



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 07:08 am GMT

PDB ID : 3M3V  
Title : SARS-CoV main protease triple mutant STI/A with two N-terminal additional residue (Gly-Ser)  
Authors : Shi, J.H.; Song, J.X.  
Deposited on : 2010-03-10  
Resolution : 2.70 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

<https://www.wwpdb.org/validation/2017/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) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

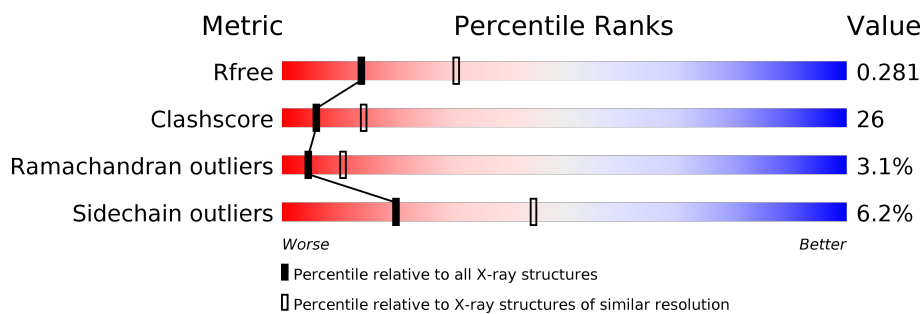
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (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. 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	308	
1	B	308	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4809 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 3C-like proteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2365	1495	405	443	22			
1	B	304	Total	C	N	O	S	0	0	0
			2343	1480	402	439	22			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P0C6U8
A	0	SER	-	EXPRESSION TAG	UNP P0C6U8
A	284	ALA	SER	ENGINEERED MUTATION	UNP P0C6U8
A	285	ALA	THR	ENGINEERED MUTATION	UNP P0C6U8
A	286	ALA	ILE	ENGINEERED MUTATION	UNP P0C6U8
B	-1	GLY	-	EXPRESSION TAG	UNP P0C6U8
B	0	SER	-	EXPRESSION TAG	UNP P0C6U8
B	284	ALA	SER	ENGINEERED MUTATION	UNP P0C6U8
B	285	ALA	THR	ENGINEERED MUTATION	UNP P0C6U8
B	286	ALA	ILE	ENGINEERED MUTATION	UNP P0C6U8

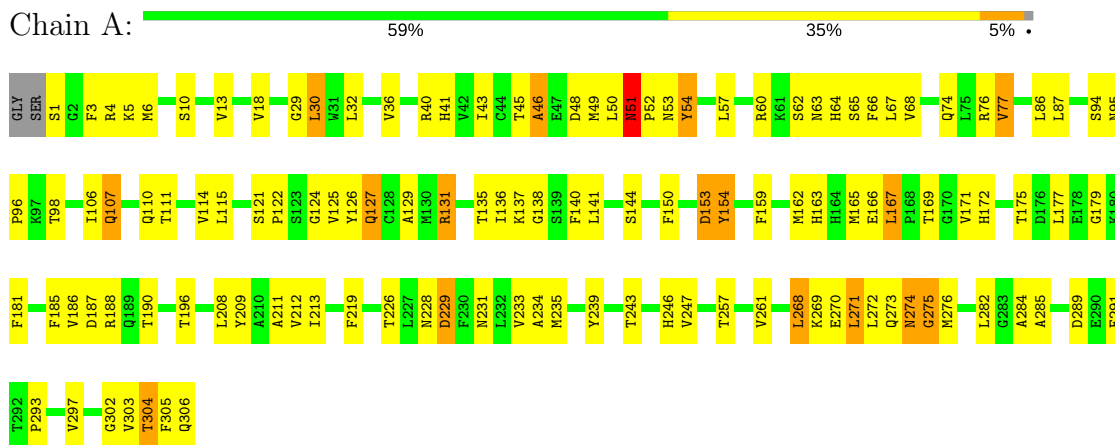
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	50	Total	O	0	0
			50	50		
2	B	51	Total	O	0	0
			51	51		

