



# Full wwPDB X-ray Structure Validation Report

Nov 7, 2014 – 11:33 AM EST

PDB ID : 3E5M  
Title : Crystal structure of the HSCARG Y81A mutant  
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Deposited on : 2008-08-14  
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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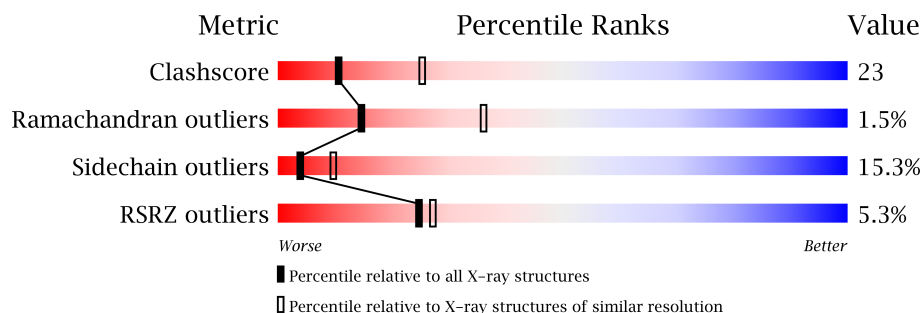
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : trunk24103  
Percentile statistics : 23426  
Refmac : 5.8.0049  
CCP4 : 6.1.3  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk24103

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
Clashscore	88313	2109 (2.70-2.70)
Ramachandran outliers	86584	2075 (2.70-2.70)
C $\alpha$ geometry	86677	2078 (2.70-2.70)
Sidechain outliers	86556	2075 (2.70-2.70)
RSRZ outliers	77580	1797 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	299	
1	B	299	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4605 atoms, of which 0 are hydrogen and 0 are deuterium.

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 NmrA-like family domain-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2298	1459	402	427	10			
1	B	295	Total	C	N	O	S	0	0	0
			2307	1465	404	428	10			

There are 2 discrepancies between the modelled and reference sequences:

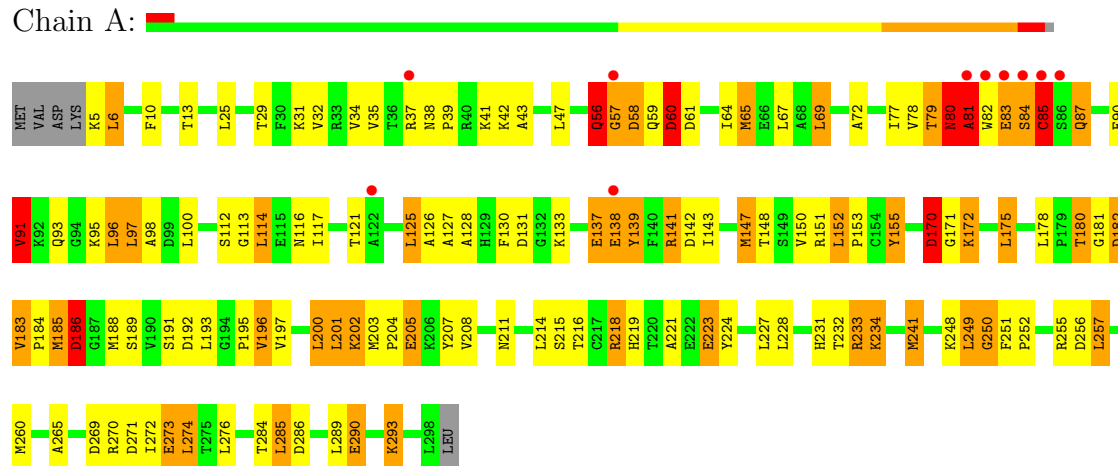
Chain	Residue	Modelled	Actual	Comment	Reference
A	81	ALA	TYR	ENGINEERED	UNP Q9HBL8
B	81	ALA	TYR	ENGINEERED	UNP Q9HBL8

