



# Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 01:14 am BST

PDB ID : 2RQW  
Title : Solution structure of Bem1p SH3CI domain complexed with Ste20p-PRR peptide  
Authors : Takaku, T.; Ogura, K.; Inagaki, F.  
Deposited on : 2009-12-21

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

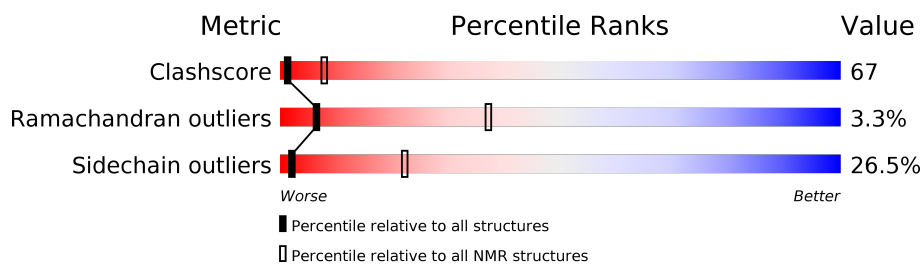
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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	105	
2	B	24	

## 2 Ensemble composition and analysis i

This entry contains 20 models. Model 15 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:159-A:197, A:203-A:215, A:226-A:244, B:470-B:480 (82)	0.32	15

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 4 single-model clusters were found.

Cluster number	Models
1	2, 5, 6, 7, 9, 12, 15, 16, 20
2	1, 3, 10, 14
3	4, 8, 13
Single-model clusters	11; 17; 18; 19

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1784 atoms, of which 816 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Bud emergence protein 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	105	1498	520	693	130	153	2	0

- Molecule 2 is a protein called 24-meric peptide from Serine/threonine-protein kinase STE20.

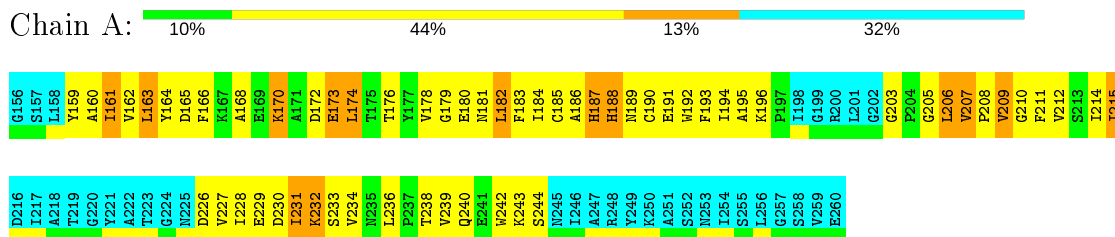
Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	B	24	286	100	123	30	33	0