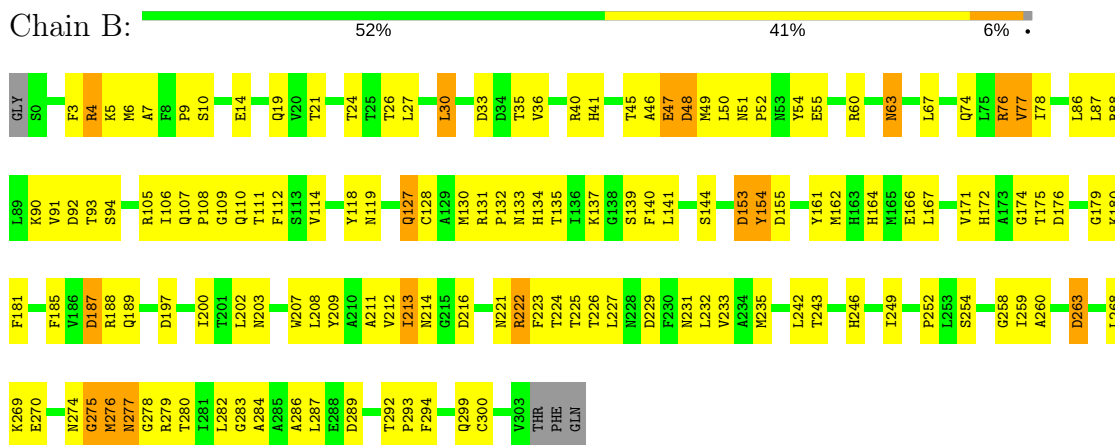
### 3 Residue-property plots [i](#)

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. 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. 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: 3C-like proteinase



- Molecule 1: 3C-like proteinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.23Å 96.52Å 67.69Å 90.00° 104.17° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 38.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	90.7 (20.00-2.70) 85.3 (38.88-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.14 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.201 , 0.274 0.212 , 0.281	Depositor DCC
$R_{free}$ test set	2828 reflections (7.76%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.6	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4809	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% 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	0.46	0/2418	0.72	0/3284
1	B	0.44	0/2395	0.67	0/3254
All	All	0.45	0/4813	0.70	0/6538