### 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.

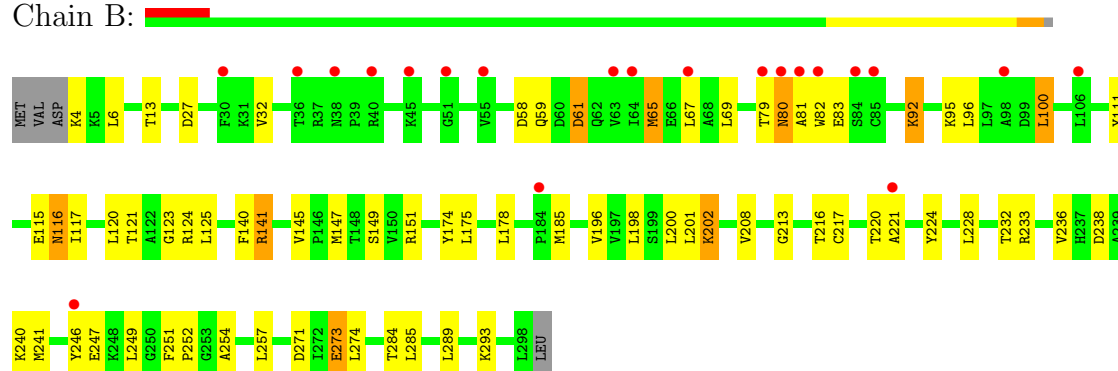
- Molecule 1: NmrA-like family domain-containing protein 1

Chain A:



- Molecule 1: NmrA-like family domain-containing protein 1

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.96Å 89.04Å 84.18Å 90.00° 88.23° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 19.73 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.1 (20.00-2.70) 89.5 (19.73-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.88 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.260 , 0.273 0.264 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	21.3	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 4.8	EDS
Estimated twinning fraction	0.308 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.34$ , $\langle L^2 \rangle = 0.17$	Xtriage
Outliers	0 of 18529 reflections	Xtriage
$F_o, F_c$ correlation	0.81	EDS
Total number of atoms	4605	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% 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	A	1.23	3/2342 (0.1%)	1.11	6/3165 (0.2%)
1	B	1.00	0/2351	0.94	5/3176 (0.2%)
All	All	1.12	3/4693 (0.1%)	1.02	11/6341 (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	10

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	196	VAL	CB-CG1	-8.36	1.35	1.52
1	A	91	VAL	CB-CG1	-6.28	1.39	1.52
1	A	234	LYS	CD-CE	5.85	1.65	1.51

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	LEU	CA-CB-CG	10.06	138.43	115.30
1	B	141	ARG	NE-CZ-NH2	-7.89	116.36	120.30
1	B	6	LEU	CA-CB-CG	7.24	131.96	115.30
1	A	96	LEU	CB-CG-CD2	6.77	122.51	111.00
1	B	141	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	60	ASP	CB-CG-OD2	-6.15	112.77	118.30
1	A	276	LEU	CA-CB-CG	-6.09	101.30	115.30
1	A	60	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	175	LEU	CA-CB-CG	5.33	127.56	115.30
1	B	100	LEU	CB-CG-CD1	5.22	119.88	111.00
1	B	61	ASP	CB-CG-OD2	-5.09	113.72	118.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	TYR	Peptide
1	A	170	ASP	Peptide
1	A	180	THR	Peptide
1	A	186	ASP	Peptide
1	A	56	GLN	Peptide
1	A	79	THR	Peptide
1	A	81	ALA	Peptide
1	A	83	GLU	Peptide
1	A	84	SER	Peptide
1	A	85	CYS	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2298	0	2321	181	0
1	B	2307	0	2334	31	0
All	All	4605	0	4655	212	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (212) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:65:MET:O	1:A:69:LEU:CD2	1.73	1.34
1:A:80:ASN:CG	1:A:84:SER:HB3	1.51	1.30
1:A:80:ASN:CA	1:A:81:ALA:HB2	1.68	1.23
1:A:80:ASN:HA	1:A:81:ALA:CB	1.62	1.21
1:A:80:ASN:ND2	1:A:84:SER:HB3	1.54	1.20
1:A:81:ALA:HB3	1:A:82:TRP:O	1.46	1.12
1:A:87:GLN:O	1:A:91:VAL:HG13	1.48	1.11
1:A:39:PRO:HG2	1:A:56:GLN:HB2	1.29	1.10
1:A:284:THR:HG22	1:A:286:ASP:H	1.13	1.09

