



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:47 PM GMT

PDB ID : 3V2A  
Title : VEGFR-2/VEGF-A COMPLEX STRUCTURE  
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Deposited on : 2011-12-12  
Resolution : 3.20 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

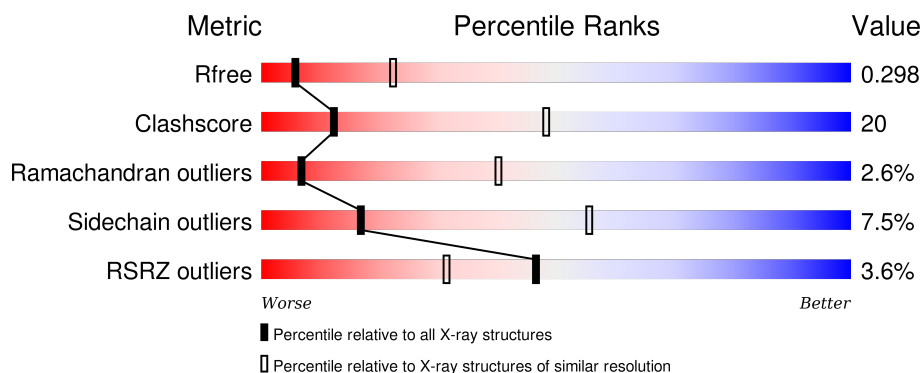
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	R	772	<div> <div style="width: 13%; background-color: red;"></div> <div style="width: 10%; background-color: orange;"></div> <div style="width: 76%; background-color: green;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>13% 10% • 76%</div>
2	A	134	<div> <div style="width: 3%; background-color: red;"></div> <div style="width: 45%; background-color: green;"></div> <div style="width: 24%; background-color: yellow;"></div> <div style="width: 29%; background-color: grey;"></div> </div> <div>3% 45% 24% • 29%</div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2114 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 Vascular endothelial growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	185	Total	C	N	O	S	0	0	0
			1369	879	216	264	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	765	ARG	-	EXPRESSION TAG	UNP P35968
R	766	THR	-	EXPRESSION TAG	UNP P35968
R	767	HIS	-	EXPRESSION TAG	UNP P35968
R	768	HIS	-	EXPRESSION TAG	UNP P35968
R	769	HIS	-	EXPRESSION TAG	UNP P35968
R	770	HIS	-	EXPRESSION TAG	UNP P35968
R	771	HIS	-	EXPRESSION TAG	UNP P35968
R	772	HIS	-	EXPRESSION TAG	UNP P35968

- Molecule 2 is a protein called Vascular endothelial growth factor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	95	Total	C	N	O	S	0	0	0
			745	468	122	143	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	ALA	-	EXPRESSION TAG	UNP P15692
A	-11	GLU	-	EXPRESSION TAG	UNP P15692
A	-10	PHE	-	EXPRESSION TAG	UNP P15692
A	-9	GLY	-	EXPRESSION TAG	UNP P15692
A	-8	SER	-	EXPRESSION TAG	UNP P15692
A	-7	HIS	-	EXPRESSION TAG	UNP P15692
A	-6	HIS	-	EXPRESSION TAG	UNP P15692
A	-5	HIS	-	EXPRESSION TAG	UNP P15692

