEU:HD12	1.85	0.57
1:A:432:GLN:HB3	1:A:460:LEU:CD1	2.34	0.57
1:A:750:LYS:HD3	1:A:751:SER:N	2.20	0.57
1:A:763:VAL:HA	1:A:766:GLN:HG3	1.85	0.57
1:A:602:GLU:H	1:A:602:GLU:CD	2.06	0.57
1:A:466:LEU:HD11	1:A:476:ARG:HD3	1.87	0.57
1:A:622:LEU:HD12	1:A:623:ASP:N	2.20	0.56
1:A:738:VAL:HG21	1:A:783:PHE:HB3	1.87	0.56
1:A:174:GLU:O	1:A:178:ARG:HG3	2.05	0.56
1:A:914:LYS:O	1:A:916:PRO:HD3	2.06	0.56
1:A:497:PHE:CD1	1:A:1042:LEU:HB3	2.34	0.56
1:A:784:ARG:O	1:A:786:PRO:HD3	2.06	0.56
1:A:775:GLN:HE22	1:A:795:ALA:HB1	1.69	0.56
1:A:1013:CYS:HB3	1:A:1068:PHE:CE2	2.41	0.56
1:A:181:VAL:HG12	1:A:185:MET:HE1	1.88	0.56
1:A:564:LEU:HD13	1:A:1049:GLU:HA	1.87	0.56
1:A:687:ARG:HG3	1:A:687:ARG:NH1	2.21	0.55
1:A:1003:SER:HB2	1:A:1004:PRO:HD2	1.87	0.55
1:A:563:PRO:HD3	1:A:1025:ASN:ND2	2.20	0.55
1:A:724:CYS:SG	1:A:729:LEU:HD13	2.47	0.55
1:A:1084:PHE:CE2	1:A:1088:LEU:HD11	2.41	0.55
1:A:1063:ASP:HA	1:A:1066:LYS:HE2	1.88	0.55
1:A:210:TYR:CE1	1:A:211:LEU:HG	2.42	0.54
1:A:1014:VAL:HG11	1:A:1065:LYS:CG	2.38	0.54
1:A:731:ASP:O	1:A:735:GLN:HG3	2.08	0.54
1:A:960:LEU:HG	1:A:961:PHE:N	2.22	0.54
1:A:1045:LYS:H	1:A:1045:LYS:CD	2.12	0.54
1:A:847:ILE:O	1:A:850:ILE:HB	2.08	0.54
1:A:464:VAL:HB	1:A:484:MET:HG2	1.90	0.54
1:A:735:GLN:O	1:A:739:ILE:HG12	2.08	0.54
1:A:834:HIS:HA	1:A:875:LYS:O	2.07	0.54
1:A:223:VAL:O	1:A:304:HIS:HA	2.07	0.54
1:A:913:GLU:HG3	1:A:914:LYS:N	2.22	0.54
1:A:386:ASN:OD1	1:A:396:GLN:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:861:ASP:C	1:A:862:LEU:HD22	2.28	0.54
1:A:364:LYS:NZ	1:A:411:ASN:O	2.41	0.53
1:A:953:MET:O	1:A:960:LEU:HD12	2.08	0.53
1:A:693:HIS:CD2	1:A:789:PRO:HB3	2.43	0.53
1:A:999:GLY:O	1:A:1000:LYS:HD3	2.08	0.53
1:A:635:PHE:O	1:A:641:ARG:HD2	2.09	0.53
1:A:846:GLN:O	1:A:850:ILE:HG12	2.09	0.53
1:A:306:VAL:HG13	1:A:308:ASP:OD1	2.08	0.52
1:A:955:THR:C	1:A:957:THR:N	2.63	0.52
1:A:732:PHE:O	1:A:736:VAL:HG23	2.09	0.52
1:A:903:LYS:HB2	1:A:906:VAL:HG23	1.90	0.52
1:A:1035:LEU:HB3	1:A:1043:THR:HG21	1.92	0.52
1:A:806:SER:C	1:A:808:LYS:H	2.13	0.52
1:A:182:THR:HB	1:A:183:PRO:HD3	1.92	0.52
1:A:360:LYS:CE	1:A:419:LYS:HG2	2.40	0.52
1:A:368:ILE:HG13	1:A:368:ILE:O	2.10	0.51
1:A:184:ARG:O	1:A:188:VAL:HG23	2.09	0.51
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.92	0.51
