



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 26, 2017 – 03:42 PM EDT

PDB ID : 3ZU7  
Title : Crystal structure of a designed selected Ankyrin Repeat protein in complex with the MAP kinase ERK2  
Authors : Kummer, L.; Mittl, P.R.; Pluckthun, A.  
Deposited on : 2011-07-16  
Resolution : 1.97 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029077
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029077

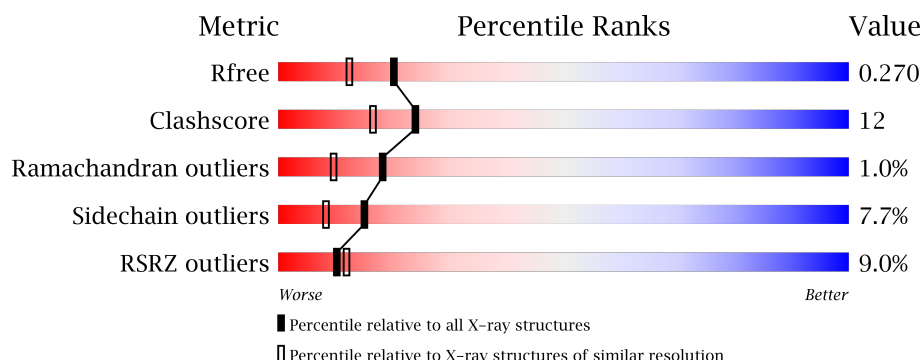
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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))
$R_{free}$	100719	9293 (2.00-1.96)
Clashscore	112137	10621 (2.00-1.96)
Ramachandran outliers	110173	10502 (2.00-1.96)
Sidechain outliers	110143	10501 (2.00-1.96)
RSRZ outliers	101464	9395 (2.00-1.96)

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	365	<div> <div>8%</div> <div> <div></div> <div>67%</div> <div>21%</div> <div>6%</div> <div>6%</div> </div> </div>
2	B	169	<div> <div>8%</div> <div> <div></div> <div>78%</div> <div>11%</div> <div>••</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4220 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 MITOGEN-ACTIVATED PROTEIN KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2817	1809	481	512	15			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ALA	-	expression tag	UNP P63086
A	-5	HIS	-	expression tag	UNP P63086
A	-4	HIS	-	expression tag	UNP P63086
A	-3	HIS	-	expression tag	UNP P63086
A	-2	HIS	-	expression tag	UNP P63086
A	-1	HIS	-	expression tag	UNP P63086
A	0	HIS	-	expression tag	UNP P63086
A	1	ALA	-	expression tag	UNP P63086
A	2	MET	-	expression tag	UNP P63086

- Molecule 2 is a protein called DESIGNED ANKYRIN REPEAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	154	Total	C	N	O	S	0	0	0
			1167	728	206	232	1			

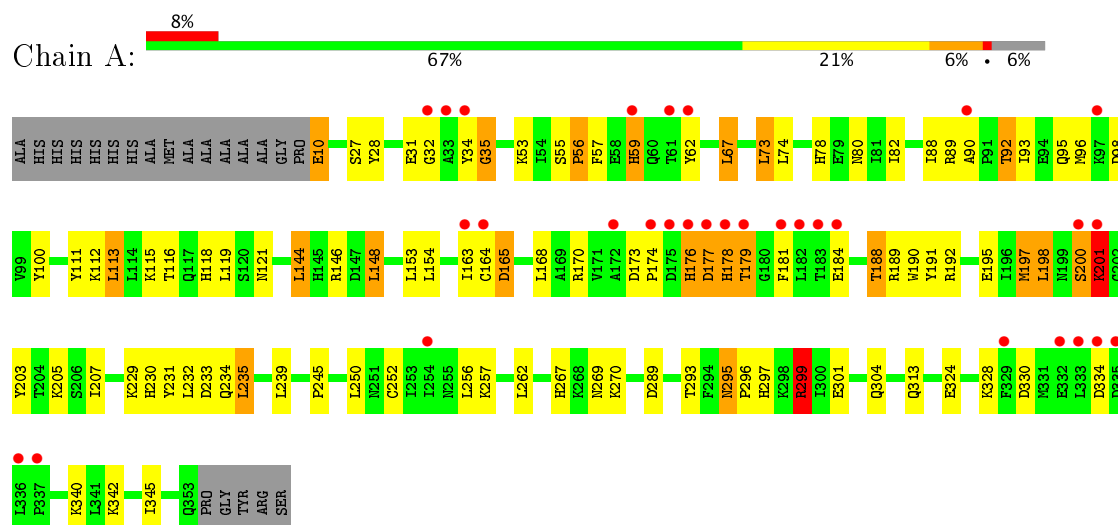
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	183	Total	O	0	0
			183	183		
3	B	53	Total	O	0	0
			53	53		