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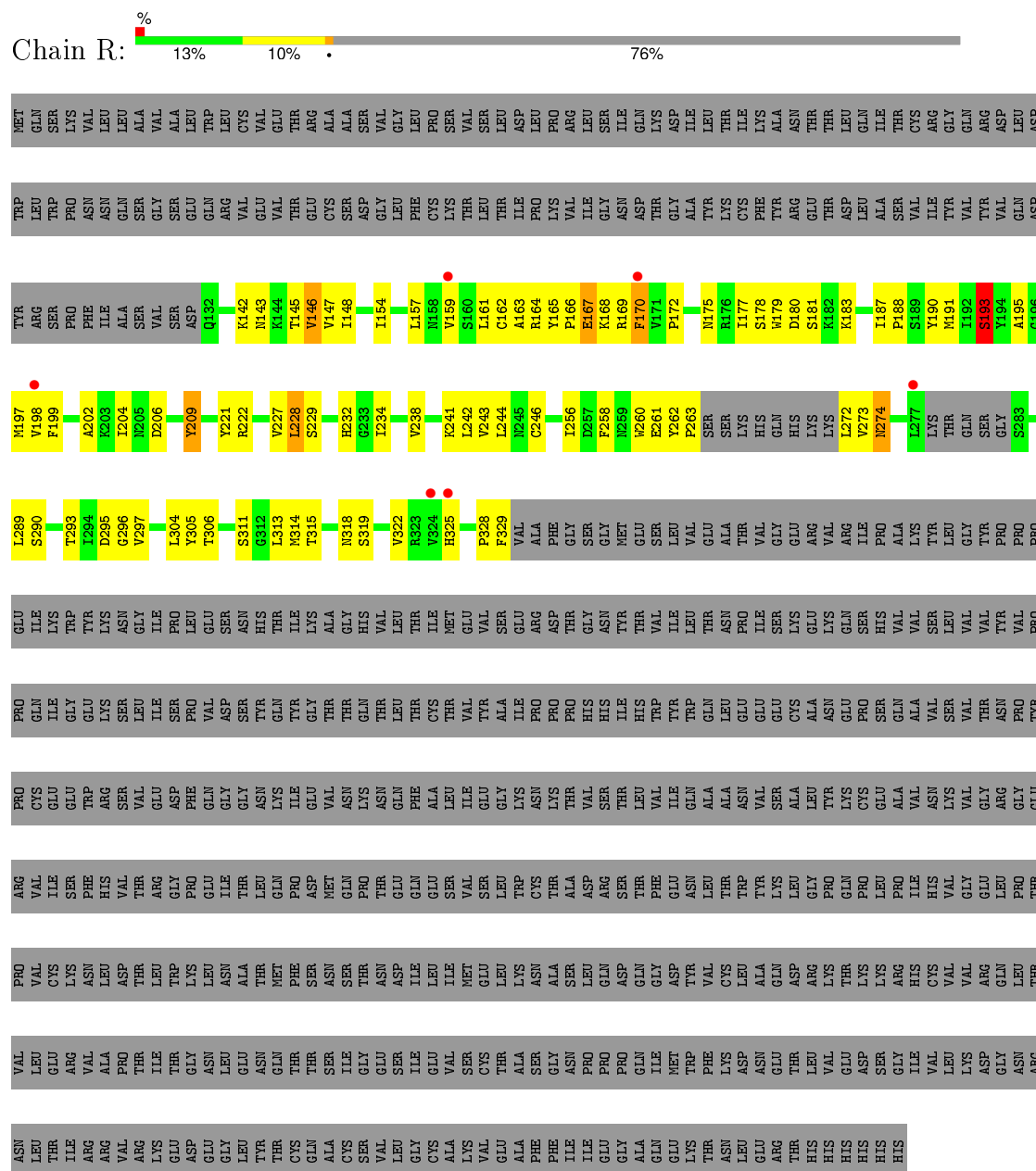
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	EXPRESSION TAG	UNP P15692
A	-3	HIS	-	EXPRESSION TAG	UNP P15692
A	-2	HIS	-	EXPRESSION TAG	UNP P15692
A	-1	GLY	-	EXPRESSION TAG	UNP P15692
A	0	SER	-	EXPRESSION TAG	UNP P15692
A	115	ASN	-	EXPRESSION TAG	UNP P15692
A	116	CYS	-	EXPRESSION TAG	UNP P15692
A	117	ASP	-	EXPRESSION TAG	UNP P15692
A	118	LYS	-	EXPRESSION TAG	UNP P15692
A	119	PRO	-	EXPRESSION TAG	UNP P15692
A	120	ARG	-	EXPRESSION TAG	UNP P15692
A	121	ARG	-	EXPRESSION TAG	UNP P15692

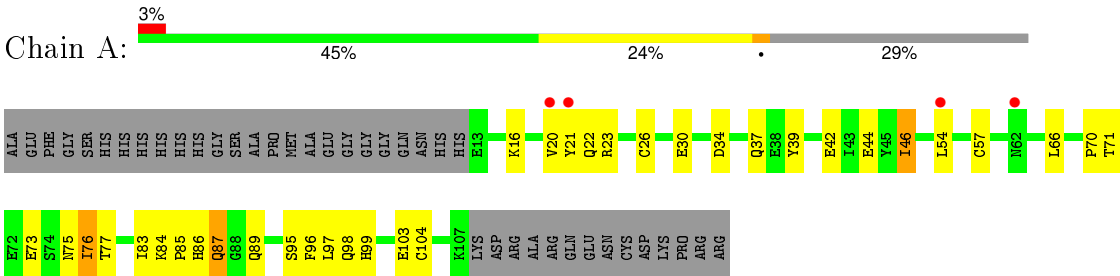
### 3 Residue-property plots

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: Vascular endothelial growth factor receptor 2



- Molecule 2: Vascular endothelial growth factor A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.97Å 80.97Å 332.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	68.61 – 3.20 68.61 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.7 (68.61-3.20) 98.7 (68.61-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.244 , 0.300 0.238 , 0.298	Depositor DCC
$R_{free}$ test set	540 reflections (4.78%)	DCC
Wilson B-factor (Å <sup>2</sup> )	109.1	Xtriage
Anisotropy	0.287	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 113.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 11301 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2114	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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

### 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	R	0.28	0/1397	0.49	0/1909
2	A	0.30	0/763	0.46	0/1035
All	All	0.29	0/2160	0.48	0/2944

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

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	R	1369	0	1272	61	0
2	A	745	0	676	22	0
All	All	2114	0	1948	80	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 20.

