



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:15 PM GMT

PDB ID : 1WR6  
Title : Crystal structure of GGA3 GAT domain in complex with ubiquitin  
Authors : Kawasaki, M.; Shiba, T.; Shiba, Y.; Yamaguchi, Y.; Matsugaki, N.; Igarashi, N.; Suzuki, M.; Kato, R.; Kato, K.; Nakayama, K.; Wakatsuki, S.  
Deposited on : 2004-10-12  
Resolution : 2.60 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

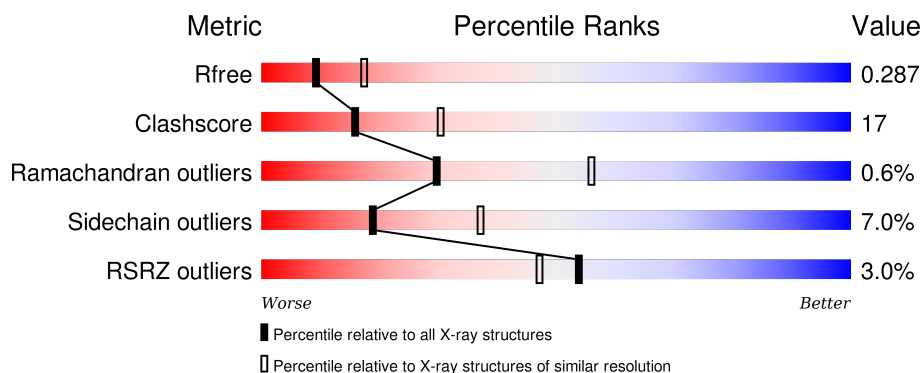
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	111	<div> <div>10%</div> <div> <div>53%</div> <div>28%</div> <div>19%</div> </div> </div>
1	B	111	<div> <div>55%</div> <div>20%</div> <div>5%</div> <div>19%</div> </div>
1	C	111	<div> <div>58%</div> <div>21%</div> <div>19%</div> </div>
1	D	111	<div> <div>5%</div> <div>52%</div> <div>22%</div> <div>5%</div> <div>21%</div> </div>
2	E	76	<div> <div>57%</div> <div>33%</div> <div>5%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	76	<div> <div> <div></div> <div>3%</div> </div> <div> <div></div> <div>45%</div> </div> <div> <div></div> <div>47%</div> </div> <div> <div></div> <div>•</div> </div> <div> <div></div> <div>•</div> </div> </div>
2	G	76	<div> <div></div> <div>70%</div> </div> <div> <div></div> <div>24%</div> </div> <div> <div></div> <div>•</div> </div> <div> <div></div> <div>5%</div> </div>
2	H	76	<div> <div></div> <div>62%</div> </div> <div> <div></div> <div>34%</div> </div> <div> <div></div> <div>•</div> </div> <div> <div></div> <div>•</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5327 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 ADP-ribosylation factor binding protein GGA3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	90	Total	C	N	O	S	Se	0	0	0
			728	442	129	154	1	2			
1	B	90	Total	C	N	O	S	Se	0	0	0
			721	438	126	154	1	2			
1	C	90	Total	C	N	O	S	Se	0	0	0
			728	442	129	154	1	2			
1	D	88	Total	C	N	O	S	Se	0	0	0
			709	432	123	151	1	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	231	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
A	248	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
B	231	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
B	248	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
C	231	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
C	248	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
D	231	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52
D	248	MSE	MET	MODIFIED RESIDUE	UNP Q9NZ52

- Molecule 2 is a protein called ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	72	Total	C	N	O	S	0	0	0
			574	362	98	113	1			
2	F	73	Total	C	N	O	S	0	0	0
			582	368	99	114	1			
2	G	72	Total	C	N	O	S	0	0	0
			574	362	98	113	1			
2	H	74	Total	C	N	O	S	0	0	0
			593	374	103	115	1			