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:148:THR:OG1	1:A:207:TYR:O	1.69	1.08
1:A:80:ASN:OD1	1:A:84:SER:HB3	1.52	1.08
1:A:65:MET:O	1:A:69:LEU:HD23	1.44	1.07
1:A:256:ASP:O	1:A:260:MET:HG3	1.55	1.06
1:A:227:LEU:HD12	1:A:285:LEU:HD13	1.38	1.03
1:A:181:GLY:O	1:A:182:ASP:HB2	1.52	1.03
1:A:69:LEU:N	1:A:69:LEU:HD22	1.74	1.02
1:A:251:PHE:HB2	1:A:252:PRO:HD2	1.40	1.02
1:A:39:PRO:CG	1:A:56:GLN:HB2	1.89	1.01
1:A:141:ARG:NH2	1:A:211:ASN:OD1	1.94	0.99
1:A:139:TYR:HA	1:A:142:ASP:HB2	1.42	0.98
1:A:87:GLN:O	1:A:91:VAL:CG1	2.13	0.97
1:A:180:THR:HG21	1:A:221:ALA:H	1.30	0.96
1:A:232:THR:O	1:A:233:ARG:HG2	1.65	0.96
1:A:138:GLU:HG3	1:A:138:GLU:O	1.63	0.95
1:A:80:ASN:ND2	1:A:84:SER:CB	2.31	0.94
1:A:69:LEU:HD22	1:A:69:LEU:H	1.32	0.92
1:A:227:LEU:HD12	1:A:285:LEU:CD1	2.01	0.90
1:A:39:PRO:HG2	1:A:56:GLN:CB	2.04	0.88
1:A:137:GLU:CD	1:A:151:ARG:HH21	1.79	0.86
1:A:80:ASN:CA	1:A:81:ALA:CB	2.35	0.86
1:A:227:LEU:CD1	1:A:285:LEU:HD13	2.07	0.84
1:A:80:ASN:HD21	1:A:84:SER:HB3	1.44	0.83
1:A:232:THR:O	1:A:233:ARG:CG	2.27	0.82
1:A:69:LEU:H	1:A:69:LEU:CD2	1.91	0.82
1:A:83:GLU:HG3	1:A:84:SER:H	1.42	0.82
1:B:82:TRP:N	1:B:83:GLU:HA	1.94	0.82
1:A:37:ARG:HG2	1:A:58:ASP:HA	1.62	0.80
1:A:151:ARG:NH2	1:A:211:ASN:ND2	2.29	0.80
1:A:251:PHE:HB2	1:A:252:PRO:CD	2.10	0.80
1:A:13:THR:CG2	1:A:41:LYS:HE2	2.11	0.80
1:A:80:ASN:OD1	1:A:84:SER:CB	2.30	0.80
1:A:78:VAL:O	1:A:79:THR:HG22	1.82	0.79
1:A:65:MET:O	1:A:69:LEU:HD21	1.80	0.79
1:A:79:THR:O	1:A:90:GLU:OE2	2.01	0.78
1:A:84:SER:HB2	1:A:85:CYS:O	1.84	0.78
1:A:65:MET:O	1:A:69:LEU:HD22	1.80	0.78
1:A:69:LEU:N	1:A:69:LEU:CD2	2.46	0.77
1:A:78:VAL:C	1:A:79:THR:CG2	2.54	0.77
1:A:290:GLU:O	1:A:293:LYS:NZ	2.16	0.75
1:A:127:ALA:HB1	1:A:256:ASP:HB3	1.67	0.74
1:A:13:THR:HG21	1:A:41:LYS:HE2	1.68	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:59:GLN:NE2	1:B:80:ASN:O	2.20	0.73
1:B:251:PHE:HB2	1:B:252:PRO:HD2	1.71	0.72
1:A:80:ASN:CG	1:A:84:SER:CB	2.46	0.72
1:A:137:GLU:OE1	1:A:151:ARG:NH2	2.22	0.72
1:A:181:GLY:O	1:A:182:ASP:CB	2.31	0.72
1:A:65:MET:HE3	1:A:65:MET:HA	1.72	0.71
1:A:180:THR:HG23	1:A:181:GLY:HA2	1.73	0.71
1:A:79:THR:O	1:A:133:LYS:NZ	2.23	0.71
1:A:203:MET:N	1:A:204:PRO:HD3	2.06	0.71
1:A:285:LEU:HD22	1:A:285:LEU:O	1.89	0.71
1:A:141:ARG:NH1	1:A:147:MET:HE3	2.06	0.71
1:A:80:ASN:HA	1:A:81:ALA:HB2	0.78	0.70
1:A:80:ASN:HD21	1:A:84:SER:CB	1.98	0.69
1:A:151:ARG:NH2	1:A:211:ASN:HD22	1.88	0.69
1:A:58:ASP:O	1:A:60:ASP:N	2.25	0.69
1:A:170:ASP:OD1	1:A:170:ASP:C	2.31	0.69
1:A:83:GLU:HG3	1:A:84:SER:N	2.06	0.69
1:A:83:GLU:CG	1:A:84:SER:H	2.06	0.69
1:A:78:VAL:HG12	1:A:112:SER:HB3	1.75	0.68
1:A:78:VAL:C	1:A:79:THR:HG23	2.13	0.68
1:A:232:THR:O	1:A:233:ARG:NE	2.27	0.68
1:A:180:THR:CG2	1:A:221:ALA:CB	2.72	0.67
1:B:228:LEU:O	1:B:232:THR:OG1	2.12	0.67
1:A:80:ASN:HB2	1:A:81:ALA:HB3	1.77	0.66
1:A:91:VAL:O	1:A:95:LYS:HG3	1.95	0.66
1:A:180:THR:HG22	1:A:221:ALA:HB2	1.76	0.66
1:A:126:ALA:O	1:A:127:ALA:HB2	1.96	0.66