All (80) 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:R:143:ASN:HA	1:R:190:TYR:CD2	2.05	0.91
1:R:179:TRP:CH2	1:R:181:SER:HA	2.18	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:73:GLU:HB3	2:A:97:LEU:HD11	1.66	0.75
1:R:274:ASN:HB3	1:R:290:SER:HA	1.69	0.74
1:R:261:GLU:HB3	1:R:306:THR:HB	1.67	0.74
1:R:143:ASN:HA	1:R:190:TYR:HD2	1.52	0.70
1:R:165:TYR:HB3	1:R:166:PRO:HA	1.74	0.69
2:A:57:CYS:H	2:A:99:HIS:HD2	1.41	0.67
1:R:161:LEU:HD11	1:R:198:VAL:HB	1.77	0.66
1:R:157:LEU:HB3	1:R:159:VAL:HG23	1.77	0.66
1:R:145:THR:HA	1:R:188:PRO:HA	1.77	0.65
1:R:314:MET:HG2	1:R:315:THR:H	1.61	0.63
1:R:221:TYR:HB3	2:A:86:HIS:HE1	1.64	0.63
2:A:57:CYS:H	2:A:99:HIS:CD2	2.17	0.63
1:R:154:ILE:HB	1:R:157:LEU:HG	1.82	0.62
1:R:304:LEU:HD11	1:R:319:SER:HB3	1.80	0.62
1:R:314:MET:HG2	1:R:315:THR:N	2.17	0.60
2:A:76:ILE:HG12	2:A:77:THR:H	1.67	0.59
2:A:83:ILE:O	2:A:85:PRO:HD3	2.03	0.58
1:R:272:LEU:HD12	1:R:273:VAL:N	2.18	0.58
1:R:146:VAL:HG13	1:R:187:ILE:O	2.05	0.57
1:R:159:VAL:HG22	1:R:202:ALA:HB2	1.86	0.57
2:A:34:ASP:O	2:A:37:GLN:HB3	2.05	0.56
1:R:162:CYS:HB3	1:R:199:PHE:CZ	2.39	0.56
1:R:163:ALA:O	1:R:167:GLU:HA	2.07	0.55
2:A:75:ASN:HB3	2:A:95:SER:OG	2.08	0.54
1:R:148:ILE:HD12	1:R:148:ILE:N	2.22	0.54
1:R:204:ILE:HB	1:R:209:TYR:CE2	2.43	0.53
1:R:262:TYR:HB2	1:R:263:PRO:HD2	1.90	0.53
1:R:143:ASN:HA	1:R:190:TYR:CE2	2.42	0.53
1:R:295:ASP:O	1:R:297:VAL:HG13	2.09	0.53
1:R:229:SER:O	1:R:244:LEU:HD12	2.08	0.53
2:A:76:ILE:HG12	2:A:77:THR:N	2.23	0.53
1:R:256:ILE:HD13	1:R:311:SER:HA	1.91	0.52
2:A:54:LEU:HA	2:A:98:GLN:HE21	1.74	0.52
2:A:22:GLN:HG3	2:A:23:ARG:N	2.24	0.52
1:R:228:LEU:HD12	1:R:228:LEU:H	1.75	0.51
2:A:75:ASN:HA	2:A:96:PHE:O	2.10	0.51
1:R:304:LEU:HD12	1:R:305:TYR:H	1.75	0.50
1:R:188:PRO:HD2	1:R:191:MET:SD	2.52	0.50
1:R:328:PRO:O	1:R:329:PHE:HB2	2.12	0.50
1:R:246:CYS:HB2	1:R:260:TRP:CH2	2.47	0.50
1:R:161:LEU:HD12	1:R:199:PHE:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:221:TYR:CG	1:R:313:LEU:HD11	2.47	0.49
1:R:165:TYR:O	1:R:195:ALA:HA	2.12	0.49
2:A:66:LEU:HD13	2:A:104:CYS:HB3	1.94	0.49
1:R:241:LYS:HD3	1:R:295:ASP:OD2	2.12	0.49
1:R:313:LEU:HG	2:A:86:HIS:ND1	2.29	0.48
1:R:170:PHE:N	1:R:170:PHE:CD2	2.82	0.48
1:R:168:LYS:HB3	1:R:170:PHE:HE2	1.79	0.47
1:R:313:LEU:HG	2:A:86:HIS:CE1	2.49	0.47
1:R:260:TRP:HA	1:R:306:THR:O	2.15	0.47
1:R:190:TYR:HA	1:R:193:SER:OG	2.15	0.46
1:R:304:LEU:HD12	1:R:305:TYR:N	2.30	0.46
1:R:222:ARG:HA	1:R:314:MET:CE	2.45	0.46
2:A:46:ILE:HG12	2:A:83:ILE:HB	1.98	0.46
1:R:164:ARG:HA	1:R:165:TYR:HA	1.69	0.46
1:R:222:ARG:HA	1:R:314:MET:HE1	1.99	0.45
1:R:188:PRO:HG2	1:R:191:MET:HG3	1.97	0.45
1:R:188:PRO:HB2	1:R:190:TYR:CE2	2.51	0.45
2:A:84:LYS:CG	2:A:87:GLN:HG2	2.46	0.45
2:A:16:LYS:O	2:A:20:VAL:HG23	2.17	0.45
1:R:177:ILE:HG22	1:R:178:SER:N	2.31	0.44
1:R:297:VAL:HG23	1:R:297:VAL:O	2.18	0.44
2:A:70:PRO:HG3	2:A:99:HIS:CD2	2.52	0.44
1:R:180:ASP:HB3	1:R:183:LYS:CB	2.48	0.44
1:R:172:PRO:HA	1:R:177:ILE:HG22	2.00	0.44
2:A:84:LYS:CD	2:A:87:GLN:HG2	2.49	0.43
1:R:243:VAL:HG22	1:R:293:THR:OG1	2.18	0.43
1:R:146:VAL:HG23	1:R:147:VAL:N	2.34	0.43
1:R:258:PHE:CD1	1:R:290:SER:HB2	2.54	0.42
1:R:238:VAL:HG23	1:R:325:HIS:O	2.19	0.42
1:R:146:VAL:CG2	1:R:147:VAL:N	2.81	0.42
1:R:242:LEU:HD23	1:R:242:LEU:O	2.19	0.42
1:R:164:ARG:HB3	1:R:165:TYR:CD2	2.55	0.42
1:R:162:CYS:HB2	1:R:169:ARG:NH1	2.34	0.42
1:R:164:ARG:O	1:R:197:MET:N	2.52	0.41
2:A:39:TYR:HB3	2:A:42:GLU:HG3	2.02	0.40
2:A:71:THR:HG21	2:A:103:GLU:OE1	2.22	0.40
1:R:234:ILE:HB	1:R:322:VAL:HG23	2.02	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	R	179/772 (23%)	144 (80%)	29 (16%)	6 (3%)	5	31
2	A	93/134 (69%)	83 (89%)	9 (10%)	1 (1%)	17	62
All	All	272/906 (30%)	227 (84%)	38 (14%)	7 (3%)	7	40

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	142	LYS
1	R	175	ASN
2	A	26	CYS
1	R	167	GLU
1	R	206	ASP
1	R	193	SER
1	R	296	GLY

### 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	R	145/691 (21%)	135 (93%)	10 (7%)	19	59
2	A	83/120 (69%)	76 (92%)	7 (8%)	14	48
All	All	228/811 (28%)	211 (92%)	17 (8%)	17	55

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	146	VAL
1	R	170	PHE
1	R	193	SER
1	R	209	TYR
1	R	227	VAL
1	R	228	LEU
1	R	232	HIS
1	R	274	ASN
1	R	289	LEU
1	R	318	ASN
2	A	21	TYR
2	A	30	GLU
2	A	44	GLU
2	A	46	ILE
2	A	76	ILE
2	A	87	GLN
2	A	89	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	132	GLN
1	R	210	GLN
1	R	232	HIS
2	A	89	GLN
2	A	98	GLN
2	A	99	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

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	R	185/772 (23%)	0.32	6 (3%)	51	36	86, 134, 176, 192	0
2	A	95/134 (70%)	0.47	4 (4%)	40	26	77, 106, 129, 153	0
All	All	280/906 (30%)	0.37	10 (3%)	46	31	77, 121, 174, 192	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	170	PHE	3.4
1	R	325	HIS	3.2
1	R	159	VAL	3.2
2	A	21	TYR	2.7
2	A	62	ASN	2.6
1	R	198	VAL	2.4
2	A	20	VAL	2.2
1	R	277	LEU	2.1
1	R	324	VAL	2.0
2	A	54	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.