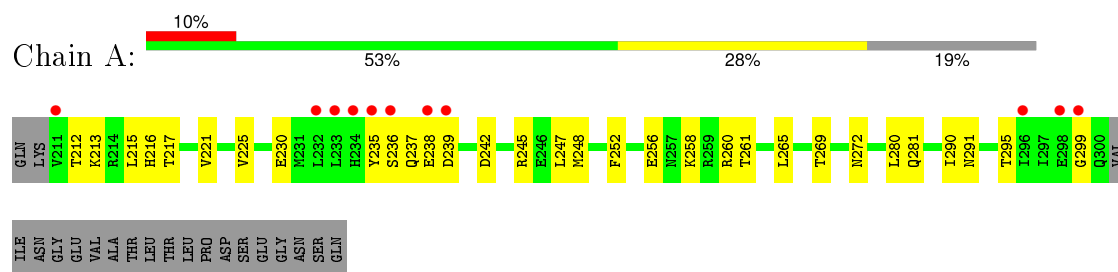
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	9	Total O 9 9	0	0
3	B	20	Total O 20 20	0	0
3	C	19	Total O 19 19	0	0
3	D	21	Total O 21 21	0	0
3	E	7	Total O 7 7	0	0
3	F	8	Total O 8 8	0	0
3	G	20	Total O 20 20	0	0
3	H	14	Total O 14 14	0	0

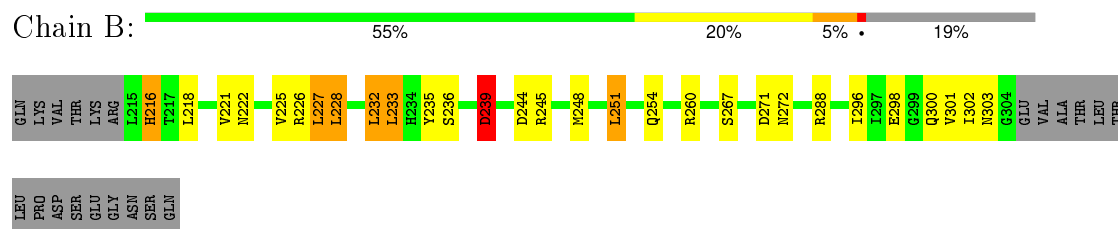
### 3 Residue-property plots

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.

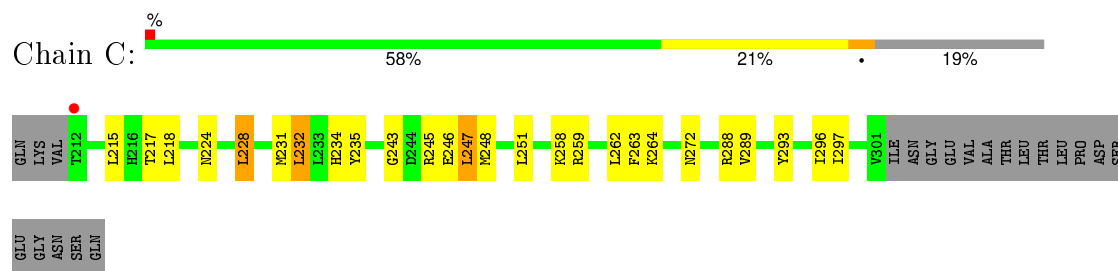
- Molecule 1: ADP-ribosylation factor binding protein GGA3



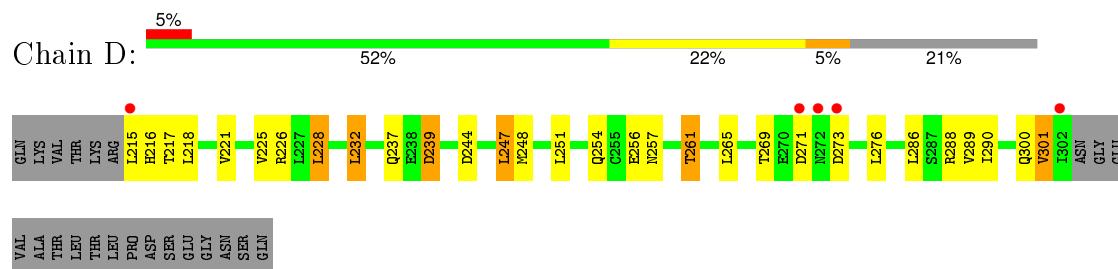
- Molecule 1: ADP-ribosylation factor binding protein GGA3



- Molecule 1: ADP-ribosylation factor binding protein GGA3



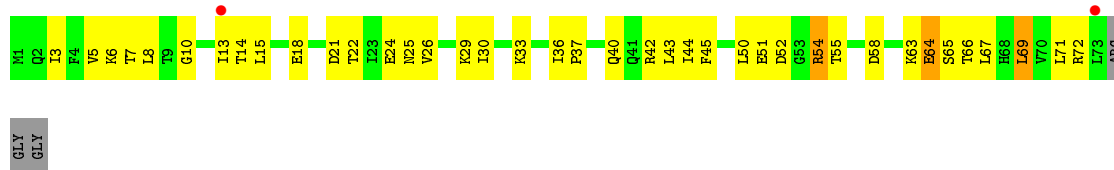
- Molecule 1: ADP-ribosylation factor binding protein GGA3



## ● Molecule 2: ubiquitin

Chain E:  57% 33% 5% 5%

## ● Molecule 2: ubiquitin

Chain F:  3% 45% 47% . .

## ● Molecule 2: ubiquitin

Chain G:  70% 24% . 5%

## ● Molecule 2: ubiquitin

Chain H:  62% 34% . .

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.03 Å 113.63 Å 114.70 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.60 46.03 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.5 (40.00-2.60) 94.5 (46.03-2.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.70 (at 2.61 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.221 , 0.290 0.218 , 0.287	Depositor DCC
$R_{free}$ test set	1105 reflections (5.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.5	Xtriage
Anisotropy	0.412	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.4	EDS
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 21951 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5327	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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](#)

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	0.35	0/731	0.51	0/978
1	B	0.42	0/724	0.55	0/970
1	C	0.41	0/731	0.58	0/978
1	D	0.41	0/712	0.62	0/954
2	E	0.35	0/580	0.54	0/781
2	F	0.34	0/588	0.54	0/792
2	G	0.39	0/580	0.66	0/781
2	H	0.43	0/599	0.71	1/806 (0.1%)
All	All	0.39	0/5245	0.59	1/7040 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	15	LEU	CA-CB-CG	5.09	127.01	115.30

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	728	0	709	26	0
1	B	721	0	696	25	0
1	C	728	0	709	24	0
1	D	709	0	687	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	574	0	599	22	0
2	F	582	0	610	45	0
2	G	574	0	599	14	0
2	H	593	0	623	17	0
3	A	9	0	0	0	0
3	B	20	0	0	1	0
3	C	19	0	0	0	0
3	D	21	0	0	1	0
3	E	7	0	0	0	0
3	F	8	0	0	0	0
3	G	20	0	0	1	0
3	H	14	0	0	0	0
All	All	5327	0	5232	177	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 17.