1:A:370:ILE:C	1:A:370:ILE:HD13	2.29	0.51
1:A:1045:LYS:O	1:A:1049:GLU:HG3	2.10	0.51
1:A:833:LYS:HG2	1:A:834:HIS:N	2.26	0.51
1:A:201:TRP:CZ3	1:A:690:ARG:NH1	2.79	0.51
1:A:470:ASP:HB3	1:A:476:ARG:NH2	2.25	0.51
1:A:892:GLN:HE22	1:A:902:PHE:HA	1.75	0.51
1:A:996:GLY:O	1:A:1001:LYS:HE3	2.10	0.51
1:A:690:ARG:NE	1:A:694:PHE:HE1	2.06	0.51
1:A:319:ARG:HG2	1:A:320:LYS:HG3	1.93	0.51
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.93	0.51
1:A:702:GLU:O	1:A:706:SER:HB3	2.10	0.51
1:A:429:LEU:HB2	1:A:468:LEU:CD2	2.40	0.51
1:A:470:ASP:OD1	1:A:472:ARG:N	2.40	0.51
1:A:464:VAL:HG11	1:A:516:ILE:HG21	1.93	0.51
1:A:583:LEU:HD22	1:A:610:LEU:HD22	1.92	0.50
1:A:955:THR:O	1:A:957:THR:N	2.44	0.50
1:A:434:TYR:HA	1:A:459:ARG:O	2.10	0.50
1:A:939:THR:OG1	1:A:945:GLY:HA2	2.10	0.50
1:A:744:LYS:HE2	1:A:748:ASP:OD1	2.12	0.50
1:A:770:LYS:O	1:A:773:ASN:HB2	2.12	0.50
1:A:640:VAL:O	1:A:643:ILE:HG12	2.12	0.50
1:A:215:ILE:HG23	1:A:220:ILE:HG22	1.93	0.50
1:A:622:LEU:HD12	1:A:623:ASP:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:997:THR:O	1:A:997:THR:HG22	2.11	0.50
1:A:772:GLU:CG	1:A:798:ILE:HG12	2.42	0.50
1:A:756:LYS:C	1:A:758:ASP:H	2.15	0.50
1:A:435:CYS:HB3	1:A:461:LEU:HD11	1.93	0.50
1:A:935:TYR:O	1:A:939:THR:HG22	2.12	0.49
1:A:223:VAL:HB	1:A:304:HIS:CD2	2.47	0.49
1:A:614:ARG:HG3	1:A:618:ASP:OD2	2.13	0.49
1:A:1038:GLY:O	1:A:1040:PRO:HD3	2.12	0.49
1:A:900:GLY:HA2	1:A:902:PHE:CE2	2.47	0.49
1:A:652:GLU:HG2	1:A:655:ASP:OD2	2.13	0.49
1:A:233:ILE:N	1:A:233:ILE:HD12	2.27	0.49
1:A:951:ASN:HA	1:A:963:ILE:CD1	2.40	0.49
1:A:271:VAL:HG22	1:A:272:LEU:N	2.28	0.49
1:A:435:CYS:SG	1:A:459:ARG:HG2	2.52	0.49
1:A:917:THR:HG23	1:A:920:LYS:HB2	1.93	0.49
1:A:226:ARG:HD3	1:A:307:LEU:HB3	1.95	0.49
1:A:887:THR:HG22	1:A:889:ALA:H	1.77	0.49
1:A:276:GLY:HA2	1:A:819:ASP:HB3	1.94	0.49
1:A:364:LYS:HD3	1:A:519:LEU:HD23	1.94	0.49
1:A:1074:VAL:O	1:A:1078:LYS:HG3	2.13	0.48
1:A:240:THR:O	1:A:244:ILE:HG13	2.12	0.48
1:A:873:GLY:HA3	1:A:876:ILE:HG12	1.94	0.48
1:A:807:LYS:HD2	1:A:807:LYS:N	2.28	0.48
1:A:757:TYR:HB3	1:A:807:LYS:HG3	1.95	0.48
1:A:803:VAL:HG22	1:A:811:LEU:CD2	2.43	0.48
1:A:705:GLN:OE1	1:A:839:ARG:NE	2.46	0.48
1:A:738:VAL:HG22	1:A:780:PRO:HD2	1.96	0.47
1:A:219:CYS:HA	1:A:236:SER:HA	1.95	0.47
1:A:625:GLY:HA2	1:A:1026:LEU:HD23	1.96	0.47