1:A:138:GLU:O	1:A:142:ASP:CG	2.34	0.66
1:A:141:ARG:CZ	1:A:147:MET:CE	2.74	0.65
1:A:137:GLU:O	1:A:139:TYR:N	2.30	0.64
1:A:78:VAL:O	1:A:79:THR:CG2	2.46	0.64
1:A:257:LEU:O	1:A:260:MET:HB2	1.97	0.63
1:A:65:MET:CE	1:A:65:MET:HA	2.28	0.63
1:A:180:THR:HG21	1:A:221:ALA:N	2.10	0.63
1:A:170:ASP:OD1	1:A:172:LYS:HB2	2.00	0.62
1:A:84:SER:OG	1:A:85:CYS:N	2.31	0.62
1:A:180:THR:HG22	1:A:221:ALA:CB	2.29	0.61
1:A:117:ILE:HG21	1:A:125:LEU:HD12	1.83	0.60
1:A:39:PRO:HG3	1:A:56:GLN:HB2	1.78	0.60
1:A:186:ASP:HB3	1:A:215:SER:OG	2.01	0.60
1:A:180:THR:CG2	1:A:221:ALA:HB2	2.31	0.60
1:A:251:PHE:O	1:A:255:ARG:NH2	2.34	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:98:ALA:O	1:A:143:ILE:HD11	2.01	0.59
1:A:284:THR:HG22	1:A:286:ASP:N	1.99	0.59
1:A:284:THR:CG2	1:A:285:LEU:N	2.66	0.59
1:A:34:VAL:HG11	1:A:47:LEU:HD13	1.85	0.59
1:A:170:ASP:OD1	1:A:171:GLY:N	2.36	0.58
1:A:93:GLN:O	1:A:97:LEU:HD22	2.03	0.58
1:A:80:ASN:CB	1:A:81:ALA:CB	2.81	0.58
1:A:180:THR:HG21	1:A:221:ALA:CB	2.32	0.58
1:A:91:VAL:O	1:A:91:VAL:HG23	2.03	0.58
1:A:285:LEU:CD2	1:A:289:LEU:HG	2.34	0.58
1:A:61:ASP:O	1:A:65:MET:HB2	2.03	0.58
1:A:141:ARG:NH1	1:A:147:MET:CE	2.67	0.57
1:B:217:CYS:HB3	1:B:284:THR:HG23	1.85	0.57
1:A:203:MET:N	1:A:204:PRO:CD	2.67	0.57
1:A:141:ARG:CZ	1:A:147:MET:HE3	2.34	0.57
1:A:231:HIS:O	1:A:293:LYS:HD3	2.04	0.57
1:A:223:GLU:O	1:A:227:LEU:HG	2.04	0.57
1:A:269:ASP:O	1:A:270:ARG:HD2	2.05	0.56
1:A:216:THR:O	1:A:216:THR:HG22	2.05	0.56
1:A:13:THR:HG21	1:A:41:LYS:CE	2.34	0.56
1:B:271:ASP:OD1	1:B:273:GLU:HG2	2.05	0.56
1:A:5:LYS:HB3	1:A:31:LYS:H	1.70	0.56
1:A:81:ALA:CB	1:A:82:TRP:O	2.38	0.56
1:B:65:MET:CE	1:B:65:MET:HA	2.35	0.56
1:A:185:MET:O	1:A:185:MET:HG3	2.02	0.55
1:B:58:ASP:HB3	1:B:61:ASP:HB2	1.89	0.55
1:A:80:ASN:HB2	1:A:81:ALA:CB	2.37	0.54
1:A:284:THR:HG22	1:A:285:LEU:N	2.22	0.54
1:A:138:GLU:O	1:A:142:ASP:OD1	2.25	0.54
1:A:214:LEU:O	1:A:215:SER:HB2	2.08	0.54
1:A:141:ARG:CZ	1:A:147:MET:HE2	2.36	0.54
1:A:117:ILE:N	1:A:131:ASP:OD1	2.41	0.54
1:A:249:LEU:O	1:A:250:GLY:C	2.46	0.54
1:A:196:VAL:HG21	1:A:214:LEU:HD21	1.89	0.54
1:B:174:TYR:HB2	1:B:236:VAL:HG22	1.90	0.54
1:A:117:ILE:CG2	1:A:125:LEU:HD12	2.39	0.53
1:A:180:THR:CG2	1:A:221:ALA:HB3	2.37	0.53
1:B:80:ASN:HA	1:B:82:TRP:HB3	1.90	0.53
1:B:81:ALA:HA	1:B:82:TRP:HB3	1.89	0.53
1:A:153:PRO:HG2	1:A:188:MET:HG2	1.90	0.53
1:A:241:MET:HA	1:A:241:MET:CE	2.39	0.53
1:B:121:THR:HG21	1:B:125:LEU:H	1.74	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:219:HIS:HB3	1:A:223:GLU:HB2	1.90	0.53
1:A:150:VAL:HB	1:A:214:LEU:HD11	1.90	0.52
1:B:121:THR:HG23	1:B:123:GLY:H	1.74	0.52
1:A:180:THR:OG1	1:A:183:VAL:O	2.27	0.52
1:A:183:VAL:HG11	1:A:265:ALA:HA	1.91	0.52
1:A:83:GLU:CG	1:A:84:SER:N	2.70	0.51
1:A:184:PRO:HB3	1:A:218:ARG:O	2.11	0.51
1:B:238:ASP:HB3	1:B:240:LYS:HE2	1.93	0.51
1:A:137:GLU:C	1:A:139:TYR:H	2.14	0.51
1:A:192:ASP:O	1:A:195:PRO:HD2	2.10	0.51
1:A:58:ASP:C	1:A:60:ASP:H	2.12	0.50
1:A:139:TYR:CA	1:A:142:ASP:HB2	2.29	0.49