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

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Bud emergence protein 1



- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

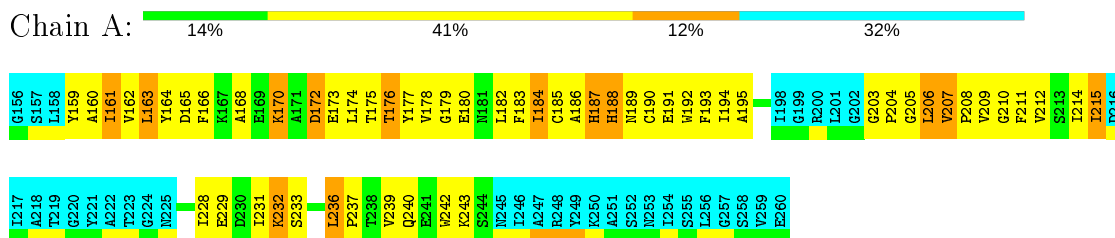


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Bud emergence protein 1

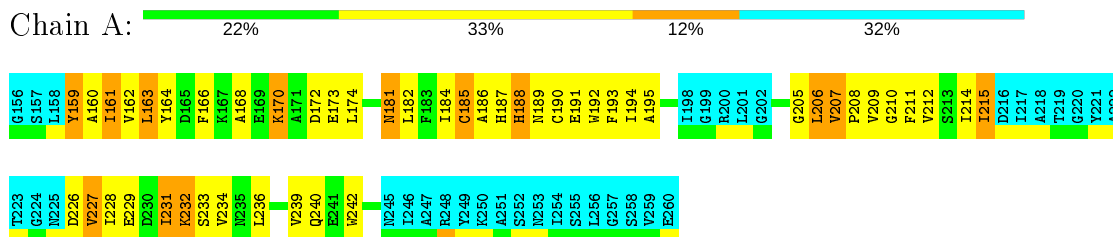


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

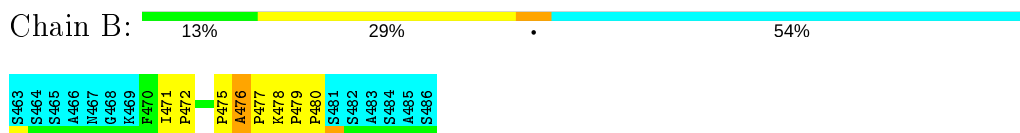


#### 4.2.2 Score per residue for model 2

- Molecule 1: Bud emergence protein 1

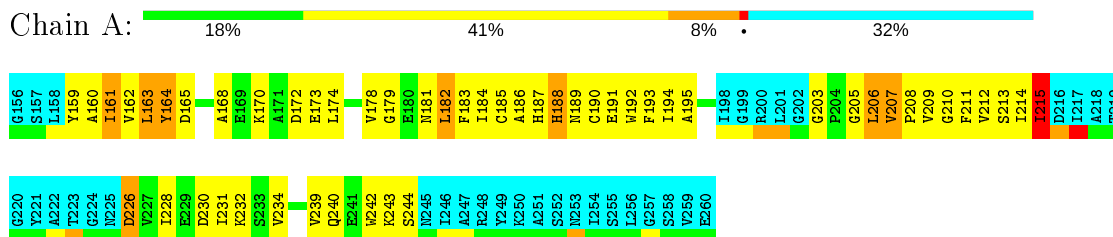


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

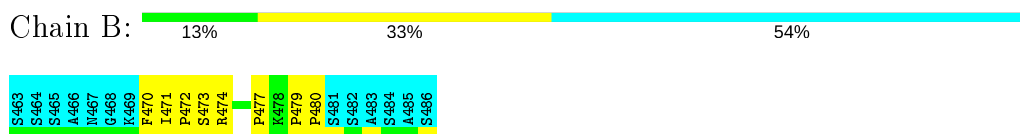


#### 4.2.3 Score per residue for model 3

- Molecule 1: Bud emergence protein 1

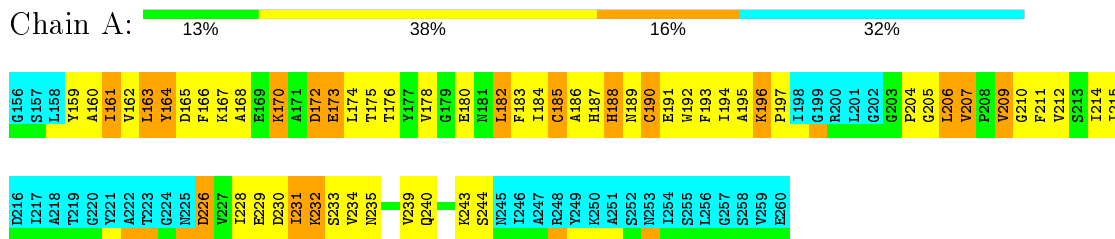


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

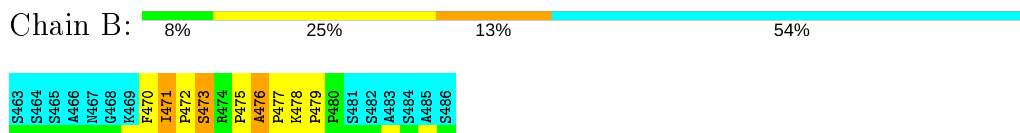


#### 4.2.4 Score per residue for model 4

- Molecule 1: Bud emergence protein 1

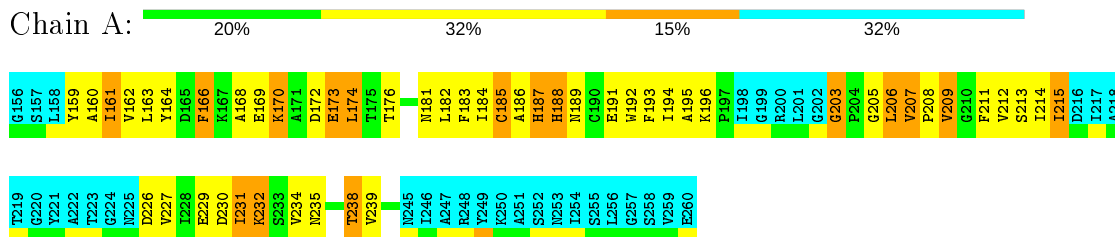


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

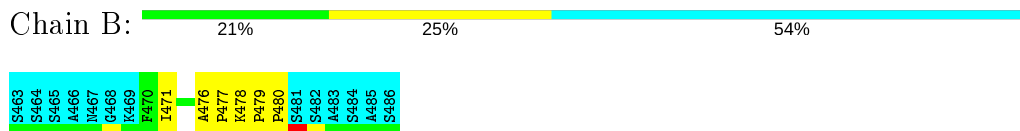


#### 4.2.5 Score per residue for model 5

- Molecule 1: Bud emergence protein 1

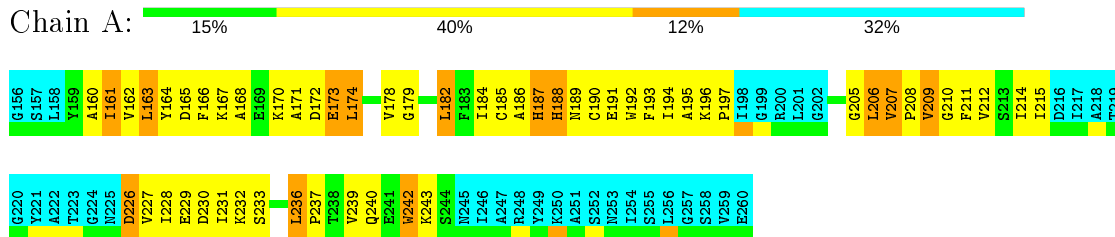


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

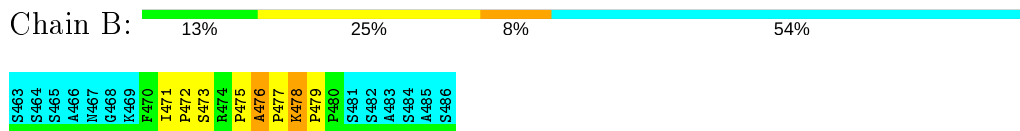


#### 4.2.6 Score per residue for model 6

- Molecule 1: Bud emergence protein 1

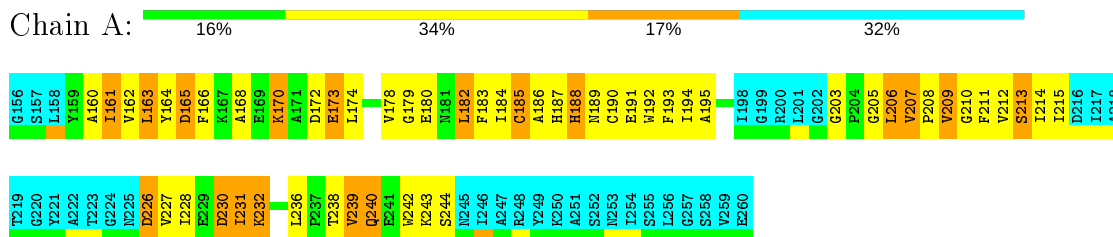


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

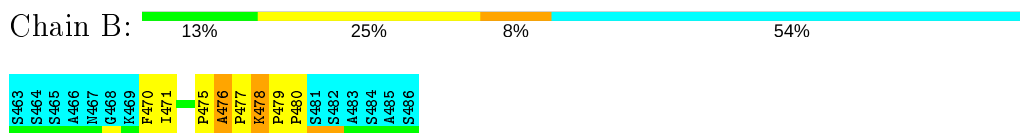


#### 4.2.7 Score per residue for model 7

- Molecule 1: Bud emergence protein 1

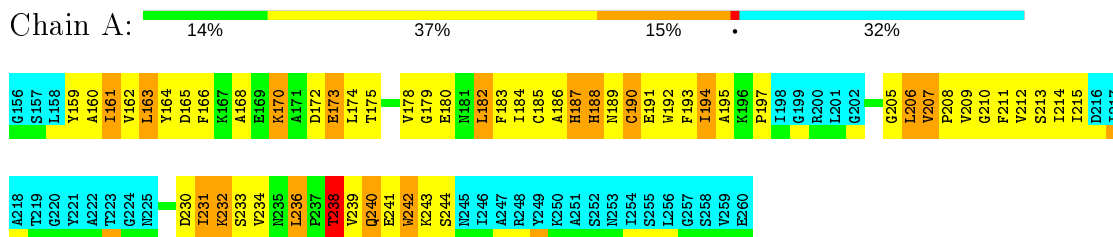


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

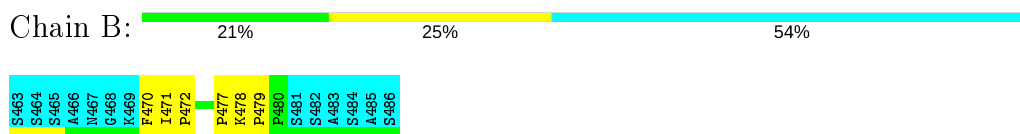


#### 4.2.8 Score per residue for model 8

- Molecule 1: Bud emergence protein 1



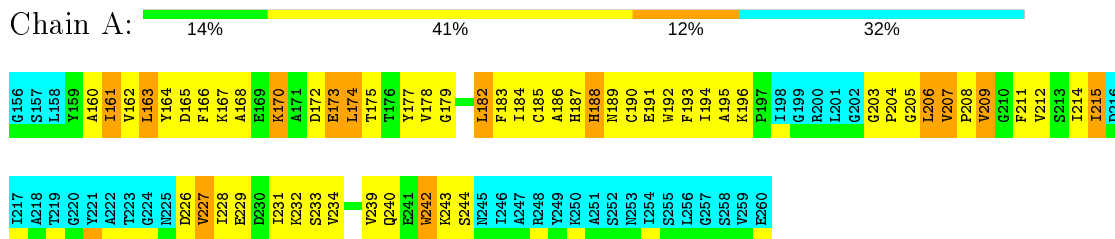
- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20



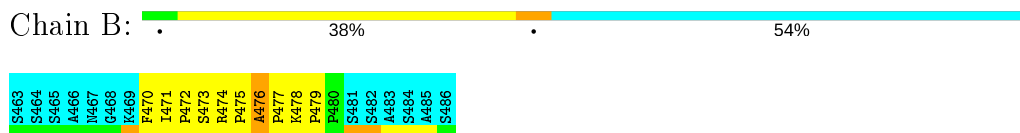
#### 4.2.9 Score per residue for model 9