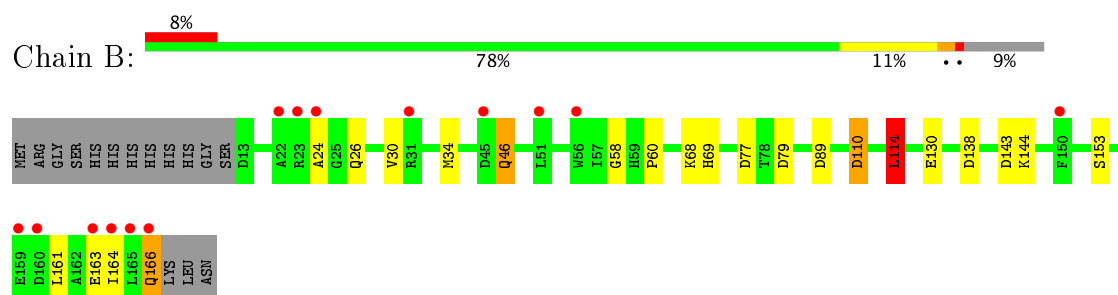
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: MITOGEN-ACTIVATED PROTEIN KINASE 1



#### • Molecule 2: DESIGNED ANKYRIN REPEAT PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.04Å 89.37Å 99.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.43 – 1.97 19.43 – 1.97	Depositor EDS
% Data completeness (in resolution range)	93.9 (19.43-1.97) 93.9 (19.43-1.97)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.64 (at 1.97Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.219 , 0.269 0.225 , 0.270	Depositor DCC
$R_{free}$ test set	2038 reflections (5.25%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 37.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4220	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	1.05	2/2884 (0.1%)	1.02	6/3907 (0.2%)
2	B	0.95	0/1187	0.95	7/1615 (0.4%)
All	All	1.02	2/4071 (0.0%)	1.00	13/5522 (0.2%)

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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	TYR	CD2-CE2	5.83	1.48	1.39
1	A	121	ASN	CB-CG	5.77	1.64	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	ARG	NE-CZ-NH2	-14.46	113.07	120.30
1	A	299	ARG	NE-CZ-NH1	13.88	127.24	120.30
1	A	148	LEU	CB-CG-CD1	7.89	124.42	111.00
2	B	77	ASP	CB-CG-OD1	6.91	124.52	118.30
2	B	77	ASP	CB-CG-OD2	-6.77	112.21	118.30
2	B	114	LEU	CA-CB-CG	6.60	130.48	115.30
1	A	144	LEU	CA-CB-CG	6.28	129.75	115.30
2	B	110	ASP	CB-CG-OD1	6.19	123.87	118.30
1	A	299	ARG	CD-NE-CZ	5.63	131.48	123.60
2	B	89	ASP	CB-CG-OD2	5.55	123.30	118.30
2	B	114	LEU	CB-CG-CD2	5.54	120.41	111.00
2	B	138	ASP	CB-CG-OD1	5.32	123.09	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	LEU	CB-CG-CD1	5.05	119.58	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	35	GLY	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	2817	0	2820	88	0
2	B	1167	0	1128	17	0
3	A	183	0	0	9	0
3	B	53	0	0	2	0
All	All	4220	0	3948	99	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 12.