1:A:838:LEU:HD12	1:A:877:GLY:CA	2.42	0.47
1:A:927:ARG:HE	1:A:959:ASN:ND2	2.11	0.47
1:A:222:ILE:O	1:A:222:ILE:HG13	2.15	0.47
1:A:867:TYR:CE2	1:A:963:ILE:HG22	2.49	0.47
1:A:483:HIS:CD2	1:A:510:LYS:HG2	2.50	0.47
1:A:477:ARG:HD3	1:A:521:ASP:O	2.15	0.47
1:A:622:LEU:HD13	1:A:647:LYS:HB3	1.97	0.47
1:A:810:PRO:O	1:A:811:LEU:HD23	2.14	0.47
1:A:474:LEU:HD22	1:A:527:ILE:HG12	1.96	0.47
1:A:652:GLU:O	1:A:656:VAL:HG23	2.15	0.47
1:A:1005:HIS:O	1:A:1008:LYS:HB3	2.15	0.46
1:A:477:ARG:HD2	1:A:478:GLY:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:TRP:O	1:A:295:HIS:HB3	2.14	0.46
1:A:552:ARG:O	1:A:556:GLU:HG3	2.15	0.46
1:A:308:ASP:N	1:A:308:ASP:OD1	2.48	0.46
1:A:662:GLN:NE2	1:A:1030:LEU:HD22	2.31	0.46
1:A:997:THR:HG21	1:A:1076:ARG:NH2	2.30	0.46
1:A:987:LEU:HD11	1:A:995:MET:CE	2.46	0.46
1:A:181:VAL:O	1:A:185:MET:HE2	2.15	0.46
1:A:418:ILE:HD13	1:A:423:LEU:HD23	1.98	0.46
1:A:1040:PRO:O	1:A:1041:GLN:C	2.54	0.46
1:A:984:PRO:HB2	1:A:985:PHE:CD2	2.50	0.46
1:A:807:LYS:HD2	1:A:807:LYS:H	1.80	0.46
1:A:428:LEU:C	1:A:428:LEU:HD23	2.36	0.46
1:A:988:THR:O	1:A:991:PHE:HB2	2.15	0.46
1:A:1052:ARG:HH11	1:A:1052:ARG:HG2	1.80	0.46
1:A:226:ARG:HG3	1:A:227:SER:H	1.80	0.46
1:A:1041:GLN:O	1:A:1043:THR:N	2.49	0.46
1:A:172:GLU:HG3	1:A:471:HIS:CG	2.50	0.46
1:A:581:GLU:OE2	1:A:584:LYS:HD2	2.16	0.45
1:A:707:ARG:HD2	1:A:710:GLN:OE1	2.16	0.45
1:A:1041:GLN:N	1:A:1041:GLN:HE21	2.14	0.45
1:A:725:GLY:O	1:A:729:LEU:HB2	2.15	0.45
1:A:622:LEU:HD21	1:A:651:LEU:HG	1.98	0.45
1:A:235:VAL:HG11	1:A:244:ILE:CD1	2.47	0.45
1:A:523:TYR:HB3	1:A:524:CYS:H	1.48	0.45
1:A:983:VAL:HB	1:A:1082:VAL:HG21	1.99	0.45
1:A:775:GLN:OE1	1:A:779:LEU:HD23	2.16	0.45
1:A:484:MET:HE3	1:A:516:ILE:HG21	1.98	0.45
1:A:212:TRP:CE3	1:A:212:TRP:HA	2.51	0.45
1:A:548:PRO:HB2	1:A:551:LEU:HB2	1.99	0.45
1:A:1031:PHE:HE2	1:A:1048:ILE:HA	1.80	0.45
1:A:696:PHE:CE1	1:A:721:LEU:HD21	2.51	0.45
1:A:319:ARG:HG2	1:A:320:LYS:N	2.29	0.45
1:A:751:SER:C	1:A:753:SER:H	2.20	0.45
1:A:729:LEU:HD12	1:A:729:LEU:HA	1.67	0.45
1:A:1052:ARG:HD3	1:A:1057:VAL:HG21	1.99	0.45
1:A:1017:TYR:O	1:A:1021:ARG:HG3	2.17	0.45
1:A:559:ILE:HD13	1:A:588:ALA:HB2	1.97	0.45
1:A:779:LEU:HD12	1:A:780:PRO:HD2	1.98	0.45
1:A:498:ASN:OD1	1:A:498:ASN:C	2.56	0.45
1:A:1060:ASN:HD22	1:A:1062:GLU:HB2	1.81	0.45