- Molecule 1: Bud emergence protein 1



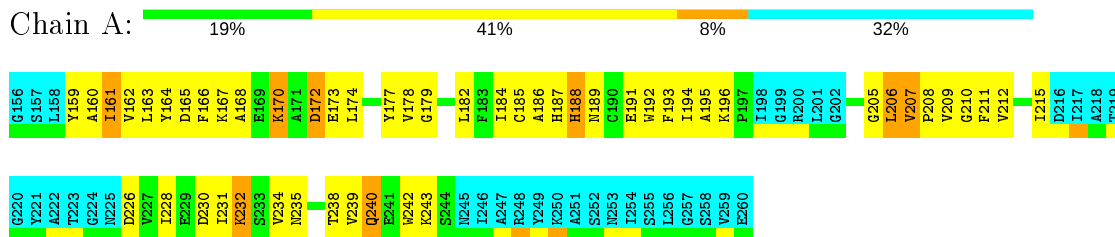


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

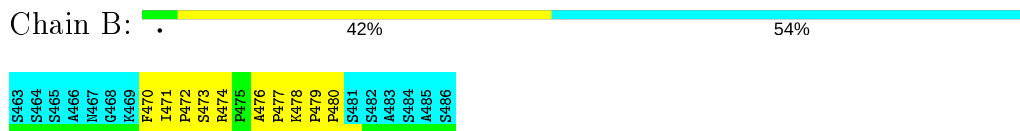


#### 4.2.10 Score per residue for model 10

- Molecule 1: Bud emergence protein 1

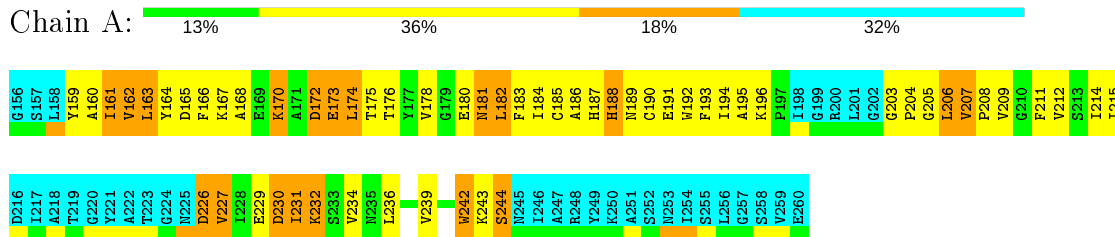


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

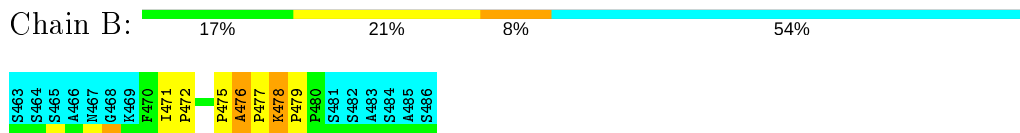


#### 4.2.11 Score per residue for model 11

- Molecule 1: Bud emergence protein 1

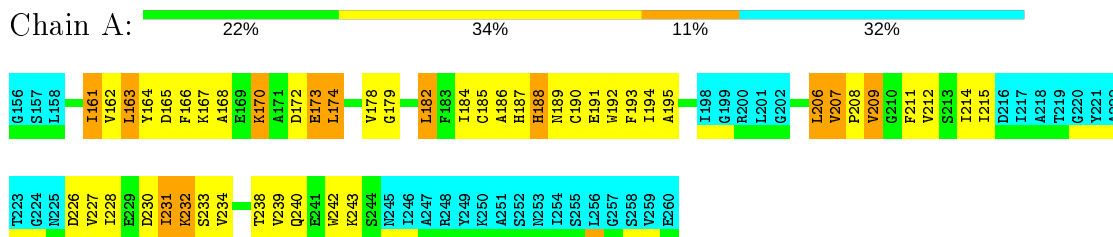


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

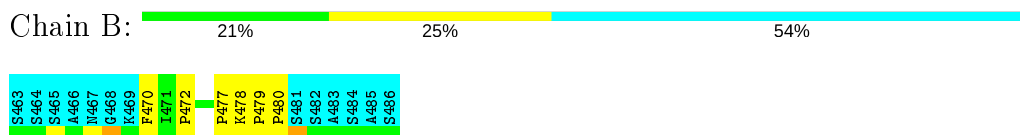


#### 4.2.12 Score per residue for model 12

- Molecule 1: Bud emergence protein 1

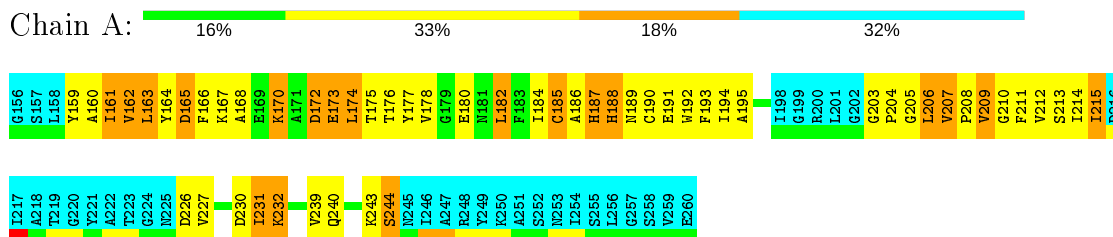


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20



#### 4.2.13 Score per residue for model 13

- Molecule 1: Bud emergence protein 1

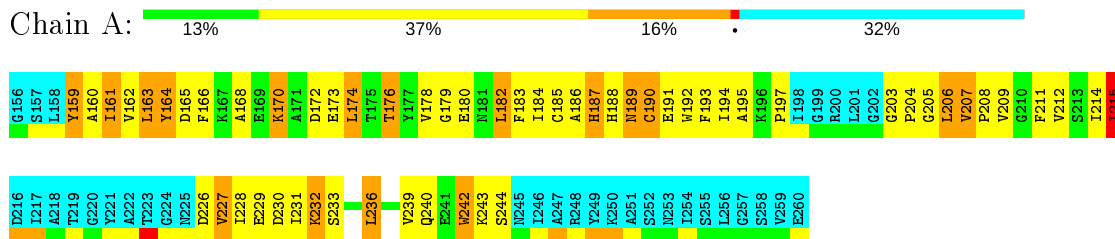


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

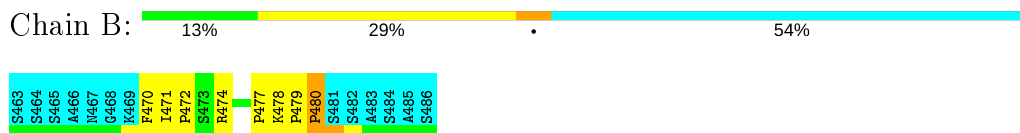


#### 4.2.14 Score per residue for model 14

- Molecule 1: Bud emergence protein 1

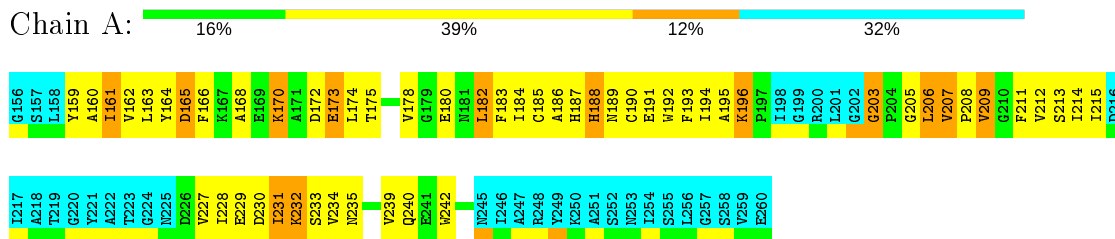


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20



#### 4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: Bud emergence protein 1

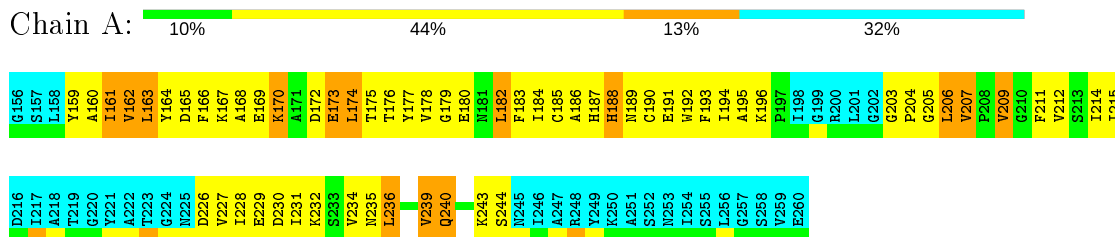


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

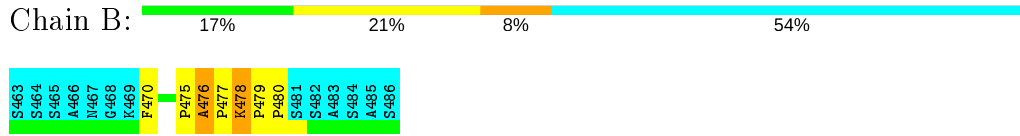


#### 4.2.16 Score per residue for model 16

- Molecule 1: Bud emergence protein 1

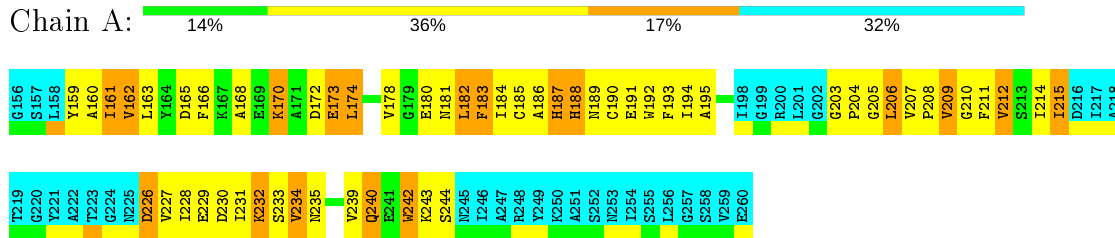


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20



#### 4.2.17 Score per residue for model 17

- Molecule 1: Bud emergence protein 1

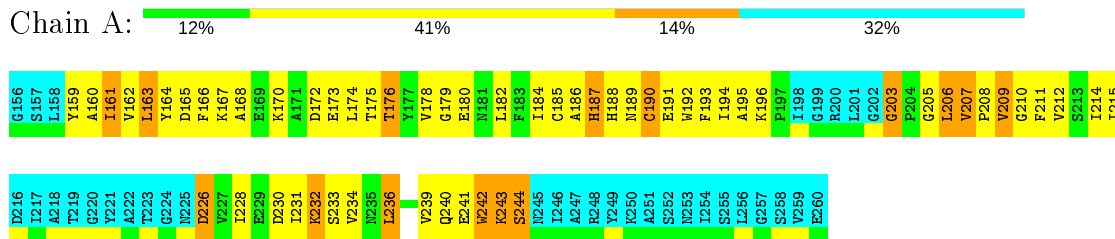


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

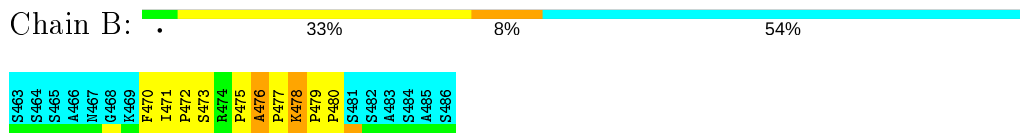


#### 4.2.18 Score per residue for model 18

- Molecule 1: Bud emergence protein 1

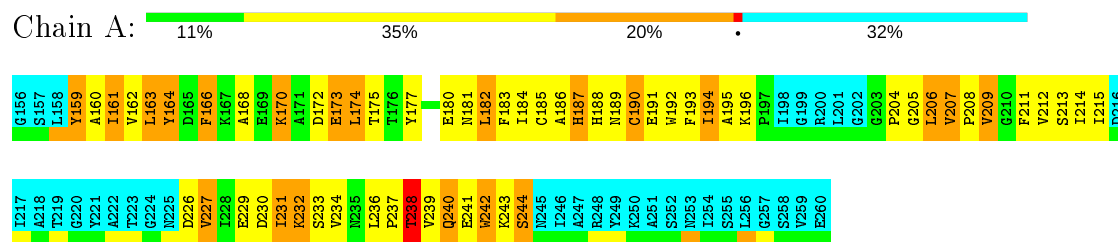


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

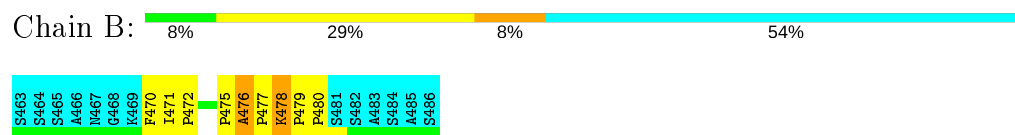


#### 4.2.19 Score per residue for model 19

- Molecule 1: Bud emergence protein 1

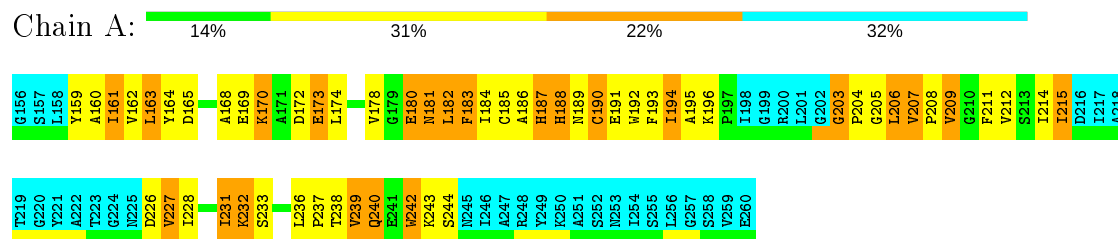


- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20

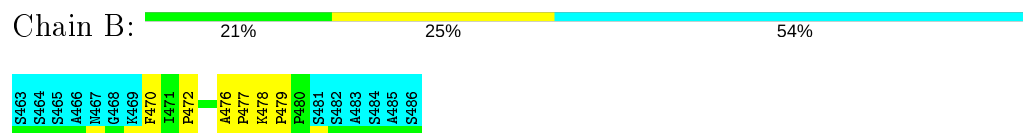


#### 4.2.20 Score per residue for model 20

- Molecule 1: Bud emergence protein 1



- Molecule 2: 24-meric peptide from Serine/threonine-protein kinase STE20



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	564	480	555	84±8
2	B	85	64	91	13±4
All	All	12980	10880	12920	1728