All (99) 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)
2:B:163:GLU:HG2	3:B:2051:HOH:O	1.56	1.04
1:A:229:LYS:NZ	2:B:79:ASP:OD2	2.03	0.91
2:B:153:SER:HB3	2:B:161:LEU:HD23	1.52	0.91
1:A:92:THR:HG23	1:A:95:GLN:HE21	1.40	0.86
1:A:78:HIS:HD2	1:A:80:ASN:H	1.28	0.81
1:A:174:PRO:O	1:A:178:HIS:CE1	2.38	0.77
1:A:78:HIS:CD2	1:A:80:ASN:H	2.07	0.72
2:B:46:GLN:O	2:B:46:GLN:HG3	1.87	0.72
1:A:230:HIS:HE1	2:B:110:ASP:OD2	1.72	0.72
1:A:270:LYS:HE2	3:A:2151:HOH:O	1.88	0.72
1:A:89:ARG:HB2	1:A:96:MET:HE2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:THR:OG1	1:A:95:GLN:HG3	1.91	0.69
1:A:154:LEU:HD11	1:A:164:CYS:SG	2.35	0.67
1:A:168:LEU:HD21	1:A:184:GLU:HG2	1.78	0.65
1:A:153:LEU:CD2	1:A:163:ILE:HG12	2.27	0.64
1:A:82:ILE:HG21	1:A:164:CYS:HB2	1.79	0.64
1:A:230:HIS:CD2	1:A:233:ASP:H	2.18	0.62
1:A:176:HIS:O	1:A:178:HIS:N	2.32	0.61
1:A:118:HIS:HE1	3:A:2071:HOH:O	1.84	0.60
1:A:92:THR:CG2	1:A:95:GLN:HE21	2.13	0.59
1:A:90:ALA:HB1	1:A:95:GLN:HB2	1.87	0.57
1:A:170:ARG:CZ	1:A:179:THR:HG22	2.35	0.56
1:A:164:CYS:O	1:A:165:ASP:CB	2.52	0.56
1:A:197:MET:SD	1:A:234:GLN:HG2	2.45	0.56
1:A:146:ARG:HG2	1:A:207:ILE:HD11	1.87	0.56
1:A:10:GLU:OE1	1:A:10:GLU:HA	2.07	0.55
1:A:168:LEU:HD11	1:A:184:GLU:HG3	1.88	0.55
1:A:289:ASP:OD2	3:A:2161:HOH:O	2.17	0.55
1:A:293:THR:O	1:A:299:ARG:HD2	2.07	0.55
1:A:31:GLU:HG2	1:A:32:GLY:N	2.23	0.54
1:A:239:LEU:HD22	1:A:245:PRO:HD3	1.89	0.54
1:A:295:ASN:C	1:A:295:ASN:HD22	2.11	0.54
1:A:35:GLY:HA2	1:A:53:LYS:O	2.09	0.52
1:A:295:ASN:HD22	1:A:296:PRO:HD2	1.75	0.52
1:A:197:MET:CE	1:A:234:GLN:HG2	2.40	0.51
1:A:28:TYR:OH	1:A:31:GLU:HB3	2.11	0.51
2:B:114:LEU:HD22	2:B:143:ASP:HB2	1.92	0.51
1:A:295:ASN:ND2	1:A:297:HIS:H	2.09	0.50
1:A:89:ARG:HD3	1:A:96:MET:HE2	1.93	0.50
1:A:55:SER:HB3	1:A:98:ASP:OD1	2.12	0.50
1:A:328:LYS:HE3	1:A:328:LYS:HA	1.92	0.49
1:A:230:HIS:CE1	2:B:110:ASP:OD2	2.60	0.49
1:A:177:ASP:OD1	1:A:177:ASP:O	2.30	0.49
1:A:295:ASN:HD22	1:A:296:PRO:N	2.10	0.49
1:A:301:GLU:H	1:A:304:GLN:HE21	1.60	0.49
1:A:178:HIS:O	1:A:179:THR:O	2.30	0.49
1:A:178:HIS:O	1:A:179:THR:C	2.51	0.49
1:A:188:THR:HG22	1:A:190:TRP:H	1.77	0.49
1:A:195:GLU:O	1:A:200:SER:HB2	2.13	0.49
1:A:174:PRO:HD3	3:A:2087:HOH:O	2.13	0.49
1:A:295:ASN:ND2	1:A:296:PRO:HD2	2.27	0.48