1:A:862:LEU:HB3	1:A:934:GLY:HA3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:989:PRO:HD2	1:A:1080:TRP:CE2	2.51	0.45
1:A:907:LEU:HD12	1:A:990:ASP:OD2	2.17	0.45
1:A:555:LEU:O	1:A:559:ILE:HG13	2.17	0.44
1:A:174:GLU:HA	1:A:177:ARG:HD3	1.99	0.44
1:A:803:VAL:HG13	1:A:810:PRO:O	2.17	0.44
1:A:1076:ARG:HB3	1:A:1076:ARG:NH1	2.28	0.44
1:A:212:TRP:HE3	1:A:212:TRP:HA	1.83	0.44
1:A:293:VAL:HG13	1:A:303:ILE:CD1	2.44	0.44
1:A:198:MET:HE3	1:A:282:VAL:HG21	1.99	0.44
1:A:947:ARG:CB	1:A:947:ARG:HH11	2.29	0.44
1:A:589:TYR:HB2	1:A:590:PRO:HD3	2.00	0.44
1:A:667:VAL:O	1:A:712:ARG:NH1	2.51	0.44
1:A:838:LEU:CD1	1:A:877:GLY:HA3	2.43	0.44
1:A:281:LEU:HA	1:A:290:PHE:CE2	2.53	0.44
1:A:745:VAL:O	1:A:749:ILE:HG12	2.18	0.44
1:A:244:ILE:HG22	1:A:245:LEU:H	1.83	0.44
1:A:281:LEU:HD22	1:A:290:PHE:CD2	2.53	0.43
1:A:862:LEU:HD12	1:A:934:GLY:N	2.33	0.43
1:A:933:ALA:O	1:A:937:VAL:HG23	2.19	0.43
1:A:733:THR:HG22	1:A:737:GLN:HE21	1.83	0.43
1:A:1024:THR:O	1:A:1028:ILE:HG13	2.18	0.43
1:A:360:LYS:HE2	1:A:419:LYS:HE2	1.99	0.43
1:A:946:ASP:OD1	1:A:983:VAL:HG12	2.18	0.43
1:A:657:LEU:HG	1:A:691:ILE:HG12	2.00	0.43
1:A:765:SER:O	1:A:769:GLN:HB2	2.19	0.43
1:A:988:THR:HG21	1:A:1083:GLN:HG3	2.00	0.43
1:A:561:THR:HG22	1:A:562:ASP:N	2.33	0.43
1:A:863:CYS:HB3	1:A:959:ASN:HD21	1.82	0.43
1:A:784:ARG:NH2	1:A:792:LYS:HE3	2.32	0.43
1:A:887:THR:O	1:A:891:ILE:HG13	2.18	0.43
1:A:271:VAL:HG23	1:A:282:VAL:HG13	2.01	0.43
1:A:892:GLN:NE2	1:A:902:PHE:HA	2.33	0.43
1:A:1070:ASP:O	1:A:1074:VAL:HG23	2.19	0.43
1:A:221:PHE:CE1	1:A:234:LYS:HG2	2.29	0.43
1:A:1013:CYS:HB3	1:A:1068:PHE:HE2	1.82	0.43
1:A:917:THR:OG1	1:A:919:GLU:HB3	2.19	0.43
1:A:853:SER:O	1:A:857:THR:HG23	2.19	0.43
1:A:463:TYR:CE1	1:A:501:LYS:HA	2.53	0.43
1:A:497:PHE:CB	1:A:1042:LEU:HD22	2.33	0.43
1:A:187:GLU:CD	1:A:687:ARG:HG2	2.39	0.43
1:A:150:PHE:O	1:A:153:GLN:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:LYS:HE2	1:A:605:ALA:CB	2.49	0.43
1:A:390:GLY:N	1:A:636:SER:HB3	2.34	0.43
1:A:287:ILE:C	1:A:287:ILE:HD13	2.40	0.42
1:A:525:HIS:N	1:A:526:PRO:HD3	2.35	0.42
1:A:198:MET:CE	1:A:282:VAL:HG21	2.48	0.42
1:A:382:PHE:CE1	1:A:434:TYR:HB2	2.55	0.42
1:A:1014:VAL:HG13	1:A:1065:LYS:HA	2.01	0.42
1:A:863:CYS:SG	1:A:927:ARG:HD3	2.59	0.42