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 67.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:184:ILE:HD13	1:A:195:ALA:HB2	1.06	1.23	17	5
1:A:188:HIS:CE1	1:A:239:VAL:HG11	1.05	1.85	16	3
1:A:162:VAL:CG1	1:A:182:LEU:HD11	0.92	1.93	17	1
1:A:192:TRP:CZ3	1:A:206:LEU:HD21	0.91	2.01	10	20
1:A:240:GLN:OE1	2:B:471:ILE:HD11	0.90	1.67	3	2
1:A:208:PRO:O	1:A:212:VAL:HG22	0.88	1.69	9	17
1:A:186:ALA:HB2	1:A:242:TRP:CZ3	0.85	2.05	18	11
1:A:160:ALA:HB3	1:A:182:LEU:CD2	0.85	2.01	20	5
1:A:239:VAL:HG22	1:A:243:LYS:NZ	0.85	1.86	11	1
1:A:188:HIS:NE2	1:A:194:ILE:HD13	0.85	1.85	7	7
1:A:188:HIS:ND1	1:A:239:VAL:HG11	0.84	1.86	7	3
1:A:191:GLU:CD	2:B:476:ALA:HB2	0.84	1.93	15	8
1:A:186:ALA:HB3	1:A:194:ILE:HB	0.84	1.50	6	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:162:VAL:HG22	1:A:212:VAL:HG12	0.82	1.50	18	16
1:A:160:ALA:O	1:A:182:LEU:HD12	0.81	1.74	6	2
1:A:160:ALA:HB2	1:A:184:ILE:HD13	0.81	1.53	14	6
1:A:182:LEU:CD2	1:A:207:VAL:HG11	0.81	2.06	6	3
1:A:161:ILE:HG21	1:A:215:ILE:HD11	0.80	1.53	17	2
1:A:186:ALA:HB1	1:A:239:VAL:HG23	0.79	1.53	8	6
1:A:159:TYR:CD1	1:A:183:PHE:CD1	0.79	2.71	11	1
1:A:169:GLU:H	1:A:170:LYS:HZ3	0.79	1.16	5	2
1:A:187:HIS:CD2	1:A:236:LEU:HD21	0.79	2.11	18	3
1:A:159:TYR:CD1	1:A:183:PHE:CE2	0.79	2.70	8	2
1:A:162:VAL:HG13	1:A:182:LEU:HD22	0.79	1.55	1	1
1:A:182:LEU:HD12	1:A:207:VAL:HG21	0.78	1.52	5	8
1:A:182:LEU:O	1:A:182:LEU:HD22	0.78	1.78	16	3
1:A:182:LEU:CD1	1:A:207:VAL:HG21	0.77	2.07	5	5
1:A:168:ALA:HB1	1:A:173:GLU:HA	0.77	1.54	4	20
1:A:162:VAL:HG23	1:A:182:LEU:HD11	0.76	1.54	20	3
1:A:182:LEU:HD13	1:A:182:LEU:N	0.76	1.95	11	3
1:A:162:VAL:CG1	1:A:182:LEU:HD21	0.76	2.09	4	1
1:A:193:PHE:CE2	1:A:209:VAL:HG12	0.76	2.15	7	20
1:A:214:ILE:O	1:A:215:ILE:HG23	0.76	1.81	12	14
1:A:162:VAL:HG23	1:A:182:LEU:HD22	0.76	1.56	2	2
1:A:182:LEU:CD1	1:A:207:VAL:HG11	0.75	2.11	18	5
1:A:186:ALA:HB1	1:A:239:VAL:HB	0.74	1.57	11	4
1:A:159:TYR:CE2	1:A:183:PHE:CZ	0.74	2.75	14	2
1:A:182:LEU:N	1:A:182:LEU:HD12	0.74	1.97	12	2
1:A:182:LEU:HD23	1:A:182:LEU:N	0.74	1.98	8	2
1:A:192:TRP:CE3	1:A:206:LEU:HD21	0.73	2.17	10	19
1:A:184:ILE:HD12	1:A:193:PHE:HB3	0.73	1.60	5	5
1:A:215:ILE:N	1:A:215:ILE:HD13	0.73	1.99	9	1
1:A:165:ASP:N	1:A:178:VAL:HG12	0.72	1.98	20	17
1:A:184:ILE:CG1	1:A:195:ALA:HB2	0.72	2.14	19	5
1:A:228:ILE:HA	1:A:231:ILE:HD12	0.72	1.61	10	8
1:A:162:VAL:HG23	1:A:182:LEU:CD2	0.71	2.16	2	4
1:A:182:LEU:N	1:A:182:LEU:HD13	0.71	2.00	15	2
1:A:162:VAL:HG12	1:A:212:VAL:HG12	0.71	1.62	1	2
1:A:239:VAL:HG22	1:A:243:LYS:HZ3	0.71	1.46	11	1
1:A:188:HIS:CE1	1:A:239:VAL:CG1	0.70	2.74	5	3
1:A:163:LEU:HD11	1:A:213:SER:HB2	0.70	1.63	8	3
1:A:159:TYR:CE2	1:A:183:PHE:CE1	0.70	2.79	15	1
1:A:161:ILE:HB	1:A:215:ILE:HD11	0.70	1.62	7	5
1:A:209:VAL:HB	1:A:227:VAL:HG21	0.70	1.62	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:160:ALA:HB2	1:A:184:ILE:HD12	0.70	1.62	16	3
1:A:182:LEU:N	1:A:182:LEU:HD23	0.70	2.01	7	5
1:A:160:ALA:O	1:A:182:LEU:HD22	0.70	1.87	17	1
1:A:184:ILE:HG12	1:A:195:ALA:HB2	0.70	1.63	19	1
1:A:162:VAL:HG11	1:A:182:LEU:HD21	0.69	1.62	4	1
2:B:471:ILE:N	2:B:471:ILE:HD13	0.69	2.00	19	3
1:A:160:ALA:CB	1:A:184:ILE:HD13	0.69	2.17	8	3
1:A:186:ALA:CB	1:A:239:VAL:HG23	0.69	2.16	8	6
1:A:161:ILE:CG2	1:A:215:ILE:HD11	0.69	2.18	17	2
1:A:227:VAL:O	1:A:231:ILE:HD12	0.69	1.86	13	1
1:A:236:LEU:HD12	1:A:237:PRO:HD2	0.69	1.63	19	2
1:A:186:ALA:HB1	1:A:239:VAL:CB	0.69	2.18	11	3
1:A:207:VAL:CG1	1:A:212:VAL:HG11	0.69	2.18	12	4
1:A:186:ALA:HB1	1:A:239:VAL:HG12	0.68	1.65	16	2
1:A:188:HIS:NE2	1:A:194:ILE:HD11	0.68	2.04	16	6
1:A:182:LEU:HD21	1:A:207:VAL:HG11	0.68	1.64	6	2
1:A:188:HIS:CD2	1:A:239:VAL:HG11	0.67	2.23	20	3
1:A:182:LEU:H	1:A:182:LEU:HD12	0.67	1.50	9	2
1:A:162:VAL:CG2	1:A:212:VAL:HG12	0.67	2.20	5	11
1:A:188:HIS:CD2	1:A:239:VAL:CG1	0.67	2.78	9	2
1:A:176:THR:HG23	1:A:180:GLU:CD	0.66	2.10	11	2
1:A:176:THR:HG23	1:A:180:GLU:HG2	0.66	1.67	14	1
1:A:182:LEU:HD13	1:A:207:VAL:HG11	0.66	1.68	10	1
1:A:214:ILE:C	1:A:215:ILE:HD13	0.66	2.12	9	1
1:A:239:VAL:HG22	1:A:243:LYS:HD3	0.65	1.68	10	2
1:A:159:TYR:CD2	1:A:215:ILE:CG1	0.65	2.79	5	1
1:A:162:VAL:HG12	1:A:212:VAL:CG1	0.65	2.21	4	2
1:A:191:GLU:OE2	2:B:476:ALA:HB2	0.65	1.91	15	3
1:A:187:HIS:CD2	1:A:236:LEU:CD2	0.65	2.79	18	2
1:A:182:LEU:HD22	1:A:182:LEU:O	0.64	1.92	15	1
1:A:182:LEU:HD11	1:A:207:VAL:HG11	0.64	1.67	18	3
1:A:166:PHE:CE2	1:A:170:LYS:NZ	0.64	2.64	10	3
1:A:195:ALA:HB3	1:A:207:VAL:HG21	0.64	1.68	10	1
1:A:193:PHE:CE2	1:A:227:VAL:HG21	0.64	2.27	14	1
2:B:475:PRO:O	2:B:476:ALA:HB2	0.64	1.93	4	9
1:A:165:ASP:H	1:A:178:VAL:HG12	0.63	1.53	4	13
1:A:169:GLU:H	1:A:170:LYS:NZ	0.63	1.90	16	2
1:A:193:PHE:CE2	1:A:209:VAL:CG1	0.63	2.81	14	18
1:A:214:ILE:HG13	1:A:227:VAL:HG23	0.63	1.71	17	1
1:A:193:PHE:CZ	1:A:209:VAL:HG12	0.63	2.28	16	10
1:A:187:HIS:C	1:A:188:HIS:CD2	0.62	2.73	7	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:193:PHE:CZ	1:A:209:VAL:CG1	0.62	2.82	16	19
1:A:162:VAL:HG13	1:A:182:LEU:HD11	0.62	1.70	17	1
1:A:188:HIS:CD2	1:A:192:TRP:O	0.62	2.53	8	9
1:A:231:ILE:HG22	1:A:232:LYS:N	0.62	2.09	12	14
1:A:192:TRP:CE3	1:A:206:LEU:HD11	0.62	2.29	10	11
1:A:160:ALA:CB	1:A:184:ILE:CD1	0.62	2.78	14	10
1:A:160:ALA:HB2	1:A:184:ILE:CD1	0.62	2.25	2	6
1:A:174:LEU:HD13	1:A:205:GLY:CA	0.62	2.25	5	2
1:A:194:ILE:HG22	1:A:194:ILE:O	0.62	1.94	17	2
1:A:162:VAL:HG13	1:A:164:TYR:O	0.61	1.95	20	15
1:A:243:LYS:NZ	2:B:470:PHE:CD2	0.61	2.65	8	3
1:A:188:HIS:CE1	1:A:192:TRP:CB	0.61	2.83	20	14
1:A:161:ILE:C	1:A:161:ILE:HD13	0.61	2.16	3	2
1:A:194:ILE:CD1	1:A:206:LEU:HD12	0.61	2.26	4	5
1:A:242:TRP:CD1	1:A:242:TRP:C	0.61	2.72	18	4
1:A:236:LEU:HD12	1:A:237:PRO:O	0.61	1.96	6	2
1:A:161:ILE:HD13	1:A:162:VAL:N	0.61	2.10	3	9
1:A:207:VAL:HB	1:A:212:VAL:HG11	0.61	1.70	6	8
1:A:185:CYS:SG	1:A:242:TRP:CH2	0.61	2.94	9	3
1:A:160:ALA:HB3	1:A:182:LEU:HD21	0.61	1.71	16	2
1:A:193:PHE:CE2	1:A:214:ILE:HD11	0.60	2.31	17	1
1:A:185:CYS:SG	1:A:242:TRP:CZ3	0.60	2.94	6	2
1:A:166:PHE:CE1	1:A:167:LYS:O	0.60	2.54	16	6
1:A:159:TYR:CE1	1:A:160:ALA:O	0.60	2.55	5	3
1:A:159:TYR:CZ	1:A:183:PHE:CD2	0.60	2.89	17	1
1:A:171:ALA:HB3	2:B:471:ILE:O	0.60	1.97	6	1
1:A:188:HIS:CE1	1:A:194:ILE:HD11	0.60	2.31	11	2
1:A:159:TYR:CD2	1:A:183:PHE:CE1	0.60	2.90	15	1
1:A:191:GLU:OE1	2:B:476:ALA:HB2	0.59	1.96	10	3
1:A:162:VAL:HG13	1:A:182:LEU:CD2	0.59	2.27	1	1
1:A:188:HIS:HD1	1:A:239:VAL:HG11	0.59	1.55	11	1
1:A:174:LEU:HD22	1:A:205:GLY:HA3	0.59	1.74	1	10
1:A:188:HIS:NE2	1:A:194:ILE:CG1	0.59	2.65	16	3
1:A:231:ILE:HG23	1:A:236:LEU:HD23	0.59	1.74	18	1