All (177) 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:F:22:THR:H	2:F:25:ASN:HD22	1.03	0.97
2:F:71:LEU:HD22	2:F:71:LEU:H	1.43	0.81
1:B:233:LEU:HD22	1:C:218:LEU:HG	1.61	0.80
1:A:247:LEU:HD13	2:E:42:ARG:HG2	1.66	0.77
2:E:24:GLU:HB2	2:E:52:ASP:HB3	1.65	0.77
1:A:212:THR:HG22	1:A:213:LYS:H	1.51	0.76
2:F:24:GLU:HG2	2:F:52:ASP:HB3	1.67	0.75
2:F:36:ILE:HD12	2:F:37:PRO:HD2	1.69	0.75
2:F:5:VAL:HG23	2:F:13:ILE:HG13	1.68	0.74
1:D:228:LEU:HD22	1:D:232:LEU:HD22	1.69	0.73
2:F:63:LYS:HB3	2:F:63:LYS:NZ	2.03	0.72
2:E:23:ILE:HB	2:E:52:ASP:HA	1.70	0.72
1:D:221:VAL:O	1:D:225:VAL:HG23	1.90	0.71
2:F:44:ILE:HD12	2:F:44:ILE:N	2.07	0.70
1:A:272:ASN:HD21	1:B:300:GLN:HE22	1.38	0.70
2:F:25:ASN:O	2:F:29:LYS:HG3	1.91	0.69
2:H:61:ILE:HD13	2:H:67:LEU:HD21	1.75	0.69
1:C:247:LEU:HG	2:G:49:GLN:HE21	1.59	0.67
2:F:36:ILE:HD11	2:F:40:GLN:HG3	1.76	0.67
1:C:231:MSE:HE1	1:C:251:LEU:HD23	1.76	0.67
2:E:22:THR:HG22	2:E:55:THR:HG22	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:61:ILE:HD13	2:G:67:LEU:HD21	1.76	0.67
1:A:252:PHE:CE1	1:A:290:ILE:HG23	2.30	0.67
1:A:215:LEU:HD12	1:A:265:LEU:HD21	1.75	0.66
2:F:22:THR:N	2:F:25:ASN:HD22	1.86	0.66
1:C:231:MSE:HE1	1:C:251:LEU:CD2	2.26	0.65
2:F:22:THR:H	2:F:25:ASN:ND2	1.87	0.65
1:B:236:SER:OG	1:B:239:ASP:HB2	1.97	0.64
1:D:226:ARG:HG2	3:D:10:HOH:O	1.98	0.64
1:D:254:GLN:HA	1:D:254:GLN:HE21	1.63	0.64
2:F:5:VAL:HB	2:F:69:LEU:HD11	1.81	0.63
2:G:22:THR:HA	2:G:55:THR:HA	1.79	0.63
2:G:42:ARG:HH21	2:G:72:ARG:HG2	1.63	0.62
2:F:14:THR:C	2:F:15:LEU:HD12	2.20	0.62
2:F:5:VAL:CG2	2:F:13:ILE:HG13	2.29	0.61
1:B:235:TYR:HD2	1:B:248:MSE:HE1	1.65	0.61
2:H:7:THR:OG1	2:H:11:LYS:HB3	2.00	0.61
2:G:25:ASN:ND2	2:G:29:LYS:HE2	2.15	0.61
2:E:62:GLN:HA	2:E:62:GLN:HE21	1.65	0.61
1:A:213:LYS:CE	1:A:261:THR:HG22	2.31	0.61
1:A:272:ASN:ND2	1:B:300:GLN:HE22	1.99	0.61
2:F:14:THR:O	2:F:15:LEU:HD12	1.99	0.60
2:E:4:PHE:HD2	2:E:14:THR:HG22	1.66	0.60
1:D:288:ARG:HH11	1:D:288:ARG:HG2	1.67	0.60
2:E:25:ASN:O	2:E:29:LYS:HG3	2.01	0.60
2:F:63:LYS:HB3	2:F:63:LYS:HZ2	1.65	0.60
2:F:40:GLN:O	2:F:71:LEU:HA	2.01	0.60
2:H:14:THR:O	2:H:33:LYS:HE3	2.01	0.60
1:A:269:THR:O	1:B:260:ARG:HD3	2.01	0.59
1:B:228:LEU:HD22	1:B:232:LEU:HD22	1.84	0.59
1:B:288:ARG:NH2	1:C:264:LYS:HD2	2.17	0.59
2:E:54:ARG:HG3	2:E:59:TYR:OH	2.03	0.58
2:F:5:VAL:HB	2:F:69:LEU:CD1	2.33	0.58
1:A:291:ASN:O	1:A:295:THR:HG22	2.04	0.57
1:A:213:LYS:HE3	1:A:261:THR:HG22	1.85	0.57
1:D:254:GLN:HA	1:D:254:GLN:NE2	2.19	0.57
2:H:26:VAL:HG21	2:H:56:LEU:HD21	1.87	0.56
2:F:71:LEU:HD22	2:F:71:LEU:N	2.17	0.56
1:B:301:VAL:O	1:B:301:VAL:HG23	2.05	0.56
2:F:71:LEU:CD2	2:F:71:LEU:H	2.14	0.55
1:C:234:HIS:HD2	3:G:81:HOH:O	1.90	0.55
1:B:222:ASN:O	1:B:226:ARG:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:LEU:HD22	1:C:232:LEU:HD22	1.89	0.54
2:F:51:GLU:CB	2:F:54:ARG:HH11	2.20	0.54
2:F:33:LYS:O	2:F:33:LYS:HG2	2.07	0.54
2:F:26:VAL:O	2:F:30:ILE:HG13	2.07	0.53
1:C:247:LEU:HD13	2:G:44:ILE:HD11	1.89	0.53
1:C:224:ASN:HD22	1:C:258:LYS:HD2	1.73	0.53
2:H:42:ARG:HH21	2:H:72:ARG:HA	1.72	0.53
2:E:4:PHE:CD2	2:E:14:THR:HG22	2.44	0.53
2:H:23:ILE:HG12	2:H:54:ARG:O	2.09	0.52
2:H:63:LYS:O	2:H:64:GLU:HB2	2.10	0.52
1:B:271:ASP:O	1:B:272:ASN:HB2	2.08	0.52
2:F:5:VAL:HG12	2:F:67:LEU:HB2	1.91	0.52
2:F:43:LEU:HD23	2:F:69:LEU:HB3	1.91	0.52
2:E:62:GLN:CA	2:E:62:GLN:HE21	2.23	0.52
1:C:293:TYR:CE1	1:C:297:ILE:HG13	2.44	0.51
2:F:6:LYS:HD2	2:F:10:GLY:HA2	1.92	0.51
1:A:256:GLU:HG2	1:B:271:ASP:OD2	2.11	0.51
1:A:252:PHE:HE1	1:A:290:ILE:HG23	1.76	0.51
1:D:254:GLN:CA	1:D:254:GLN:HE21	2.22	0.51
2:E:5:VAL:HB	2:E:13:ILE:HG13	1.91	0.51
2:G:54:ARG:HB2	2:G:59:TYR:CE1	2.46	0.50
2:F:63:LYS:HG2	2:F:64:GLU:N	2.27	0.50
2:G:54:ARG:HB2	2:G:59:TYR:HE1	1.76	0.50
2:F:45:PHE:HB3	2:F:50:LEU:HD21	1.93	0.50
1:C:245:ARG:HA	1:C:248:MSE:HE3	1.93	0.50
1:A:245:ARG:HA	1:A:248:MSE:HE3	1.94	0.50
2:F:69:LEU:N	2:F:69:LEU:HD13	2.26	0.50
2:H:23:ILE:HG22	2:H:27:LYS:HE3	1.94	0.49
1:D:301:VAL:O	1:D:301:VAL:HG13	2.12	0.49
1:A:216:HIS:CD2	1:A:258:LYS:HG2	2.47	0.49
2:E:49:GLN:HG2	2:E:50:LEU:N	2.28	0.49
1:B:296:ILE:HD13	1:C:217:THR:CG2	2.43	0.49
1:A:221:VAL:O	1:A:225:VAL:HG23	2.12	0.49
2:F:63:LYS:HG2	2:F:64:GLU:OE1	2.13	0.48
2:F:36:ILE:HD12	2:F:37:PRO:CD	2.40	0.48
1:A:215:LEU:HD23	1:A:216:HIS:N	2.29	0.48
2:G:29:LYS:O	2:G:32:ASP:HB2	2.14	0.48
2:F:5:VAL:HA	2:F:67:LEU:O	2.14	0.48
1:A:260:ARG:HG2	1:B:267:SER:O	2.13	0.48
2:F:55:THR:O	2:F:58:ASP:HB2	2.14	0.48
1:B:228:LEU:O	1:B:232:LEU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:272:ASN:HB2	2:F:65:SER:HA	1.96	0.47
2:H:43:LEU:O	2:H:49:GLN:HA	2.13	0.47
1:D:257:ASN:O	1:D:261:THR:HG23	2.14	0.47
1:B:221:VAL:O	1:B:225:VAL:HG23	2.13	0.47
1:A:238:GLU:H	1:A:238:GLU:CD	2.17	0.47
1:D:269:THR:HG21	1:D:276:LEU:HB2	1.96	0.47
1:C:243:GLY:O	1:C:246:GLU:HG2	2.14	0.47
1:C:247:LEU:O	1:C:251:LEU:HD23	2.15	0.47
2:F:42:ARG:O	2:F:69:LEU:HA	2.14	0.47
1:C:235:TYR:CD1	1:C:248:MSE:HE1	2.49	0.47
2:E:1:MET:HG2	2:E:17:VAL:O	2.14	0.47
2:F:6:LYS:N	2:F:67:LEU:O	2.45	0.47
1:C:247:LEU:HD22	1:C:251:LEU:CD2	2.45	0.47
1:D:288:ARG:NH1	1:D:288:ARG:HG2	2.30	0.47
1:B:222:ASN:HD21	1:B:226:ARG:HD2	1.81	0.46
1:A:245:ARG:HG3	1:A:245:ARG:HH11	1.80	0.46
2:F:18:GLU:HB2	2:F:21:ASP:OD2	2.16	0.46
2:E:39:ASP:N	2:E:39:ASP:OD2	2.48	0.46
2:F:40:GLN:HA	2:F:72:ARG:HB3	1.98	0.46
1:C:228:LEU:HD13	1:C:289:VAL:HG22	1.98	0.46
1:D:247:LEU:HD11	2:H:44:ILE:HD11	1.98	0.46
1:B:298:GLU:HG2	3:B:116:HOH:O	2.15	0.46
2:H:5:VAL:HB	2:H:13:ILE:CG1	2.46	0.46
2:E:41:GLN:O	2:E:42:ARG:HD3	2.15	0.45
1:C:247:LEU:CD1	2:G:44:ILE:HD11	2.46	0.45
2:G:41:GLN:O	2:G:42:ARG:HG3	2.17	0.45
1:D:239:ASP:OD2	1:D:239:ASP:N	2.50	0.45
1:A:235:TYR:CD2	1:A:248:MSE:HE1	2.51	0.45
1:D:216:HIS:C	1:D:218:LEU:H	2.20	0.45
1:C:215:LEU:HD12	1:C:215:LEU:C	2.37	0.45
2:F:42:ARG:NH2	2:F:72:ARG:HA	2.31	0.45
1:B:235:TYR:OH	1:B:245:ARG:NH1	2.50	0.45
1:A:217:THR:O	1:A:221:VAL:HG23	2.17	0.45
1:D:256:GLU:HG2	1:D:290:ILE:HD13	1.99	0.45
1:D:300:GLN:O	1:D:301:VAL:C	2.56	0.45
1:A:272:ASN:HD21	1:B:300:GLN:NE2	2.11	0.45
2:H:44:ILE:N	2:H:44:ILE:HD12	2.32	0.45
1:B:216:HIS:C	1:B:218:LEU:H	2.19	0.45
1:C:247:LEU:HD12	2:G:49:GLN:HG3	2.00	0.44
1:B:227:LEU:HD13	1:B:251:LEU:HD21	2.00	0.44
1:B:244:ASP:HB3	1:B:248:MSE:HE2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:54:ARG:HB2	2:E:59:TYR:CE1	2.52	0.44
2:E:40:GLN:HA	2:E:72:ARG:CD	2.47	0.44
2:H:37:PRO:HA	2:H:38:PRO:HD3	1.94	0.44
2:H:42:ARG:HB2	2:H:70:VAL:O	2.18	0.43
1:A:213:LYS:HE2	1:A:261:THR:HG22	1.99	0.43
2:F:44:ILE:HD12	2:F:44:ILE:H	1.81	0.43
2:E:4:PHE:O	2:E:66:THR:HA	2.18	0.43
2:E:40:GLN:HA	2:E:72:ARG:HD3	2.00	0.43
1:D:225:VAL:HG22	1:D:286:LEU:HD23	2.00	0.43
2:E:49:GLN:HG2	2:E:50:LEU:H	1.82	0.43
1:C:243:GLY:HA2	1:C:246:GLU:OE2	2.19	0.43
2:E:26:VAL:HG21	2:E:56:LEU:HD21	2.00	0.43
1:A:212:THR:HG22	1:A:213:LYS:N	2.27	0.42
2:H:56:LEU:HB3	2:H:61:ILE:HB	2.01	0.42
2:F:3:ILE:HG13	2:F:3:ILE:O	2.19	0.42
1:C:232:LEU:HG	1:C:296:ILE:HD12	2.02	0.42
2:F:7:THR:HG22	2:F:8:LEU:N	2.35	0.42
2:E:19:PRO:O	2:E:57:SER:HB2	2.20	0.41
1:D:215:LEU:C	1:D:217:THR:H	2.22	0.41
1:D:244:ASP:HB3	1:D:248:MSE:HE3	2.03	0.41
1:B:235:TYR:CD2	1:B:248:MSE:HE1	2.52	0.41
1:B:254:GLN:HA	1:B:254:GLN:OE1	2.21	0.41
2:H:63:LYS:O	2:H:64:GLU:CB	2.67	0.41
2:H:63:LYS:O	2:H:63:LYS:HG3	2.20	0.41
1:C:259:ARG:HG2	1:C:263:PHE:CE1	2.56	0.41
1:A:215:LEU:C	1:A:215:LEU:HD23	2.41	0.41
2:F:51:GLU:HB2	2:F:54:ARG:HH11	1.86	0.40
2:G:37:PRO:HA	2:G:38:PRO:HD3	1.89	0.40
2:G:1:MET:HB2	2:G:63:LYS:HB3	2.02	0.40
1:D:271:ASP:C	1:D:273:ASP:N	2.74	0.40
1:A:236:SER:HB3	1:A:239:ASP:HB2	2.02	0.40
2:F:44:ILE:CD1	2:F:44:ILE:N	2.77	0.40
2:F:7:THR:HG22	2:F:8:LEU:H	1.86	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	88/111 (79%)	79 (90%)	8 (9%)	1 (1%)	17	36
1	B	88/111 (79%)	82 (93%)	4 (4%)	2 (2%)	8	14
1	C	88/111 (79%)	88 (100%)	0	0	100	100
1	D	86/111 (78%)	78 (91%)	7 (8%)	1 (1%)	16	33
2	E	70/76 (92%)	69 (99%)	1 (1%)	0	100	100
2	F	71/76 (93%)	66 (93%)	5 (7%)	0	100	100
2	G	70/76 (92%)	67 (96%)	3 (4%)	0	100	100
2	H	72/76 (95%)	68 (94%)	4 (6%)	0	100	100
All	All	633/748 (85%)	597 (94%)	32 (5%)	4 (1%)	30	56

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	301	VAL
1	B	303	ASN
1	A	299	GLY
1	B	239	ASP

### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	85/101 (84%)	80 (94%)	5 (6%)	24	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	84/101 (83%)	76 (90%)	8 (10%)	11	20
1	C	85/101 (84%)	80 (94%)	5 (6%)	24	47
1	D	83/101 (82%)	74 (89%)	9 (11%)	8	15
2	E	66/68 (97%)	61 (92%)	5 (8%)	16	32
2	F	67/68 (98%)	63 (94%)	4 (6%)	24	47
2	G	66/68 (97%)	64 (97%)	2 (3%)	48	76
2	H	68/68 (100%)	64 (94%)	4 (6%)	24	47
All	All	604/676 (89%)	562 (93%)	42 (7%)	19	37

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	GLU
1	A	237	GLN
1	A	242	ASP
1	A	280	LEU
1	A	281	GLN
1	B	216	HIS
1	B	227	LEU
1	B	228	LEU
1	B	232	LEU
1	B	233	LEU
1	B	239	ASP
1	B	251	LEU
1	B	302	ILE
1	C	228	LEU
1	C	232	LEU
1	C	247	LEU
1	C	262	LEU
1	C	288	ARG
1	D	228	LEU
1	D	232	LEU
1	D	237	GLN
1	D	239	ASP
1	D	247	LEU
1	D	251	LEU
1	D	261	THR
1	D	265	LEU
1	D	289	VAL
2	E	16	GLU

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Mol	Chain	Res	Type
2	E	25	ASN
2	E	39	ASP
2	E	54	ARG
2	E	62	GLN
2	F	54	ARG
2	F	64	GLU
2	F	66	THR
2	F	69	LEU
2	G	63	LYS
2	G	64	GLU
2	H	15	LEU
2	H	34	GLU
2	H	39	ASP
2	H	71	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	224	ASN
1	A	285	ASN
1	A	291	ASN
1	B	222	ASN
1	B	223	ASN
1	B	237	GLN
1	B	285	ASN
1	B	291	ASN
1	B	300	GLN
1	C	222	ASN
1	C	224	ASN
1	C	291	ASN
1	D	234	HIS
1	D	237	GLN
1	D	254	GLN
1	D	272	ASN
1	D	285	ASN
1	D	300	GLN
2	E	2	GLN
2	E	25	ASN
2	E	40	GLN
2	E	60	ASN
2	E	62	GLN
2	F	25	ASN

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Mol	Chain	Res	Type
2	F	40	GLN
2	F	49	GLN
2	F	60	ASN
2	F	62	GLN
2	G	25	ASN
2	G	40	GLN
2	G	49	GLN
2	H	62	GLN
2	H	68	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](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	88/111 (79%)	0.59	11 (12%) 5 3	31, 61, 105, 108	0
1	B	88/111 (79%)	-0.33	0 100 100	27, 40, 80, 99	0
1	C	88/111 (79%)	-0.32	1 (1%) 82 79	23, 38, 65, 74	0
1	D	86/111 (77%)	0.03	5 (5%) 26 20	31, 44, 92, 101	0
2	E	72/76 (94%)	-0.06	0 100 100	48, 69, 78, 86	0
2	F	73/76 (96%)	0.11	2 (2%) 58 51	38, 68, 79, 86	0
2	G	72/76 (94%)	-0.39	0 100 100	28, 44, 59, 64	0
2	H	74/76 (97%)	-0.46	0 100 100	27, 38, 51, 57	0
All	All	641/748 (85%)	-0.10	19 (2%) 54 47	23, 47, 84, 108	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	302	ILE	7.4
1	D	272	ASN	3.9
1	A	235	TYR	3.7
1	A	211	VAL	3.7
1	D	271	ASP	3.5
1	A	239	ASP	2.9
1	D	273	ASP	2.9
1	A	299	GLY	2.9
1	A	234	HIS	2.8
1	A	238	GLU	2.7
1	A	232	LEU	2.7
1	A	233	LEU	2.6
2	F	73	LEU	2.5
1	A	296	ILE	2.5
1	C	212	THR	2.4
2	F	13	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	215	LEU	2.4
1	A	298	GLU	2.2
1	A	236	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.