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	A	2365	0	2314	116	0
1	B	2343	0	2295	141	0
2	A	50	0	0	9	0
2	B	51	0	0	12	0
All	All	4809	0	4609	246	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 (246) 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:226:THR:HG22	1:A:228:ASN:H	1.24	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:PHE:HB2	2:B:311:HOH:O	1.64	0.95
1:B:63:ASN:HD22	1:B:63:ASN:H	0.99	0.94
1:B:63:ASN:HD22	1:B:63:ASN:N	1.64	0.94
1:B:41:HIS:HB2	1:B:49:MET:HE3	1.55	0.89
1:B:63:ASN:ND2	1:B:63:ASN:H	1.71	0.86
1:B:6:MET:O	1:B:127:GLN:HG3	1.80	0.82
1:B:226:THR:HG22	1:B:229:ASP:HB2	1.63	0.79
1:B:167:LEU:HD21	1:B:185:PHE:CE1	2.17	0.78
1:B:141:LEU:HD11	2:B:345:HOH:O	1.84	0.78
1:B:140:PHE:HB2	1:B:172:HIS:CE1	2.20	0.76
1:B:280:THR:HB	1:B:284:ALA:O	1.86	0.76
1:A:285:ALA:HB3	1:B:286:ALA:HB2	1.67	0.75
1:A:226:THR:HG22	1:A:228:ASN:N	1.99	0.75
1:A:57:LEU:HD23	1:A:60:ARG:HH21	1.51	0.75
1:A:303:VAL:HG12	1:A:304:THR:HG22	1.69	0.74
1:A:4:ARG:HB2	1:B:139:SER:HB2	1.70	0.74
1:B:131:ARG:HH22	1:B:289:ASP:CG	1.91	0.73
1:A:140:PHE:HB3	1:A:144:SER:OG	1.89	0.73
1:A:30:LEU:HD22	1:A:32:LEU:HG	1.70	0.72
1:A:219:PHE:HB2	1:A:271:LEU:HD21	1.71	0.72
1:B:127:GLN:HE21	1:B:128:CYS:N	1.90	0.70
1:B:33:ASP:O	1:B:94:SER:HA	1.93	0.69
1:A:234:ALA:HB1	1:A:239:TYR:HB2	1.72	0.69
1:A:169:THR:HB	1:A:171:VAL:HG12	1.75	0.68
1:B:52:PRO:HD2	1:B:188:ARG:HG2	1.74	0.67
1:A:126:TYR:HD2	1:B:6:MET:HG2	1.60	0.67
1:B:118:TYR:O	1:B:119:ASN:HB2	1.95	0.67
1:B:127:GLN:CA	1:B:127:GLN:HE21	2.08	0.66
1:A:131:ARG:HD2	1:A:137:LYS:HE3	1.78	0.66
1:B:166:GLU:HG3	1:B:172:HIS:CD2	2.30	0.66
1:B:131:ARG:HB2	1:B:135:THR:O	1.95	0.65
1:B:105:ARG:NH1	1:B:180:LYS:HB3	2.11	0.65
1:A:6:MET:O	1:A:127:GLN:HG3	1.97	0.65
1:B:67:LEU:HD11	1:B:74:GLN:HE21	1.60	0.65
1:A:140:PHE:HB2	1:A:172:HIS:CD2	2.32	0.64
1:B:33:ASP:HA	2:B:328:HOH:O	1.97	0.64
1:B:63:ASN:ND2	1:B:63:ASN:N	2.38	0.64
1:B:212:VAL:HA	1:B:216:ASP:O	1.98	0.64
1:B:213:ILE:HD13	1:B:214:ASN:N	2.11	0.64
1:B:48:ASP:O	1:B:52:PRO:HB3	1.98	0.64
1:B:106:ILE:HG12	1:B:110:GLN:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:HIS:CE1	1:A:172:HIS:HB3	2.33	0.64
1:B:299:GLN:O	1:B:299:GLN:HG2	1.99	0.63
1:B:19:GLN:NE2	1:B:119:ASN:HB3	2.14	0.63
1:B:140:PHE:C	1:B:141:LEU:HD12	2.18	0.63
1:B:276:MET:O	1:B:278:GLY:N	2.31	0.62
1:B:78:ILE:O	1:B:78:ILE:HD12	1.99	0.62
1:A:285:ALA:HA	2:A:312:HOH:O	1.99	0.62
1:B:76:ARG:HB3	1:B:92:ASP:OD2	2.00	0.61
1:A:243:THR:H	1:A:246:HIS:CD2	2.19	0.61
1:B:7:ALA:HA	1:B:127:GLN:HG2	1.82	0.61
1:B:254:SER:HB2	1:B:259:ILE:O	2.01	0.61
1:A:209:TYR:O	1:A:213:ILE:HG12	1.99	0.61
1:A:48:ASP:HA	2:A:356:HOH:O	2.01	0.60
1:B:109:GLY:HA2	1:B:200:ILE:HD13	1.82	0.60
1:B:161:TYR:CE1	1:B:174:GLY:HA3	2.37	0.60