1:A:211:PHE:CZ	2:B:479:PRO:HA	0.59	2.33	2	20
1:A:182:LEU:HD22	1:A:207:VAL:HG21	0.59	1.75	6	2
1:A:234:VAL:HG23	1:A:234:VAL:O	0.59	1.98	17	3
1:A:188:HIS:CD2	1:A:188:HIS:N	0.58	2.71	5	8
1:A:175:THR:HG23	1:A:175:THR:O	0.58	1.98	4	5
1:A:159:TYR:CD1	1:A:159:TYR:N	0.58	2.72	16	4
1:A:242:TRP:CE3	1:A:243:LYS:NZ	0.58	2.71	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:188:HIS:N	1:A:188:HIS:CD2	0.58	2.72	4	10
1:A:162:VAL:HG23	1:A:182:LEU:HD21	0.58	1.76	14	4
1:A:168:ALA:HB1	1:A:173:GLU:CA	0.58	2.29	7	13
1:A:183:PHE:CE1	1:A:184:ILE:O	0.58	2.57	20	1
1:A:185:CYS:O	1:A:242:TRP:CZ3	0.57	2.58	7	6
1:A:194:ILE:HG21	2:B:470:PHE:CD2	0.57	2.34	3	3
1:A:185:CYS:O	1:A:236:LEU:HD12	0.57	2.00	18	1
2:B:471:ILE:HG22	2:B:472:PRO:HD2	0.57	1.77	18	1
2:B:471:ILE:CD1	2:B:471:ILE:N	0.57	2.68	13	2
1:A:174:LEU:HD13	1:A:205:GLY:HA3	0.57	1.76	15	10
1:A:182:LEU:N	1:A:182:LEU:CD2	0.57	2.68	7	3
1:A:166:PHE:CZ	1:A:168:ALA:HB2	0.57	2.34	13	1
1:A:236:LEU:C	1:A:236:LEU:HD12	0.57	2.20	1	1
1:A:182:LEU:H	1:A:182:LEU:HD13	0.57	1.58	16	1
1:A:170:LYS:NZ	1:A:192:TRP:CH2	0.56	2.73	17	3
1:A:159:TYR:CE2	1:A:215:ILE:CD1	0.56	2.88	10	2
1:A:193:PHE:HE2	1:A:227:VAL:HG21	0.56	1.59	14	1
1:A:214:ILE:C	1:A:215:ILE:HG22	0.56	2.20	3	2
1:A:170:LYS:NZ	1:A:206:LEU:HD23	0.56	2.15	12	1
1:A:159:TYR:CD1	1:A:215:ILE:O	0.56	2.59	3	1
1:A:159:TYR:CE2	1:A:183:PHE:CG	0.56	2.94	17	1
2:B:471:ILE:HG23	2:B:472:PRO:HD2	0.56	1.78	15	4
1:A:185:CYS:O	1:A:242:TRP:CE3	0.56	2.58	19	1
1:A:243:LYS:CE	2:B:470:PHE:CD2	0.56	2.89	19	2
1:A:181:ASN:C	1:A:182:LEU:HD13	0.56	2.21	11	1
1:A:188:HIS:NE2	1:A:194:ILE:CD1	0.56	2.69	14	13
1:A:191:GLU:O	1:A:209:VAL:HG13	0.55	2.00	11	14
1:A:162:VAL:HG23	1:A:212:VAL:HG12	0.55	1.76	13	1
1:A:187:HIS:CD2	1:A:236:LEU:HD11	0.55	2.36	1	1
1:A:239:VAL:HG13	1:A:240:GLN:N	0.55	2.15	18	7
1:A:184:ILE:N	1:A:184:ILE:CD1	0.55	2.69	1	2
1:A:184:ILE:HG13	1:A:195:ALA:HB2	0.55	1.77	10	2
1:A:163:LEU:HD11	1:A:213:SER:OG	0.55	2.01	15	1
1:A:188:HIS:NE2	1:A:239:VAL:HG11	0.55	2.15	16	1
1:A:188:HIS:CE1	1:A:192:TRP:HB3	0.55	2.37	20	14
1:A:188:HIS:CE1	2:B:472:PRO:HD3	0.55	2.37	4	14
1:A:170:LYS:CE	1:A:192:TRP:CH2	0.55	2.90	15	2
1:A:186:ALA:HB1	1:A:239:VAL:CG2	0.55	2.31	3	2
1:A:238:THR:CG2	1:A:240:GLN:NE2	0.55	2.70	8	2
1:A:182:LEU:CD1	1:A:182:LEU:N	0.55	2.67	11	2
1:A:159:TYR:OH	1:A:183:PHE:CD2	0.55	2.59	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:194:ILE:O	1:A:194:ILE:HG22	0.55	2.00	20	4
1:A:182:LEU:CD2	1:A:182:LEU:N	0.54	2.69	8	2
1:A:161:ILE:HD12	1:A:163:LEU:HD23	0.54	1.79	3	2
1:A:188:HIS:HE1	1:A:194:ILE:HD11	0.54	1.62	9	1
1:A:174:LEU:CD2	1:A:205:GLY:CA	0.54	2.85	13	1
1:A:172:ASP:OD1	1:A:194:ILE:HD12	0.54	2.01	16	1
1:A:242:TRP:CD2	1:A:243:LYS:HD3	0.54	2.37	18	1
1:A:211:PHE:CZ	2:B:479:PRO:CA	0.54	2.91	2	14
1:A:186:ALA:HB3	1:A:194:ILE:CB	0.54	2.32	11	10
1:A:194:ILE:CD1	1:A:194:ILE:N	0.54	2.70	8	1
1:A:182:LEU:HD22	1:A:207:VAL:HG11	0.54	1.79	14	1
2:B:478:LYS:O	2:B:478:LYS:CD	0.54	2.55	11	2
1:A:188:HIS:CE1	1:A:192:TRP:HB2	0.54	2.38	19	11
1:A:238:THR:HG21	1:A:240:GLN:NE2	0.54	2.18	8	2
1:A:182:LEU:N	1:A:182:LEU:CD1	0.54	2.70	16	3
1:A:215:ILE:CD1	1:A:215:ILE:N	0.54	2.69	9	1
1:A:192:TRP:CZ3	1:A:206:LEU:CD2	0.53	2.87	10	4
1:A:243:LYS:NZ	2:B:470:PHE:CG	0.53	2.70	14	3
1:A:195:ALA:O	1:A:205:GLY:N	0.53	2.41	16	19
1:A:174:LEU:HD12	1:A:205:GLY:HA3	0.53	1.80	7	2
1:A:243:LYS:NZ	2:B:470:PHE:CE2	0.53	2.66	20	1
2:B:471:ILE:N	2:B:471:ILE:CD1	0.53	2.69	19	1
1:A:170:LYS:NZ	1:A:206:LEU:CD2	0.53	2.72	7	2
1:A:170:LYS:HZ1	1:A:206:LEU:HD23	0.53	1.63	12	1
1:A:183:PHE:CD1	1:A:184:ILE:O	0.53	2.61	20	1
1:A:166:PHE:CE2	1:A:168:ALA:HB2	0.53	2.39	13	1
1:A:211:PHE:CE1	2:B:479:PRO:N	0.53	2.77	17	1
1:A:211:PHE:CE1	2:B:479:PRO:HB3	0.52	2.39	16	10
1:A:161:ILE:HG22	1:A:213:SER:O	0.52	2.04	3	1
1:A:243:LYS:HD2	2:B:470:PHE:CD2	0.52	2.40	17	3
1:A:185:CYS:HB3	1:A:242:TRP:CH2	0.52	2.40	11	2
1:A:182:LEU:HD13	1:A:182:LEU:H	0.52	1.61	15	1
1:A:239:VAL:CG2	1:A:240:GLN:N	0.52	2.72	16	2
1:A:207:VAL:HG11	1:A:212:VAL:HG11	0.52	1.80	16	4
1:A:174:LEU:HD21	1:A:205:GLY:CA	0.52	2.34	13	1
1:A:170:LYS:O	1:A:173:GLU:CG	0.52	2.57	7	3
1:A:206:LEU:O	1:A:207:VAL:HG13	0.52	2.04	5	4
1:A:163:LEU:HD12	1:A:164:TYR:CE1	0.52	2.39	19	1
1:A:192:TRP:HB3	1:A:206:LEU:HD11	0.52	1.82	15	9
2:B:475:PRO:O	2:B:476:ALA:CB	0.51	2.58	19	8
1:A:209:VAL:O	1:A:209:VAL:HG23	0.51	2.04	3	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:162:VAL:CG2	1:A:182:LEU:HD21	0.51	2.34	14	1
1:A:170:LYS:HZ2	1:A:174:LEU:H	0.51	1.48	20	1
1:A:170:LYS:HE3	1:A:192:TRP:CZ3	0.51	2.40	15	1
1:A:159:TYR:CZ	1:A:183:PHE:CE2	0.51	2.99	14	1
1:A:243:LYS:HD3	2:B:470:PHE:CD2	0.51	2.41	1	2
1:A:184:ILE:CG2	1:A:185:CYS:N	0.51	2.74	14	8
1:A:228:ILE:O	1:A:232:LYS:CE	0.51	2.59	4	6
1:A:161:ILE:CD1	1:A:180:GLU:O	0.51	2.59	14	10
1:A:161:ILE:HD13	1:A:180:GLU:O	0.51	2.05	13	9
1:A:185:CYS:C	1:A:242:TRP:CZ3	0.51	2.83	19	4
1:A:184:ILE:HD12	1:A:193:PHE:CB	0.51	2.34	17	2
1:A:230:ASP:O	1:A:234:VAL:HG13	0.51	2.06	15	2
1:A:174:LEU:HD22	1:A:205:GLY:CA	0.51	2.35	2	9
1:A:185:CYS:SG	1:A:186:ALA:N	0.51	2.83	3	3
2:B:471:ILE:HD13	2:B:471:ILE:N	0.51	2.21	17	2
1:A:182:LEU:HD11	1:A:207:VAL:HG21	0.51	1.83	18	1
1:A:211:PHE:CE2	2:B:479:PRO:HB3	0.50	2.41	3	5
1:A:185:CYS:HB2	1:A:242:TRP:CH2	0.50	2.41	14	2
2:B:478:LYS:O	2:B:478:LYS:CG	0.50	2.59	11	2
1:A:192:TRP:CZ2	2:B:477:PRO:HD3	0.50	2.42	14	20
1:A:170:LYS:HE3	1:A:192:TRP:CH2	0.50	2.41	15	2
1:A:162:VAL:CG1	1:A:164:TYR:O	0.50	2.60	2	1
1:A:234:VAL:O	1:A:234:VAL:HG23	0.50	2.06	19	5
1:A:236:LEU:HD12	1:A:236:LEU:C	0.50	2.26	6	1
1:A:159:TYR:CD1	1:A:183:PHE:CZ	0.50	2.99	8	1
1:A:236:LEU:O	1:A:236:LEU:HD23	0.50	2.06	16	1
1:A:161:ILE:HG23	1:A:163:LEU:HD21	0.50	1.83	12	4
1:A:194:ILE:CG2	1:A:194:ILE:O	0.50	2.59	17	2
1:A:159:TYR:CE2	1:A:215:ILE:HD12	0.50	2.40	16	1
1:A:210:GLY:O	2:B:479:PRO:CG	0.50	2.59	8	11
1:A:236:LEU:CD1	1:A:237:PRO:O	0.50	2.60	6	2
1:A:185:CYS:O	1:A:236:LEU:CD1	0.50	2.60	18	2
1:A:228:ILE:O	1:A:231:ILE:N	0.50	2.45	15	2
1:A:191:GLU:OE1	2:B:476:ALA:CA	0.50	2.60	20	2
1:A:192:TRP:CD1	2:B:472:PRO:HG3	0.50	2.42	3	2
1:A:159:TYR:CD2	1:A:183:PHE:CZ	0.50	3.00	14	1
1:A:160:ALA:HB3	1:A:182:LEU:HD22	0.50	1.82	15	2
1:A:173:GLU:N	1:A:173:GLU:CD	0.50	2.65	19	1
1:A:214:ILE:O	1:A:215:ILE:CG2	0.50	2.60	5	12
2:B:478:LYS:CD	2:B:478:LYS:O	0.50	2.60	7	2
1:A:170:LYS:HE2	1:A:192:TRP:CH2	0.49	2.42	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:239:VAL:CG2	1:A:243:LYS:NZ	0.49	2.75	6	1
1:A:191:GLU:OE2	2:B:476:ALA:CB	0.49	2.60	16	1
1:A:181:ASN:ND2	1:A:181:ASN:N	0.49	2.60	20	1