1:B:117:ILE:O	1:B:121:THR:HG22	2.12	0.49
1:B:111:TYR:O	1:B:149:SER:HA	2.12	0.49
1:A:80:ASN:HB2	1:A:83:GLU:HG3	1.93	0.49
1:A:80:ASN:CB	1:A:81:ALA:HB2	2.40	0.49
1:B:289:LEU:O	1:B:293:LYS:HB3	2.13	0.49
1:A:59:GLN:HA	1:A:65:MET:SD	2.53	0.49
1:A:80:ASN:CB	1:A:81:ALA:HB3	2.43	0.49
1:A:87:GLN:CG	1:A:128:ALA:HB1	2.43	0.48
1:A:113:GLY:HA2	1:A:133:LYS:HD2	1.94	0.48
1:A:180:THR:HG23	1:A:181:GLY:CA	2.42	0.48
1:A:87:GLN:HG3	1:A:128:ALA:HB1	1.94	0.48
1:A:251:PHE:CB	1:A:252:PRO:CD	2.86	0.47
1:B:198:LEU:O	1:B:202:LYS:HG2	2.14	0.47
1:B:80:ASN:HA	1:B:82:TRP:CB	2.44	0.47
1:B:249:LEU:HB3	1:B:251:PHE:HD2	1.79	0.47
1:A:13:THR:HG23	1:A:43:ALA:HB3	1.95	0.47
1:A:114:LEU:HB3	1:A:130:PHE:CD2	2.49	0.47
1:A:271:ASP:OD2	1:A:274:LEU:HB2	2.14	0.47
1:B:247:GLU:HA	1:B:254:ALA:HB1	1.97	0.46
1:B:92:LYS:HA	1:B:95:LYS:HB2	1.97	0.46
1:A:285:LEU:O	1:A:285:LEU:CD2	2.59	0.46
1:A:61:ASP:HB3	1:A:64:ILE:HB	1.98	0.46
1:A:25:LEU:HG	1:A:32:VAL:HG11	1.97	0.46
1:A:273:GLU:H	1:A:273:GLU:HG2	1.51	0.45
1:B:241:MET:HG2	1:B:246:TYR:HE1	1.82	0.45
1:A:152:LEU:HD22	1:A:214:LEU:HD12	1.98	0.45
1:A:139:TYR:O	1:A:143:ILE:HG12	2.17	0.45
1:A:203:MET:HA	1:A:205:GLU:OE2	2.17	0.45
1:A:117:ILE:O	1:A:121:THR:HG22	2.16	0.45
1:A:58:ASP:C	1:A:60:ASP:N	2.65	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:58:ASP:O	1:A:59:GLN:C	2.55	0.44
1:A:10:PHE:HB2	1:A:77:ILE:HA	2.00	0.44
1:B:79:THR:O	1:B:80:ASN:C	2.55	0.44
1:A:228:LEU:O	1:A:232:THR:HB	2.18	0.44
1:A:139:TYR:O	1:A:143:ILE:HG23	2.17	0.44
1:A:186:ASP:OD1	1:A:218:ARG:HG3	2.17	0.44
1:A:221:ALA:HA	1:A:224:TYR:HB2	2.00	0.44
1:A:285:LEU:HD22	1:A:289:LEU:HG	2.00	0.44
1:B:121:THR:HG23	1:B:124:ARG:H	1.83	0.44
1:A:126:ALA:O	1:A:127:ALA:CB	2.60	0.43
1:A:189:SER:C	1:A:191:SER:N	2.69	0.43
1:A:79:THR:O	1:A:80:ASN:O	2.36	0.43
1:B:151:ARG:HB2	1:B:213:GLY:HA2	1.99	0.43
1:A:216:THR:HA	1:A:272:ILE:HG23	1.99	0.43
1:A:285:LEU:HD22	1:A:285:LEU:C	2.40	0.43
1:A:193:LEU:O	1:A:197:VAL:HG23	2.19	0.42
1:A:151:ARG:CZ	1:A:211:ASN:HD22	2.32	0.42
1:B:140:PHE:HD1	1:B:145:VAL:HB	1.84	0.42
1:A:200:LEU:O	1:A:202:LYS:N	2.51	0.42
1:A:35:VAL:HG11	1:A:65:MET:HE1	2.00	0.42
1:A:79:THR:C	1:A:90:GLU:OE2	2.56	0.42
1:B:220:THR:HG22	1:B:221:ALA:N	2.34	0.42
1:A:6:LEU:HB3	1:A:72:ALA:HA	2.00	0.42
1:A:80:ASN:HD21	1:A:84:SER:HB2	1.78	0.42
1:B:221:ALA:HA	1:B:224:TYR:HB2	2.02	0.42
1:A:61:ASP:CG	1:A:64:ILE:HG12	2.40	0.41
1:A:251:PHE:CD2	1:A:251:PHE:N	2.88	0.41
1:A:290:GLU:HA	1:A:293:LYS:HE3	2.03	0.41
1:A:38:ASN:HA	1:A:39:PRO:HD3	1.51	0.41
1:B:116:ASN:C	1:B:116:ASN:HD22	2.23	0.41
1:B:178:LEU:HD22	1:B:185:MET:HE1	2.03	0.41
1:A:84:SER:CB	1:A:85:CYS:O	2.63	0.41
1:A:155:TYR:CD2	1:A:155:TYR:N	2.89	0.40
1:A:241:MET:HE2	1:A:241:MET:HA	2.04	0.40
1:A:56:GLN:HG2	1:A:57:GLY:N	2.33	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	292/299 (98%)	261 (89%)	23 (8%)	8 (3%)	7	18
1	B	293/299 (98%)	272 (93%)	20 (7%)	1 (0%)	49	80
All	All	585/598 (98%)	533 (91%)	43 (7%)	9 (2%)	15	36

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	ALA
1	A	182	ASP
1	A	201	LEU
1	A	250	GLY
1	B	80	ASN
1	A	137	GLU
1	A	138	GLU
1	A	80	ASN
1	A	57	GLY

### 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	245/250 (98%)	197 (80%)	48 (20%)	2	5
1	B	246/250 (98%)	219 (89%)	27 (11%)	9	20
All	All	491/500 (98%)	416 (85%)	75 (15%)	4	10

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	29	THR
1	A	42	LYS
1	A	56	GLN
1	A	58	ASP
1	A	60	ASP
1	A	65	MET
1	A	67	LEU
1	A	69	LEU
1	A	80	ASN
1	A	85	CYS
1	A	87	GLN
1	A	91	VAL
1	A	96	LEU
1	A	97	LEU
1	A	100	LEU
1	A	114	LEU
1	A	116	ASN
1	A	125	LEU
1	A	141	ARG
1	A	147	MET
1	A	152	LEU
1	A	155	TYR
1	A	170	ASP
1	A	172	LYS
1	A	175	LEU
1	A	178	LEU
1	A	183	VAL
1	A	185	MET
1	A	186	ASP
1	A	200	LEU
1	A	201	LEU
1	A	202	LYS
1	A	205	GLU
1	A	208	VAL
1	A	218	ARG
1	A	223	GLU
1	A	233	ARG
1	A	234	LYS
1	A	241	MET
1	A	248	LYS
1	A	249	LEU
1	A	257	LEU

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Mol	Chain	Res	Type
1	A	273	GLU
1	A	274	LEU
1	A	285	LEU
1	A	290	GLU
1	A	293	LYS
1	B	4	LYS
1	B	13	THR
1	B	27	ASP
1	B	32	VAL
1	B	65	MET
1	B	67	LEU
1	B	69	LEU
1	B	92	LYS
1	B	96	LEU
1	B	100	LEU
1	B	115	GLU
1	B	116	ASN
1	B	120	LEU
1	B	141	ARG
1	B	147	MET
1	B	175	LEU
1	B	196	VAL
1	B	200	LEU
1	B	201	LEU
1	B	202	LYS
1	B	208	VAL
1	B	216	THR
1	B	233	ARG
1	B	257	LEU
1	B	273	GLU
1	B	274	LEU
1	B	285	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	80	ASN
1	A	87	GLN
1	A	93	GLN
1	A	116	ASN
1	A	259	ASN

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Mol	Chain	Res	Type
1	B	16	GLN
1	B	87	GLN
1	B	93	GLN
1	B	116	ASN
1	B	210	GLN
1	B	259	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

### 5.5 Carbohydrates ⓘ

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 ⓘ

### 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	294/299 (98%)	0.27	10 (3%) 42 48	2, 15, 31, 40	0
1	B	295/299 (98%)	0.51	21 (7%) 15 16	2, 17, 37, 45	0
All	All	589/598 (98%)	0.39	31 (5%) 25 27	2, 16, 34, 45	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	84	SER	5.4
1	B	38	ASN	4.2
1	B	80	ASN	3.8
1	A	82	TRP	3.4
1	B	67	LEU	3.3
1	B	79	THR	3.2
1	B	81	ALA	3.2
1	B	63	VAL	3.1
1	A	57	GLY	3.0
1	B	106	LEU	3.0
1	A	85	CYS	3.0
1	B	40	ARG	2.9
1	B	82	TRP	2.8
1	A	83	GLU	2.8
1	B	51	GLY	2.8
1	B	55	VAL	2.6
1	B	36	THR	2.6
1	B	85	CYS	2.5
1	B	84	SER	2.5
1	B	64	ILE	2.5
1	A	86	SER	2.4
1	A	81	ALA	2.4
1	B	184	PRO	2.2
1	B	45	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	37	ARG	2.2
1	B	98	ALA	2.1
1	B	246	TYR	2.1
1	B	30	PHE	2.1
1	A	138	GLU	2.0
1	A	122	ALA	2.0
1	B	221	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.