1:A:205:LYS:HG3	3:A:2120:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:ASN:HD22	1:A:296:PRO:CD	2.26	0.48
1:A:174:PRO:O	1:A:178:HIS:NE2	2.45	0.48
1:A:89:ARG:HD3	1:A:96:MET:CE	2.44	0.48
1:A:229:LYS:HZ1	2:B:46:GLN:HE22	1.62	0.48
2:B:58:GLY:O	2:B:60:PRO:HD3	2.14	0.48
1:A:189:ARG:HD3	1:A:192:ARG:NH1	2.29	0.48
1:A:154:LEU:CD1	1:A:164:CYS:SG	3.01	0.48
1:A:78:HIS:HE1	3:A:2077:HOH:O	1.96	0.47
1:A:178:HIS:HB2	3:A:2102:HOH:O	2.15	0.47
1:A:301:GLU:H	1:A:304:GLN:NE2	2.12	0.47
1:A:111:TYR:CE1	1:A:115:LYS:HE3	2.50	0.47
2:B:26:GLN:O	2:B:30:VAL:HG23	2.14	0.47
1:A:293:THR:O	1:A:299:ARG:CD	2.63	0.47
1:A:112:LYS:O	1:A:116:THR:HG23	2.14	0.47
1:A:168:LEU:HD11	1:A:184:GLU:CG	2.44	0.46
1:A:82:ILE:HG23	1:A:82:ILE:O	2.14	0.46
1:A:88:ILE:HB	1:A:100:TYR:HB2	1.97	0.46
1:A:229:LYS:NZ	2:B:46:GLN:HE22	2.14	0.45
1:A:82:ILE:HB	1:A:164:CYS:HB3	1.98	0.45
1:A:197:MET:HE1	1:A:234:GLN:HG2	1.99	0.44
2:B:130:GLU:OE2	2:B:164:ILE:HG21	2.17	0.44
1:A:201:LYS:HD3	1:A:201:LYS:HA	1.30	0.44
2:B:130:GLU:OE2	2:B:164:ILE:CG2	2.65	0.44
1:A:113:LEU:HD13	1:A:119:LEU:HD21	2.00	0.44
1:A:198:LEU:HD13	1:A:235:LEU:HD21	1.99	0.44
1:A:153:LEU:HD22	1:A:163:ILE:HG12	1.99	0.43
1:A:197:MET:HG3	1:A:231:TYR:HB2	1.98	0.43
1:A:67:LEU:HG	1:A:345:ILE:HG13	2.01	0.43
1:A:198:LEU:HD21	1:A:262:LEU:HD11	2.00	0.43
2:B:166:GLN:C	3:B:2053:HOH:O	2.57	0.43
1:A:111:TYR:HE1	1:A:115:LYS:HE3	1.84	0.42
1:A:252:CYS:HB3	3:A:2146:HOH:O	2.18	0.42
1:A:82:ILE:HG21	1:A:164:CYS:CB	2.46	0.42
1:A:176:HIS:O	1:A:177:ASP:C	2.58	0.42
1:A:232:LEU:HD13	2:B:144:LYS:HG2	2.01	0.42
1:A:56:PRO:HD2	1:A:57:PHE:CE2	2.54	0.42
1:A:89:ARG:CD	1:A:96:MET:CE	2.98	0.42
2:B:34:MET:CE	2:B:69:HIS:CG	3.04	0.41
1:A:57:PHE:CD1	1:A:342:LYS:HG3	2.55	0.41
1:A:82:ILE:CG2	1:A:164:CYS:CB	2.99	0.41
1:A:267:HIS:HE1	1:A:269:ASN:OD1	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:HIS:HB3	1:A:62:TYR:CD2	2.56	0.41
2:B:24:ALA:CB	2:B:26:GLN:HE21	2.34	0.41
1:A:324:GLU:HG2	3:A:2080:HOH:O	2.20	0.40
1:A:257:LYS:HE2	1:A:257:LYS:HB3	1.79	0.40
1:A:170:ARG:NH1	1:A:330:ASP:OD1	2.53	0.40
1:A:144:LEU:HD22	1:A:205:LYS:HA	2.04	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	342/365 (94%)	318 (93%)	19 (6%)	5 (2%)	12	5
2	B	152/169 (90%)	147 (97%)	5 (3%)	0	100	100
All	All	494/534 (92%)	465 (94%)	24 (5%)	5 (1%)	18	10

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	177	ASP
1	A	179	THR
1	A	165	ASP
1	A	56	PRO
1	A	201	LYS

### 5.3.2 Protein sidechains [i](#)

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	312/324 (96%)	283 (91%)	29 (9%)	10	5
2	B	119/132 (90%)	115 (97%)	4 (3%)	42	37
All	All	431/456 (94%)	398 (92%)	33 (8%)	15	8

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLU
1	A	27	SER
1	A	34	TYR
1	A	59	HIS
1	A	67	LEU
1	A	73	LEU
1	A	74	LEU
1	A	92	THR
1	A	93	ILE
1	A	113	LEU
1	A	148	LEU
1	A	173	ASP
1	A	176	HIS
1	A	178	HIS
1	A	181	PHE
1	A	188	THR
1	A	197	MET
1	A	198	LEU
1	A	200	SER
1	A	201	LYS
1	A	203	TYR
1	A	235	LEU
1	A	250	LEU
1	A	256	LEU
1	A	295	ASN
1	A	299	ARG
1	A	313	GLN
1	A	334	ASP
1	A	340	LYS
2	B	46	GLN
2	B	68	LYS
2	B	114	LEU
2	B	166	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	78	HIS
1	A	95	GLN
1	A	118	HIS
1	A	121	ASN
1	A	176	HIS
1	A	199	ASN
1	A	230	HIS
1	A	234	GLN
1	A	247	GLN
1	A	251	ASN
1	A	267	HIS
1	A	295	ASN
1	A	297	HIS
1	A	304	GLN
2	B	26	GLN
2	B	36	ASN
2	B	46	GLN
2	B	59	HIS
2	B	69	HIS
2	B	156	ASN

### 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](#)

There are no ligands in this entry.

## 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	344/365 (94%)	0.63	31 (9%) 10 12	13, 25, 59, 81	0
2	B	154/169 (91%)	0.50	14 (9%) 10 12	17, 29, 52, 68	0
All	All	498/534 (93%)	0.59	45 (9%) 10 12	13, 27, 57, 81	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	HIS	7.5
1	A	34	TYR	7.3
1	A	177	ASP	6.2
1	A	32	GLY	6.2
1	A	33	ALA	6.0
1	A	174	PRO	5.5
1	A	179	THR	4.9
1	A	175	ASP	4.8
1	A	334	ASP	4.5
1	A	329	PHE	4.4
1	A	201	LYS	4.4
1	A	337	PRO	4.3
1	A	62	TYR	4.0
1	A	178	HIS	3.9
1	A	59	HIS	3.8
2	B	45	ASP	3.6
1	A	164	CYS	3.6
1	A	336	LEU	3.5
2	B	163	GLU	3.5
1	A	200	SER	3.4
2	B	165	LEU	3.4
2	B	51	LEU	3.2
2	B	166	GLN	3.1
1	A	97	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	181	PHE	3.0
1	A	335	ASP	2.9
1	A	184	GLU	2.9
1	A	163	ILE	2.8
1	A	183	THR	2.8
2	B	150	PHE	2.7
1	A	90	ALA	2.6
1	A	61	THR	2.6
2	B	24	ALA	2.5
1	A	182	LEU	2.4
1	A	332	GLU	2.4
2	B	56	TRP	2.3
1	A	333	LEU	2.3
2	B	159	GLU	2.3
1	A	172	ALA	2.2
2	B	22	ALA	2.2
1	A	254	ILE	2.1
2	B	164	ILE	2.1
2	B	160	ASP	2.1
2	B	31	ARG	2.0
2	B	23	ARG	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.