1:A:159:TYR:CD2	1:A:215:ILE:HG12	0.49	2.41	5	1
1:A:160:ALA:HB3	1:A:184:ILE:HD11	0.49	1.84	13	1
1:A:243:LYS:HE3	2:B:470:PHE:CE2	0.49	2.41	19	1
1:A:175:THR:CG2	1:A:175:THR:O	0.49	2.60	4	1
1:A:239:VAL:HG22	1:A:243:LYS:HZ2	0.49	1.60	11	1
1:A:196:LYS:CD	1:A:197:PRO:O	0.49	2.60	4	1
1:A:214:ILE:HG21	1:A:230:ASP:HB3	0.49	1.85	17	1
1:A:189:ASN:C	1:A:191:GLU:N	0.49	2.65	13	20
1:A:163:LEU:C	1:A:164:TYR:CG	0.49	2.85	4	4
1:A:170:LYS:NZ	1:A:174:LEU:H	0.49	2.05	20	1
1:A:211:PHE:CD1	2:B:479:PRO:HB3	0.49	2.42	17	9
1:A:231:ILE:CG2	1:A:232:LYS:N	0.49	2.75	12	5
1:A:173:GLU:CD	1:A:173:GLU:N	0.49	2.66	11	1
1:A:204:PRO:HG2	2:B:470:PHE:CE2	0.49	2.42	20	4
1:A:182:LEU:H	1:A:182:LEU:HD23	0.49	1.68	5	3
1:A:240:GLN:OE1	1:A:241:GLU:N	0.49	2.46	19	2
1:A:162:VAL:HG11	1:A:177:TYR:O	0.49	2.07	13	4
1:A:240:GLN:O	1:A:244:SER:CB	0.49	2.61	18	1
1:A:161:ILE:HG23	1:A:163:LEU:CD2	0.49	2.38	13	11
1:A:170:LYS:CE	1:A:206:LEU:CD2	0.49	2.91	13	3
1:A:165:ASP:OD1	1:A:178:VAL:CG1	0.49	2.61	16	1
1:A:234:VAL:O	1:A:235:ASN:CB	0.49	2.61	16	2
1:A:166:PHE:HE2	1:A:170:LYS:HZ1	0.48	1.51	2	1
1:A:192:TRP:CH2	2:B:477:PRO:HD3	0.48	2.43	19	5
1:A:186:ALA:HB2	1:A:242:TRP:CE3	0.48	2.43	19	2
1:A:174:LEU:CD2	1:A:205:GLY:HA2	0.48	2.39	13	1
1:A:170:LYS:CE	1:A:192:TRP:CZ3	0.48	2.96	15	1
1:A:239:VAL:HG13	1:A:240:GLN:H	0.48	1.69	17	1
1:A:240:GLN:OE1	2:B:471:ILE:CD1	0.48	2.61	9	3
1:A:169:GLU:N	1:A:170:LYS:HZ3	0.48	1.97	5	2
1:A:170:LYS:O	1:A:173:GLU:CB	0.48	2.61	13	3
1:A:162:VAL:CG1	1:A:177:TYR:O	0.48	2.61	19	2
1:A:185:CYS:SG	1:A:196:LYS:CG	0.48	3.01	15	1
1:A:185:CYS:N	1:A:194:ILE:O	0.48	2.46	1	11
1:A:161:ILE:CG2	1:A:213:SER:OG	0.48	2.62	5	1
1:A:166:PHE:HB3	1:A:211:PHE:CE1	0.48	2.43	5	1
1:A:165:ASP:OD1	1:A:178:VAL:HG13	0.48	2.08	16	1
1:A:227:VAL:HG13	1:A:228:ILE:HD12	0.48	1.85	9	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:159:TYR:CD2	1:A:215:ILE:HG13	0.48	2.43	5	1
1:A:187:HIS:O	1:A:239:VAL:HG13	0.48	2.09	16	1
1:A:231:ILE:HG13	1:A:236:LEU:HD23	0.48	1.86	19	1
1:A:184:ILE:HD12	1:A:195:ALA:HB2	0.48	1.84	1	1
1:A:189:ASN:O	1:A:191:GLU:N	0.48	2.47	4	20
1:A:172:ASP:O	1:A:173:GLU:C	0.48	2.52	10	20
1:A:242:TRP:CD2	1:A:243:LYS:CD	0.48	2.97	18	1
1:A:186:ALA:HB3	1:A:194:ILE:CG1	0.48	2.39	13	2
1:A:188:HIS:CD2	1:A:239:VAL:HB	0.48	2.44	18	1
1:A:175:THR:O	1:A:175:THR:HG23	0.48	2.09	1	3
1:A:211:PHE:CE1	2:B:479:PRO:CB	0.48	2.97	16	8
1:A:161:ILE:HG22	1:A:213:SER:OG	0.48	2.09	5	1
1:A:243:LYS:HE2	2:B:470:PHE:CD2	0.48	2.44	12	1
1:A:211:PHE:CE1	2:B:479:PRO:CA	0.48	2.97	17	3
1:A:174:LEU:HD22	1:A:205:GLY:C	0.47	2.29	4	3
1:A:188:HIS:ND1	1:A:239:VAL:CG1	0.47	2.71	7	1
1:A:210:GLY:O	2:B:479:PRO:CB	0.47	2.62	10	3
1:A:174:LEU:HD23	1:A:205:GLY:HA3	0.47	1.87	14	3
1:A:166:PHE:HB3	1:A:211:PHE:CE2	0.47	2.44	19	2
1:A:187:HIS:HB2	1:A:193:PHE:CD1	0.47	2.44	19	8
1:A:159:TYR:CZ	1:A:183:PHE:CG	0.47	3.02	17	1
1:A:204:PRO:HG2	2:B:470:PHE:CZ	0.47	2.44	4	4
2:B:478:LYS:CD	2:B:478:LYS:N	0.47	2.78	19	1
1:A:160:ALA:CB	1:A:182:LEU:CD2	0.47	2.86	20	1
2:B:470:PHE:N	2:B:470:PHE:CD1	0.47	2.76	8	1
1:A:239:VAL:CG1	1:A:240:GLN:N	0.47	2.77	18	3
1:A:160:ALA:HB3	1:A:182:LEU:HG	0.47	1.86	10	1
1:A:159:TYR:CD1	1:A:183:PHE:CG	0.47	3.03	11	1
1:A:166:PHE:CZ	1:A:167:LYS:O	0.47	2.67	12	1
1:A:183:PHE:CD1	1:A:183:PHE:N	0.47	2.81	11	3
1:A:166:PHE:CE2	2:B:477:PRO:HG3	0.47	2.45	11	4
1:A:211:PHE:CD2	2:B:479:PRO:HB3	0.47	2.45	4	2
1:A:192:TRP:CE3	1:A:206:LEU:CD2	0.47	2.95	10	2
1:A:163:LEU:HB2	1:A:164:TYR:CE1	0.47	2.45	11	2
2:B:470:PHE:C	2:B:471:ILE:HD12	0.47	2.30	13	1
2:B:471:ILE:N	2:B:471:ILE:HD12	0.47	2.24	13	1
1:A:159:TYR:CD1	1:A:160:ALA:N	0.46	2.83	2	2
1:A:193:PHE:O	1:A:207:VAL:HG23	0.46	2.11	10	1
1:A:159:TYR:CE1	1:A:183:PHE:HB2	0.46	2.44	4	1
1:A:161:ILE:CD1	1:A:161:ILE:C	0.46	2.83	3	1
1:A:172:ASP:O	1:A:174:LEU:N	0.46	2.48	20	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:172:ASP:CB	1:A:206:LEU:CB	0.46	2.92	14	3
1:A:211:PHE:C	1:A:212:VAL:CG1	0.46	2.83	17	6
1:A:226:ASP:O	1:A:229:GLU:N	0.46	2.49	2	10
1:A:163:LEU:HB2	1:A:164:TYR:CE2	0.46	2.45	20	11
1:A:227:VAL:HG13	1:A:228:ILE:H	0.46	1.71	12	2
1:A:209:VAL:HG23	1:A:209:VAL:O	0.46	2.08	1	4
1:A:194:ILE:HG21	2:B:470:PHE:CE2	0.46	2.46	3	1
1:A:159:TYR:O	1:A:215:ILE:HD13	0.46	2.11	5	1
1:A:166:PHE:CD1	1:A:167:LYS:N	0.46	2.83	6	3
1:A:159:TYR:O	1:A:215:ILE:CD1	0.46	2.64	5	1
1:A:211:PHE:CZ	2:B:479:PRO:HB3	0.46	2.45	14	3
1:A:166:PHE:HB2	1:A:211:PHE:CE2	0.46	2.45	6	5
1:A:183:PHE:CD1	1:A:183:PHE:C	0.46	2.86	20	1
1:A:226:ASP:O	1:A:230:ASP:N	0.46	2.49	7	9
1:A:182:LEU:HD12	1:A:182:LEU:H	0.46	1.71	6	1
1:A:240:GLN:C	1:A:240:GLN:OE1	0.46	2.54	18	1
1:A:185:CYS:SG	1:A:242:TRP:CZ2	0.46	3.09	19	1
2:B:478:LYS:N	2:B:478:LYS:CD	0.46	2.78	16	1
1:A:191:GLU:O	1:A:209:VAL:CG1	0.46	2.63	10	2
1:A:176:THR:HG23	1:A:180:GLU:CG	0.46	2.40	14	1
1:A:229:GLU:O	1:A:233:SER:CB	0.45	2.64	15	1
1:A:162:VAL:HG22	1:A:180:GLU:N	0.45	2.26	17	1
1:A:228:ILE:HG22	1:A:232:LYS:CD	0.45	2.42	20	1
1:A:195:ALA:C	1:A:196:LYS:CG	0.45	2.85	5	2
1:A:187:HIS:O	1:A:239:VAL:N	0.45	2.50	8	1
1:A:243:LYS:HE2	2:B:470:PHE:CG	0.45	2.47	20	4
2:B:478:LYS:HG2	2:B:478:LYS:O	0.45	2.12	19	2
1:A:187:HIS:HA	1:A:192:TRP:O	0.45	2.11	16	1
1:A:162:VAL:HG13	1:A:182:LEU:CD1	0.45	2.41	17	1
1:A:184:ILE:HD13	1:A:193:PHE:CD2	0.45	2.47	9	1
1:A:174:LEU:HD23	1:A:207:VAL:HG13	0.45	1.87	4	1
1:A:159:TYR:CE1	1:A:183:PHE:CE2	0.45	3.04	8	1
1:A:207:VAL:CG2	1:A:212:VAL:HG11	0.45	2.41	12	3
1:A:162:VAL:CG1	1:A:182:LEU:CD1	0.45	2.81	17	1
1:A:161:ILE:HG23	1:A:163:LEU:HD23	0.45	1.89	14	2
1:A:242:TRP:C	1:A:242:TRP:CD1	0.45	2.89	19	1
1:A:185:CYS:CB	1:A:194:ILE:O	0.45	2.65	1	1
1:A:160:ALA:HB3	1:A:182:LEU:HD13	0.45	1.89	6	1
1:A:170:LYS:HE2	1:A:206:LEU:CD2	0.45	2.42	13	2
1:A:242:TRP:C	1:A:244:SER:N	0.45	2.70	18	1
1:A:175:THR:O	1:A:175:THR:CG2	0.45	2.64	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:166:PHE:HZ	1:A:170:LYS:HZ1	0.45	1.51	17	1
1:A:159:TYR:OH	1:A:161:ILE:CG1	0.45	2.65	19	1
1:A:172:ASP:OD2	1:A:206:LEU:N	0.45	2.49	1	1
1:A:159:TYR:OH	1:A:181:ASN:ND2	0.45	2.50	2	2
1:A:192:TRP:CG	2:B:472:PRO:HG3	0.45	2.47	13	2
1:A:166:PHE:HB2	1:A:211:PHE:CD1	0.45	2.47	10	2
1:A:159:TYR:O	1:A:215:ILE:N	0.45	2.50	14	1
1:A:242:TRP:CG	1:A:243:LYS:N	0.45	2.85	18	1
1:A:183:PHE:CE2	1:A:185:CYS:HB2	0.45	2.47	19	1
2:B:470:PHE:CD1	2:B:470:PHE:N	0.44	2.84	1	1
1:A:188:HIS:NE2	1:A:194:ILE:HG12	0.44	2.26	16	3
1:A:208:PRO:O	1:A:212:VAL:CG2	0.44	2.60	20	3
1:A:211:PHE:CE2	2:B:479:PRO:CB	0.44	3.00	8	2
1:A:160:ALA:HB3	1:A:182:LEU:O	0.44	2.12	10	2
1:A:192:TRP:NE1	2:B:474:ARG:O	0.44	2.50	9	1