1:A:309:THR:HG22	1:A:310:PRO:HD2	2.02	0.42
1:A:501:LYS:HB3	1:A:501:LYS:HE2	1.83	0.42
1:A:997:THR:HG23	1:A:1001:LYS:HG3	2.00	0.42
1:A:983:VAL:HG22	1:A:984:PRO:CD	2.45	0.42
1:A:370:ILE:O	1:A:370:ILE:HG23	2.19	0.42
1:A:918:GLU:O	1:A:922:GLN:HG2	2.19	0.42
1:A:831:ILE:CG2	1:A:832:PHE:N	2.83	0.42
1:A:162:VAL:O	1:A:177:ARG:NH1	2.53	0.42
1:A:947:ARG:CB	1:A:947:ARG:NH1	2.83	0.42
1:A:806:SER:C	1:A:808:LYS:N	2.73	0.42
1:A:804:MET:CE	1:A:812:TRP:HB2	2.49	0.42
1:A:275:CYS:SG	1:A:821:THR:HG22	2.60	0.42
1:A:390:GLY:C	1:A:392:GLN:H	2.23	0.42
1:A:382:PHE:CZ	1:A:434:TYR:HB2	2.55	0.42
1:A:829:GLY:HA3	1:A:881:ILE:HB	2.03	0.41
1:A:766:GLN:HE21	1:A:766:GLN:HB3	1.56	0.41
1:A:682:LEU:HD21	1:A:720:TYR:HA	2.02	0.41
1:A:531:LYS:HD2	1:A:608:TYR:CD1	2.46	0.41
1:A:720:TYR:CZ	1:A:724:CYS:HB3	2.55	0.41
1:A:889:ALA:O	1:A:893:GLN:HG3	2.20	0.41
1:A:844:ILE:O	1:A:848:LEU:HD13	2.21	0.41
1:A:400:SER:HA	1:A:401:PRO:HD3	1.88	0.41
1:A:164:ASP:C	1:A:166:SER:H	2.24	0.41
1:A:529:LEU:HA	1:A:530:PRO:HD3	1.95	0.41
1:A:904:ASP:OD2	1:A:904:ASP:N	2.52	0.41
1:A:775:GLN:HE22	1:A:796:LEU:H	1.68	0.41
1:A:1068:PHE:O	1:A:1071:GLN:HB2	2.20	0.41
1:A:845:LEU:HD12	1:A:845:LEU:HA	1.84	0.41
1:A:239:ASP:O	1:A:286:PRO:HA	2.20	0.41
1:A:583:LEU:HD22	1:A:610:LEU:CD2	2.51	0.41
1:A:749:ILE:HG21	1:A:803:VAL:HG21	2.03	0.41
1:A:201:TRP:CD1	1:A:291:GLN:HG3	2.55	0.41
1:A:862:LEU:HA	1:A:862:LEU:HD13	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:PHE:CD1	1:A:721:LEU:HD21	2.56	0.41
1:A:764:ILE:O	1:A:768:LYS:HG3	2.21	0.41
1:A:1035:LEU:C	1:A:1043:THR:HG21	2.41	0.41
1:A:823:LEU:HD22	1:A:823:LEU:H	1.86	0.41
1:A:632:ASP:OD1	1:A:634:ASN:HB2	2.20	0.41
1:A:418:ILE:CG1	1:A:419:LYS:H	2.16	0.41
1:A:963:ILE:O	1:A:964:ASP:C	2.59	0.41
1:A:370:ILE:HD13	1:A:372:VAL:N	2.36	0.41
1:A:643:ILE:O	1:A:647:LYS:HG2	2.21	0.41
1:A:551:LEU:HA	1:A:551:LEU:HD12	1.72	0.41
1:A:286:PRO:O	1:A:289:ASN:HB2	2.20	0.41
1:A:550:GLN:O	1:A:550:GLN:NE2	2.53	0.41
1:A:373:LEU:HA	1:A:373:LEU:HD12	1.94	0.41
1:A:520:LEU:O	1:A:521:ASP:C	2.59	0.41
1:A:945:GLY:C	1:A:985:PHE:HA	2.41	0.41
1:A:1032:SER:O	1:A:1036:MET:HG2	2.20	0.41
1:A:477:ARG:HG3	1:A:478:GLY:N	2.36	0.40
1:A:354:LEU:N	1:A:354:LEU:HD23	2.36	0.40
1:A:806:SER:HB3	1:A:810:PRO:CD	2.51	0.40
1:A:1053:ASP:N	1:A:1053:ASP:OD1	2.53	0.40
1:A:1027:LEU:HA	1:A:1027:LEU:HD12	1.78	0.40
1:A:637:ASP:OD1	1:A:639:ASN:HB2	2.21	0.40
1:A:996:GLY:O	1:A:1003:SER:HB3	2.21	0.40
1:A:796:LEU:HB3	1:A:797:ALA:H	1.65	0.40
1:A:312:ASP:HA	1:A:313:PRO:HD2	1.84	0.40
1:A:726:THR:CG2	1:A:727:ALA:N	2.85	0.40
1:A:651:LEU:HD22	1:A:655:ASP:CB	2.51	0.40
1:A:1078:LYS:O	1:A:1079:GLY:C	2.60	0.40
1:A:741:MET:O	1:A:744:LYS:HB3	2.21	0.40
1:A:773:ASN:HA	1:A:776:ASN:ND2	2.37	0.40
1:A:944:ILE:HD12	1:A:965:PHE:HD2	1.87	0.40
1:A:245:LEU:CA	1:A:248:PHE:HB3	2.52	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	830/966 (86%)	690 (83%)	115 (14%)	25 (3%)	5	19

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	916	PRO
1	A	165	VAL
1	A	214	LYS
1	A	251	LYS
1	A	776	ASN
1	A	956	GLU
1	A	1042	LEU
1	A	226	ARG
1	A	239	ASP
1	A	752	LEU
1	A	796	LEU
1	A	216	ALA
1	A	354	LEU
1	A	757	TYR
1	A	874	ASP
1	A	162	VAL
1	A	425	LYS
1	A	896	VAL
1	A	964	ASP
1	A	418	ILE
1	A	798	ILE
1	A	906	VAL
1	A	1079	GLY
1	A	759	VAL
1	A	780	PRO

### 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	761/864 (88%)	694 (91%)	67 (9%)	12	33

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	GLU
1	A	202	VAL
1	A	238	ASP
1	A	245	LEU
1	A	246	GLN
1	A	249	PHE
1	A	282	VAL
1	A	285	THR
1	A	287	ILE
1	A	309	THR
1	A	320	LYS
1	A	354	LEU
1	A	357	CYS
1	A	360	LYS
1	A	370	ILE
1	A	391	GLN
1	A	395	CYS
1	A	396	GLN
1	A	410	TRP
1	A	417	SER
1	A	471	HIS
1	A	477	ARG
1	A	482	LEU
1	A	516	ILE
1	A	524	CYS
1	A	525	HIS
1	A	546	GLU
1	A	550	GLN
1	A	551	LEU
1	A	575	LEU
1	A	579	ARG
1	A	580	TYR
1	A	601	GLN
1	A	613	ARG
1	A	626	LEU
1	A	636	SER
1	A	682	LEU
1	A	687	ARG

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Mol	Chain	Res	Type
1	A	705	GLN
1	A	717	LEU
1	A	729	LEU
1	A	743	GLN
1	A	750	LYS
1	A	756	LYS
1	A	766	GLN
1	A	807	LYS
1	A	841	ASP
1	A	843	LEU
1	A	845	LEU
1	A	858	GLU
1	A	860	LEU
1	A	874	ASP
1	A	876	ILE
1	A	905	GLU
1	A	913	GLU
1	A	917	THR
1	A	919	GLU
1	A	927	ARG
1	A	947	ARG
1	A	957	THR
1	A	960	LEU
1	A	1026	LEU
1	A	1027	LEU
1	A	1037	THR
1	A	1039	MET
1	A	1041	GLN
1	A	1076	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	A	225	HIS
1	A	388	GLN
1	A	391	GLN
1	A	396	GLN
1	A	483	HIS
1	A	550	GLN
1	A	565	ASN
1	A	577	HIS

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Mol	Chain	Res	Type
1	A	619	GLN