1:B:203:ASN:OD1	1:B:292:THR:HA	2.02	0.59
1:B:213:ILE:C	1:B:213:ILE:HD13	2.22	0.59
1:B:209:TYR:O	1:B:213:ILE:HG22	2.03	0.59
1:B:153:ASP:O	1:B:154:TYR:HB2	2.03	0.59
1:B:132:PRO:HD2	1:B:197:ASP:OD2	2.02	0.59
1:A:49:MET:CE	1:A:49:MET:HA	2.32	0.58
1:A:1:SER:HA	1:B:137:LYS:HG2	1.83	0.58
1:B:171:VAL:HG22	1:B:172:HIS:H	1.67	0.58
1:B:88:ARG:HD3	2:B:330:HOH:O	2.04	0.58
1:B:49:MET:HB3	1:B:189:GLN:HG2	1.86	0.57
1:A:175:THR:HG22	1:A:181:PHE:HA	1.87	0.57
1:A:270:GLU:C	1:A:272:LEU:N	2.58	0.57
1:B:105:ARG:HH12	1:B:180:LYS:HB3	1.69	0.57
1:A:136:ILE:O	1:A:171:VAL:HG23	2.05	0.56
1:A:305:PHE:O	1:A:306:GLN:HB3	2.06	0.56
1:B:270:GLU:CG	1:B:274:ASN:HD22	2.17	0.56
1:A:304:THR:OG1	1:A:305:PHE:N	2.35	0.56
1:A:135:THR:OG1	1:A:171:VAL:HG21	2.06	0.56
1:A:270:GLU:O	1:A:272:LEU:N	2.39	0.56
1:A:4:ARG:HH21	1:B:128:CYS:CB	2.18	0.56
1:A:243:THR:H	1:A:246:HIS:HD2	1.53	0.55
1:A:60:ARG:NH2	2:A:348:HOH:O	2.38	0.55
1:A:305:PHE:O	1:A:306:GLN:CB	2.54	0.55
1:A:111:THR:HG22	1:A:129:ALA:HB2	1.88	0.55
1:A:153:ASP:O	1:A:154:TYR:HB2	2.05	0.55
1:A:186:VAL:HA	2:A:328:HOH:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:TYR:CD2	1:B:6:MET:HG2	2.40	0.54
1:A:270:GLU:C	1:A:272:LEU:H	2.09	0.54
1:B:231:ASN:O	1:B:235:MET:HG3	2.07	0.54
1:A:86:LEU:HD12	1:A:179:GLY:N	2.22	0.54
1:B:127:GLN:C	1:B:127:GLN:HE21	2.10	0.54
1:B:10:SER:O	1:B:14:GLU:HG3	2.07	0.54
1:B:187:ASP:O	1:B:188:ARG:HG3	2.08	0.54
1:A:10:SER:HB2	1:A:115:LEU:HD13	1.89	0.54
1:B:105:ARG:NH1	1:B:176:ASP:OD2	2.40	0.54
1:A:52:PRO:HG2	1:A:54:TYR:CE1	2.43	0.53
1:B:275:GLY:O	1:B:277:ASN:N	2.41	0.53
1:A:114:VAL:HG11	1:A:140:PHE:HZ	1.73	0.53
1:B:260:ALA:O	1:B:263:ASP:HB2	2.08	0.53
1:B:77:VAL:HA	1:B:91:VAL:HG12	1.91	0.53
1:A:4:ARG:HG2	1:A:4:ARG:HH11	1.72	0.53
1:A:4:ARG:HH21	1:B:128:CYS:HB3	1.74	0.53
1:B:45:THR:HG22	1:B:48:ASP:OD2	2.09	0.53
1:A:114:VAL:HG11	1:A:140:PHE:CZ	2.44	0.53
1:A:57:LEU:HD23	1:A:60:ARG:NH2	2.22	0.52
1:A:293:PRO:O	1:A:297:VAL:HG23	2.09	0.52
1:B:252:PRO:HG2	2:B:346:HOH:O	2.07	0.52
1:A:167:LEU:HD21	1:A:185:PHE:CE1	2.44	0.52
1:A:302:GLY:HA3	2:A:353:HOH:O	2.10	0.52
1:A:95:ASN:HB3	1:A:98:THR:OG1	2.09	0.52
1:A:138:GLY:O	1:A:172:HIS:HE1	1.93	0.52
1:A:86:LEU:HD21	1:A:162:MET:SD	2.49	0.52
1:B:226:THR:HG22	1:B:229:ASP:CB	2.36	0.52
1:B:88:ARG:CD	2:B:330:HOH:O	2.57	0.52
1:A:166:GLU:OE2	1:A:166:GLU:N	2.42	0.52
1:A:66:PHE:HB2	1:A:77:VAL:HG11	1.92	0.51
1:B:276:MET:C	1:B:278:GLY:H	2.14	0.51
1:B:50:LEU:HD23	1:B:189:GLN:HB2	1.93	0.51
1:A:30:LEU:HD22	1:A:32:LEU:CG	2.40	0.51
1:B:21:THR:HG23	1:B:26:THR:OG1	2.10	0.51
1:B:226:THR:HG23	1:B:229:ASP:H	1.74	0.51
1:A:3:PHE:HB2	1:A:282:LEU:HD22	1.92	0.51
1:B:110:GLN:HG2	2:B:323:HOH:O	2.10	0.51
1:A:45:THR:O	1:A:46:ALA:HB3	2.11	0.51
1:A:86:LEU:HD12	1:A:179:GLY:H	1.75	0.51
1:A:30:LEU:O	1:A:36:VAL:HA	2.12	0.50
1:A:274:ASN:O	1:A:275:GLY:C	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ASP:O	1:A:233:VAL:HG23	2.12	0.50
1:A:276:MET:HB3	2:A:340:HOH:O	2.12	0.50
1:B:140:PHE:HB3	1:B:144:SER:OG	2.12	0.50
1:B:246:HIS:O	1:B:249:ILE:HB	2.12	0.50
1:B:227:LEU:C	1:B:227:LEU:HD13	2.33	0.49
1:A:165:MET:SD	1:A:187:ASP:HA	2.52	0.49
1:B:242:LEU:HA	1:B:246:HIS:HD2	1.77	0.49
1:A:62:SER:O	1:A:65:SER:HB2	2.11	0.49
1:A:124:GLY:HA3	1:B:6:MET:CE	2.43	0.49
1:B:86:LEU:HG	1:B:179:GLY:HA2	1.93	0.49
1:A:140:PHE:HB2	1:A:172:HIS:NE2	2.27	0.49
1:B:270:GLU:HG2	1:B:274:ASN:HD22	1.78	0.48
1:B:4:ARG:HG2	1:B:4:ARG:HH11	1.78	0.48
1:B:107:GLN:N	1:B:110:GLN:OE1	2.46	0.48
1:A:5:LYS:NZ	1:A:5:LYS:HB2	2.28	0.48
1:B:112:PHE:O	1:B:127:GLN:NE2	2.46	0.48
1:B:233:VAL:HG11	1:B:269:LYS:HG3	1.94	0.48
1:A:273:GLN:O	1:A:275:GLY:N	2.46	0.48
1:A:107:GLN:HA	1:A:107:GLN:HE21	1.78	0.47
1:A:171:VAL:HG22	1:A:172:HIS:N	2.28	0.47
1:B:47:GLU:O	1:B:48:ASP:C	2.52	0.47
1:B:171:VAL:HG22	1:B:172:HIS:N	2.29	0.47
1:A:131:ARG:HH22	1:A:289:ASP:CG	2.17	0.47
1:A:63:ASN:HB3	1:A:77:VAL:O	2.15	0.47
1:A:231:ASN:O	1:A:235:MET:HG3	2.15	0.47
1:B:243:THR:H	1:B:246:HIS:CD2	2.33	0.47
1:B:269:LYS:HD3	2:B:329:HOH:O	2.14	0.47
1:B:221:ASN:O	1:B:221:ASN:OD1	2.33	0.47
1:B:162:MET:O	1:B:164:HIS:HD2	1.97	0.47
1:B:282:LEU:C	1:B:284:ALA:H	2.18	0.47
1:A:131:ARG:HB2	1:A:135:THR:O	2.15	0.46
1:A:303:VAL:HG12	1:A:304:THR:N	2.31	0.46
1:B:111:THR:HG23	1:B:292:THR:HG23	1.97	0.46
1:B:19:GLN:HE21	1:B:119:ASN:CB	2.29	0.46
1:B:3:PHE:HE1	1:B:300:CYS:SG	2.39	0.46
1:B:40:ARG:HG3	1:B:54:TYR:CE2	2.50	0.46
1:A:106:ILE:HG12	1:A:110:GLN:HB2	1.97	0.46
1:A:94:SER:O	1:A:96:PRO:HD3	2.16	0.46
1:A:124:GLY:HA3	1:B:6:MET:HE3	1.97	0.46
1:B:24:THR:HG23	2:B:308:HOH:O	2.15	0.46
1:A:247:VAL:HG13	1:A:261:VAL:HG11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:THR:HB	1:B:180:LYS:O	2.16	0.46
1:B:226:THR:CG2	1:B:229:ASP:H	2.29	0.46
1:B:224:THR:HB	1:B:263:ASP:OD1	2.15	0.46
1:A:53:ASN:HB3	2:A:351:HOH:O	2.16	0.45
1:B:155:ASP:OD1	1:B:155:ASP:N	2.50	0.45
1:B:225:THR:OG1	1:B:226:THR:N	2.50	0.45
1:B:45:THR:HG23	1:B:45:THR:O	2.16	0.45
1:A:5:LYS:HB2	1:A:5:LYS:HZ2	1.81	0.45
1:B:164:HIS:CD2	1:B:175:THR:HG23	2.51	0.45
1:A:30:LEU:HD12	1:A:177:LEU:HD11	1.97	0.45
1:A:285:ALA:CB	1:B:286:ALA:HB2	2.43	0.45
1:B:52:PRO:HG2	1:B:54:TYR:CE1	2.51	0.45
1:B:140:PHE:HB3	1:B:144:SER:HG	1.82	0.45
1:B:88:ARG:HB3	1:B:88:ARG:CZ	2.46	0.45
1:B:55:GLU:H	1:B:55:GLU:CD	2.20	0.45
1:B:180:LYS:HE2	2:B:341:HOH:O	2.16	0.44
1:B:276:MET:C	1:B:278:GLY:N	2.70	0.44
1:A:188:ARG:O	1:A:190:THR:N	2.51	0.44
1:A:268:LEU:HD22	1:A:272:LEU:HG	1.99	0.44
1:B:49:MET:HA	1:B:49:MET:HE2	2.00	0.44
1:A:49:MET:HA	1:A:49:MET:HE2	2.00	0.44
1:B:106:ILE:CG2	1:B:130:MET:HE3	2.46	0.44
1:A:40:ARG:O	1:A:43:ILE:HG12	2.18	0.44
1:B:213:ILE:CD1	1:B:213:ILE:C	2.85	0.44
1:A:247:VAL:HG13	1:A:261:VAL:CB	2.48	0.43
1:A:45:THR:O	1:A:45:THR:HG23	2.18	0.43
1:A:40:ARG:HG3	1:A:54:TYR:CE2	2.52	0.43
1:A:125:VAL:O	1:A:125:VAL:HG13	2.19	0.43
1:A:211:ALA:HA	1:A:282:LEU:HD11	2.00	0.43
1:B:127:GLN:HA	1:B:127:GLN:HE21	1.81	0.43
1:B:30:LEU:HA	1:B:30:LEU:HD23	1.74	0.43
1:A:243:THR:N	1:A:246:HIS:HD2	2.17	0.43
1:B:299:GLN:CG	1:B:299:GLN:O	2.66	0.43
1:B:92:ASP:OD1	1:B:93:THR:N	2.51	0.43
1:A:213:ILE:HD13	1:A:257:THR:CG2	2.49	0.43
1:A:50:LEU:O	1:A:51:ASN:HB3	2.17	0.43
1:A:13:VAL:HG13	1:A:159:PHE:HE1	1.83	0.43
1:B:242:LEU:HD12	1:B:246:HIS:CD2	2.53	0.43
1:A:67:LEU:HD12	1:A:68:VAL:N	2.34	0.43
1:B:127:GLN:HE21	1:B:128:CYS:H	1.66	0.43
1:B:133:ASN:O	1:B:134:HIS:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:PHE:HB2	2:B:354:HOH:O	2.18	0.43
1:A:135:THR:HB	1:A:171:VAL:HG22	2.01	0.43
1:A:67:LEU:HD13	1:A:74:GLN:NE2	2.34	0.43
1:A:18:VAL:HG22	1:A:29:GLY:O	2.19	0.42
1:B:5:LYS:HD3	1:B:127:GLN:O	2.19	0.42
1:A:153:ASP:O	1:A:154:TYR:CB	2.67	0.42
1:B:19:GLN:HE21	1:B:119:ASN:HB3	1.82	0.42
1:B:211:ALA:HA	1:B:282:LEU:HG	2.02	0.42
1:A:208:LEU:O	1:A:211:ALA:HB3	2.19	0.42
1:A:111:THR:HG22	1:A:129:ALA:CB	2.50	0.42
1:A:13:VAL:HG21	1:A:150:PHE:CD2	2.55	0.41
1:B:60:ARG:HB3	1:B:60:ARG:HH11	1.85	0.41
1:A:276:MET:HA	2:A:309:HOH:O	2.21	0.41
1:A:136:ILE:HD11	1:A:140:PHE:HE1	1.85	0.41
1:B:19:GLN:HE21	1:B:119:ASN:CA	2.33	0.41
1:A:212:VAL:O	1:A:213:ILE:C	2.59	0.41
1:A:86:LEU:HA	1:A:86:LEU:HD23	1.88	0.41
1:B:229:ASP:O	1:B:233:VAL:HG23	2.20	0.41
1:A:1:SER:HA	1:B:137:LYS:CG	2.50	0.41
1:A:247:VAL:HG13	1:A:261:VAL:HG21	2.01	0.41
1:B:127:GLN:CA	1:B:127:GLN:NE2	2.80	0.41
1:A:41:HIS:HB2	1:A:49:MET:HE3	2.03	0.41
1:B:114:VAL:HG11	1:B:140:PHE:CZ	2.56	0.41
1:B:258:GLY:HA2	2:B:352:HOH:O	2.21	0.41
1:B:30:LEU:O	1:B:36:VAL:HA	2.21	0.41
1:A:269:LYS:O	1:A:273:GLN:HG3	2.21	0.41
1:A:291:PHE:HB2	2:A:311:HOH:O	2.20	0.41
1:A:121:SER:HA	1:A:122:PRO:HD3	1.93	0.41
1:B:108:PRO:HA	1:B:130:MET:CG	2.50	0.41
1:B:211:ALA:CB	1:B:282:LEU:HG	2.50	0.41
1:B:127:GLN:NE2	1:B:128:CYS:N	2.64	0.41
1:B:202:LEU:HD11	1:B:293:PRO:HG2	2.03	0.41
1:B:208:LEU:O	1:B:212:VAL:HG23	2.20	0.41
1:B:35:THR:OG1	1:B:90:LYS:HE3	2.21	0.41
1:B:60:ARG:HB3	1:B:60:ARG:NH1	2.35	0.41
1:A:4:ARG:NH1	1:A:4:ARG:HG2	2.35	0.40
1:A:51:ASN:ND2	1:A:51:ASN:C	2.75	0.40
1:B:207:TRP:HZ3	1:B:287:LEU:HD23	1.86	0.40
1:B:277:ASN:HB3	1:B:279:ARG:HG3	2.02	0.40
1:B:131:ARG:NH2	1:B:289:ASP:OD2	2.54	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	304/308 (99%)	253 (83%)	41 (14%)	10 (3%)	4	10
1	B	302/308 (98%)	259 (86%)	34 (11%)	9 (3%)	5	11
All	All	606/616 (98%)	512 (84%)	75 (12%)	19 (3%)	4	11

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	ALA
1	A	304	THR
1	B	276	MET
1	B	277	ASN
1	A	141	LEU
1	A	274	ASN
1	A	275	GLY
1	B	48	ASP
1	B	222	ARG
1	B	275	GLY
1	A	154	TYR
1	B	47	GLU
1	A	46	ALA
1	A	54	TYR
1	B	46	ALA
1	A	271	LEU
1	B	154	TYR
1	B	283	GLY
1	A	51	ASN

### 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	260/261 (100%)	246 (95%)	14 (5%)	24	51
1	B	258/261 (99%)	240 (93%)	18 (7%)	16	38
All	All	518/522 (99%)	486 (94%)	32 (6%)	20	44

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	LEU
1	A	51	ASN
1	A	64	HIS
1	A	76	ARG
1	A	77	VAL
1	A	87	LEU
1	A	107	GLN
1	A	127	GLN
1	A	131	ARG
1	A	153	ASP
1	A	167	LEU
1	A	196	THR
1	A	229	ASP
1	A	268	LEU
1	B	4	ARG
1	B	9	PRO
1	B	27	LEU
1	B	30	LEU
1	B	51	ASN
1	B	63	ASN
1	B	76	ARG
1	B	77	VAL
1	B	87	LEU
1	B	127	GLN
1	B	153	ASP
1	B	181	PHE
1	B	187	ASP
1	B	213	ILE
1	B	222	ARG
1	B	232	LEU
1	B	263	ASP
1	B	268	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	19	GLN
1	A	41	HIS
1	A	51	ASN
1	A	53	ASN
1	A	69	GLN
1	A	74	GLN
1	A	80	HIS
1	A	107	GLN
1	A	127	GLN
1	A	142	ASN
1	A	151	ASN
1	A	172	HIS
1	A	192	GLN
1	A	246	HIS
1	A	277	ASN
1	A	299	GLN
1	B	19	GLN
1	B	51	ASN
1	B	63	ASN
1	B	69	GLN
1	B	74	GLN
1	B	107	GLN
1	B	119	ASN
1	B	127	GLN
1	B	163	HIS
1	B	164	HIS
1	B	172	HIS
1	B	192	GLN
1	B	221	ASN
1	B	238	ASN
1	B	246	HIS
1	B	274	ASN
1	B	277	ASN

### 5.3.3 RNA ⓘ

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 [i](#)

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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.