1:A:196:LYS:CB	1:A:204:PRO:HA	0.44	2.42	11	1
1:A:185:CYS:CB	1:A:242:TRP:CH2	0.44	3.00	11	2
1:A:189:ASN:O	1:A:190:CYS:C	0.44	2.55	9	18
1:A:163:LEU:O	1:A:164:TYR:CD1	0.44	2.71	3	2
1:A:162:VAL:O	1:A:179:GLY:CA	0.44	2.66	8	11
1:A:162:VAL:HG22	1:A:180:GLU:CB	0.44	2.43	4	2
2:B:473:SER:OG	2:B:474:ARG:CZ	0.44	2.66	3	1
1:A:159:TYR:CD1	1:A:183:PHE:CD2	0.44	3.05	1	1
1:A:165:ASP:OD1	1:A:166:PHE:N	0.44	2.50	1	2
1:A:168:ALA:CB	1:A:174:LEU:N	0.44	2.81	5	6
1:A:191:GLU:CD	2:B:476:ALA:CB	0.44	2.80	20	2
1:A:239:VAL:HG13	1:A:240:GLN:HG3	0.44	1.89	10	3
1:A:172:ASP:HB3	1:A:206:LEU:CB	0.44	2.43	14	1
1:A:209:VAL:CB	1:A:227:VAL:HG21	0.44	2.37	17	1
1:A:239:VAL:HG21	2:B:470:PHE:HB3	0.44	1.90	4	1
1:A:174:LEU:HD21	1:A:205:GLY:HA2	0.44	1.90	13	1
2:B:472:PRO:O	2:B:473:SER:CB	0.44	2.66	4	1
1:A:207:VAL:CG2	1:A:212:VAL:CG1	0.44	2.95	16	1
2:B:478:LYS:CG	2:B:478:LYS:O	0.44	2.66	16	1
1:A:232:LYS:HZ3	1:A:232:LYS:HB3	0.44	1.73	4	1
1:A:160:ALA:HB2	1:A:184:ILE:HG12	0.43	1.90	5	1
1:A:160:ALA:HB3	1:A:184:ILE:CD1	0.43	2.43	7	1
1:A:207:VAL:HG13	1:A:212:VAL:HG11	0.43	1.88	13	2
1:A:243:LYS:HG2	2:B:470:PHE:CD1	0.43	2.47	18	1
1:A:232:LYS:HZ2	1:A:232:LYS:HB3	0.43	1.73	8	1
1:A:243:LYS:HZ2	2:B:470:PHE:CB	0.43	2.26	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:188:HIS:CE1	2:B:472:PRO:HG3	0.43	2.48	6	2
1:A:190:CYS:HB3	1:A:231:ILE:HD13	0.43	1.90	17	1
1:A:172:ASP:N	1:A:172:ASP:OD2	0.43	2.51	4	1
1:A:243:LYS:CD	2:B:470:PHE:CD2	0.43	3.02	17	2
1:A:195:ALA:HB3	1:A:207:VAL:CG2	0.43	2.40	10	1
1:A:242:TRP:HB3	1:A:243:LYS:NZ	0.43	2.28	18	1
1:A:166:PHE:HB2	1:A:211:PHE:CE1	0.43	2.49	10	2
1:A:206:LEU:HG	1:A:207:VAL:N	0.43	2.28	11	3
1:A:211:PHE:O	1:A:212:VAL:CG1	0.43	2.67	14	1
1:A:174:LEU:CB	1:A:205:GLY:HA2	0.43	2.43	16	1
1:A:162:VAL:N	1:A:180:GLU:O	0.43	2.51	13	1
1:A:160:ALA:O	1:A:182:LEU:CD2	0.43	2.63	17	1
1:A:176:THR:HG22	1:A:177:TYR:N	0.43	2.29	13	1
1:A:203:GLY:HA2	1:A:204:PRO:C	0.43	2.34	14	2
1:A:161:ILE:C	1:A:161:ILE:CD1	0.43	2.87	4	1
1:A:174:LEU:HD13	1:A:205:GLY:HA2	0.42	1.90	5	1
1:A:174:LEU:HG	1:A:205:GLY:CA	0.42	2.44	9	3
1:A:173:GLU:OE1	1:A:173:GLU:O	0.42	2.37	11	1
1:A:234:VAL:HG23	1:A:236:LEU:CB	0.42	2.44	11	1
1:A:162:VAL:CG2	1:A:177:TYR:O	0.42	2.67	1	1
1:A:214:ILE:C	1:A:215:ILE:HG23	0.42	2.35	5	1
1:A:162:VAL:O	1:A:179:GLY:N	0.42	2.52	8	1
1:A:172:ASP:CB	1:A:206:LEU:HB2	0.42	2.44	15	2
1:A:194:ILE:HD11	1:A:206:LEU:HD12	0.42	1.91	19	1
1:A:239:VAL:HG21	2:B:470:PHE:HB2	0.42	1.91	9	1
1:A:166:PHE:CE1	2:B:477:PRO:HB3	0.42	2.49	7	2
1:A:227:VAL:HG13	1:A:228:ILE:N	0.42	2.28	12	3
1:A:234:VAL:CG2	1:A:234:VAL:O	0.42	2.68	17	1
1:A:242:TRP:CE2	1:A:243:LYS:HD3	0.42	2.49	18	1
1:A:243:LYS:O	1:A:244:SER:C	0.42	2.58	3	7
1:A:184:ILE:HG22	1:A:185:CYS:N	0.42	2.29	5	2
1:A:160:ALA:O	1:A:182:LEU:CD1	0.42	2.63	9	1
1:A:234:VAL:HG23	1:A:236:LEU:HB2	0.42	1.92	11	1
1:A:172:ASP:CB	1:A:206:LEU:HB3	0.42	2.44	14	1
1:A:170:LYS:HE2	1:A:192:TRP:CZ3	0.42	2.49	19	1
1:A:173:GLU:CG	1:A:173:GLU:O	0.42	2.67	11	2
1:A:189:ASN:C	1:A:190:CYS:SG	0.42	2.98	14	6
1:A:211:PHE:C	1:A:212:VAL:HG13	0.42	2.35	14	1
1:A:195:ALA:N	1:A:205:GLY:O	0.42	2.53	1	3
1:A:234:VAL:C	1:A:236:LEU:N	0.42	2.73	18	2
1:A:203:GLY:HA3	1:A:204:PRO:C	0.42	2.34	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:478:LYS:O	2:B:478:LYS:HG2	0.42	2.15	16	1
1:A:187:HIS:CD2	1:A:238:THR:HA	0.42	2.50	7	2
1:A:183:PHE:O	1:A:195:ALA:HA	0.42	2.15	19	4
1:A:163:LEU:HD21	1:A:213:SER:OG	0.42	2.15	5	1
1:A:239:VAL:HG21	2:B:470:PHE:CB	0.42	2.45	9	1
1:A:194:ILE:HD12	1:A:206:LEU:HD12	0.42	1.92	4	1
1:A:239:VAL:CG1	1:A:240:GLN:OE1	0.41	2.68	3	1
1:A:183:PHE:O	1:A:183:PHE:CD1	0.41	2.73	9	1
1:A:159:TYR:CE2	1:A:215:ILE:HD11	0.41	2.49	10	1
1:A:214:ILE:CG1	1:A:227:VAL:HG23	0.41	2.43	17	1
1:A:242:TRP:O	1:A:244:SER:N	0.41	2.53	18	1
1:A:194:ILE:O	1:A:194:ILE:CG2	0.41	2.68	20	1
1:A:191:GLU:O	1:A:208:PRO:HA	0.41	2.15	12	3
1:A:159:TYR:C	1:A:215:ILE:O	0.41	2.59	17	1
1:A:189:ASN:O	1:A:190:CYS:SG	0.41	2.77	8	4
1:A:187:HIS:CG	1:A:236:LEU:HD21	0.41	2.50	18	1
1:A:173:GLU:O	1:A:173:GLU:OE1	0.41	2.38	19	1
1:A:160:ALA:CB	1:A:184:ILE:HD11	0.41	2.45	13	2
1:A:232:LYS:H	1:A:232:LYS:NZ	0.41	2.13	8	1
2:B:471:ILE:CG2	2:B:472:PRO:HD2	0.41	2.46	14	4
1:A:226:ASP:O	1:A:227:VAL:C	0.41	2.57	19	3
1:A:209:VAL:O	1:A:209:VAL:CG2	0.41	2.68	3	1
1:A:184:ILE:N	1:A:184:ILE:HD12	0.41	2.30	4	2
1:A:238:THR:HG22	1:A:239:VAL:H	0.41	1.76	5	1
1:A:191:GLU:OE1	2:B:476:ALA:CB	0.41	2.66	15	1
1:A:242:TRP:CE2	1:A:243:LYS:CD	0.41	3.04	18	1
1:A:188:HIS:HB3	1:A:239:VAL:HG12	0.41	1.91	3	2
1:A:196:LYS:NZ	1:A:196:LYS:CB	0.41	2.83	6	1
1:A:173:GLU:O	1:A:174:LEU:HD22	0.41	2.15	17	1
1:A:234:VAL:O	1:A:235:ASN:C	0.41	2.59	17	4
1:A:160:ALA:O	1:A:182:LEU:O	0.41	2.38	15	2
1:A:172:ASP:HB2	1:A:206:LEU:CB	0.41	2.46	4	2
1:A:173:GLU:O	1:A:173:GLU:CD	0.41	2.59	14	1
1:A:232:LYS:O	1:A:235:ASN:N	0.41	2.54	15	1
1:A:184:ILE:C	1:A:185:CYS:SG	0.41	2.98	17	1
1:A:173:GLU:O	1:A:173:GLU:CG	0.41	2.68	19	1
1:A:184:ILE:HD12	1:A:184:ILE:N	0.41	2.30	2	1
1:A:170:LYS:HZ3	1:A:192:TRP:HZ3	0.41	1.48	2	1
1:A:174:LEU:CG	1:A:205:GLY:HA3	0.41	2.46	11	2
1:A:174:LEU:HD13	1:A:174:LEU:HA	0.41	1.80	12	1
1:A:162:VAL:O	1:A:162:VAL:CG2	0.41	2.69	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:184:ILE:HA	1:A:195:ALA:CB	0.41	2.46	10	1
1:A:159:TYR:CE2	1:A:215:ILE:HG13	0.41	2.51	10	1
1:A:170:LYS:O	1:A:173:GLU:OE2	0.41	2.38	11	1
1:A:227:VAL:O	1:A:230:ASP:N	0.41	2.54	12	1
1:A:182:LEU:CD1	1:A:207:VAL:CG2	0.41	2.95	18	1
1:A:159:TYR:CE2	1:A:215:ILE:CG1	0.40	3.04	13	1
1:A:165:ASP:OD1	1:A:176:THR:O	0.40	2.40	1	1
1:A:159:TYR:O	1:A:215:ILE:O	0.40	2.40	4	1
1:A:229:GLU:HA	1:A:232:LYS:CD	0.40	2.47	1	1
1:A:163:LEU:HB2	1:A:164:TYR:CZ	0.40	2.51	3	1
1:A:196:LYS:CG	1:A:197:PRO:HD2	0.40	2.46	6	1
1:A:193:PHE:O	1:A:207:VAL:CG2	0.40	2.69	10	1
1:A:176:THR:HG23	1:A:180:GLU:OE2	0.40	2.16	11	1
1:A:172:ASP:OD1	2:B:470:PHE:C	0.40	2.60	13	1
1:A:214:ILE:HG21	1:A:230:ASP:CB	0.40	2.46	17	1
2:B:478:LYS:N	2:B:478:LYS:HD2	0.40	2.31	19	1
1:A:228:ILE:H	1:A:228:ILE:HD12	0.40	1.76	20	1
1:A:234:VAL:CG2	1:A:236:LEU:HB3	0.40	2.46	8	1
1:A:193:PHE:CE2	1:A:227:VAL:CG2	0.40	3.04	14	1
1:A:175:THR:C	1:A:176:THR:HG1	0.40	2.19	16	1
1:A:174:LEU:CD2	1:A:205:GLY:HA3	0.40	2.46	5	1
1:A:163:LEU:HD11	1:A:213:SER:HB3	0.40	1.92	7	1
1:A:172:ASP:CG	1:A:206:LEU:CB	0.40	2.90	10	1
1:A:182:LEU:HD23	1:A:195:ALA:CB	0.40	2.47	15	1
1:A:174:LEU:CB	1:A:205:GLY:CA	0.40	3.00	16	1
1:A:193:PHE:N	1:A:207:VAL:O	0.40	2.55	16	1
1:A:191:GLU:OE1	2:B:475:PRO:O	0.40	2.40	16	1
1:A:239:VAL:CG1	1:A:240:GLN:H	0.40	2.29	18	1