1	A	634	ASN
1	A	639	ASN
1	A	662	GLN
1	A	711	GLN
1	A	734	GLN
1	A	737	GLN
1	A	766	GLN
1	A	776	ASN
1	A	825	ASN
1	A	840	GLN
1	A	892	GLN
1	A	893	GLN
1	A	908	ASN
1	A	951	ASN
1	A	959	ASN
1	A	1007	GLN
1	A	1023	HIS
1	A	1041	GLN
1	A	1083	GLN
1	A	1085	ASN
1	A	1089	HIS

### 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](#)

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	41A	A	2040	-	15,20,20	1.42	3 (20%)	19,30,30	1.42	3 (15%)

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	41A	A	2040	-	-	0/2/26/26	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2040	41A	C17-N12	2.17	1.50	1.46
2	A	2040	41A	C04-C02	2.83	1.57	1.53
2	A	2040	41A	C11-N12	3.12	1.37	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2040	41A	C17-N12-C11	-2.42	112.29	120.30
2	A	2040	41A	C08-C02-C04	3.27	110.57	107.83
2	A	2040	41A	C02-C08-C07	3.71	118.32	113.80

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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	846/966 (87%)	0.31	59 (6%) 19 13	14, 58, 106, 126	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	979	ASN	6.0
1	A	212	TRP	5.7
1	A	895	THR	5.1
1	A	249	PHE	4.6
1	A	529	LEU	4.6
1	A	211	LEU	4.5
1	A	143	MET	4.1
1	A	353	SER	4.0
1	A	250	THR	4.0
1	A	379	LEU	3.9
1	A	755	GLU	3.7
1	A	761	SER	3.4
1	A	1090	LEU	3.4
1	A	762	GLN	3.4
1	A	270	PHE	3.4
1	A	1091	VAL	3.4
1	A	892	GLN	3.3
1	A	217	ASN	3.3
1	A	210	TYR	3.2
1	A	995	MET	3.2
1	A	144	SER	3.1
1	A	896	VAL	3.0
1	A	1042	LEU	3.0
1	A	524	CYS	3.0
1	A	525	HIS	2.9
1	A	527	ILE	2.9
1	A	1092	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	986	VAL	2.8
1	A	251	LYS	2.7
1	A	523	TYR	2.6
1	A	531	LYS	2.5
1	A	310	PRO	2.5
1	A	352	VAL	2.5
1	A	152	ARG	2.4
1	A	148	GLN	2.4
1	A	235	VAL	2.4
1	A	307	LEU	2.4
1	A	403	PRO	2.4
1	A	981	GLU	2.3
1	A	1040	PRO	2.3
1	A	532	HIS	2.3
1	A	215	ILE	2.3
1	A	1060	ASN	2.3
1	A	980	LYS	2.3
1	A	252	MET	2.2
1	A	750	LYS	2.2
1	A	894	SER	2.1
1	A	218	ASN	2.1
1	A	245	LEU	2.1
1	A	404	PHE	2.1
1	A	912	LYS	2.1
1	A	820	PRO	2.1
1	A	757	TYR	2.1
1	A	823	LEU	2.1
1	A	147	SER	2.1
1	A	1077	ASP	2.0
1	A	213	LYS	2.0
1	A	1082	VAL	2.0
1	A	751	SER	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	41A	A	2040	18/18	0.95	0.18	-0.03	49,60,66,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.