## 6.3 Torsion angles [i](#)

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	71/105 (68%)	58±2 (82±3%)	11±2 (16±2%)	2±1 (3±2%)	8	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	11/24 (46%)	8±1 (70±8%)	3±1 (23±9%)	1±1 (8±6%)	2	15
All	All	1640/2580 (64%)	1314 (80%)	272 (17%)	54 (3%)	6	37

All 9 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	173	GLU	12
1	A	203	GLY	10
2	B	476	ALA	9
2	B	480	PRO	8
1	A	190	CYS	6
1	A	215	ILE	4
1	A	238	THR	3
1	A	169	GLU	1
1	A	177	TYR	1

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	62/86 (72%)	45±3 (72±5%)	18±3 (28±5%)	2	19
2	B	10/19 (53%)	8±1 (84±9%)	2±1 (16±9%)	5	43
All	All	1440/2100 (69%)	1059 (74%)	381 (26%)	2	22

All 50 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	161	ILE	20
1	A	170	LYS	20
1	A	206	LEU	20
1	A	207	VAL	20
1	A	232	LYS	20
2	B	478	LYS	19
1	A	187	HIS	17

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Mol	Chain	Res	Type	Models (Total)
1	A	188	HIS	17
1	A	163	LEU	17
1	A	182	LEU	15
1	A	209	VAL	13
1	A	233	SER	12
1	A	240	GLN	11
1	A	231	ILE	11
1	A	227	VAL	10
1	A	244	SER	10
1	A	174	LEU	10
1	A	242	TRP	9
1	A	226	ASP	8
1	A	196	LYS	7
1	A	215	ILE	7
1	A	236	LEU	7
1	A	181	ASN	6
2	B	473	SER	6
1	A	238	THR	5
1	A	172	ASP	5
1	A	176	THR	5
1	A	185	CYS	5
2	B	474	ARG	4
1	A	164	TYR	4
1	A	162	VAL	4
1	A	159	TYR	4
1	A	230	ASP	4
1	A	239	VAL	3
1	A	194	ILE	3
1	A	165	ASP	3
1	A	183	PHE	3
1	A	173	GLU	2
1	A	213	SER	2
1	A	166	PHE	2
2	B	471	ILE	2
1	A	234	VAL	1
1	A	243	LYS	1
1	A	241	GLU	1
1	A	212	VAL	1
1	A	175	THR	1
1	A	180	GLU	1
1	A	189	ASN	1
1	A	167	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	184	ILE	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

There are no such molecules in this entry.

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

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided