



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 05:58 pm GMT

PDB ID : 1EMO
Title : NMR STUDY OF A PAIR OF FIBRILLIN CA²⁺ BINDING EPIDERMAL GROWTH FACTOR-LIKE DOMAINS, 22 STRUCTURES
Authors : Downing, A.K.; Campbell, I.D.; Handford, P.A.
Deposited on : 1996-08-05

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

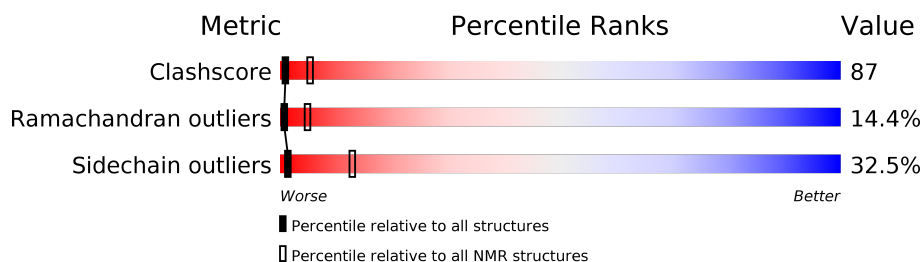
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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 ≥ 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	82	

2 Ensemble composition and analysis

This entry contains 22 models. Model 3 is the overall representative, medoid model (most similar to other models).

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:2129-A:2205 (77)	0.51	3

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 5 clusters and 1 single-model cluster was found.

Cluster number	Models
1	2, 4, 6, 10, 11, 17, 22
2	1, 3, 5, 8, 9, 13
3	7, 19, 20
4	15, 16, 21
5	14, 18
Single-model clusters	12

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1120 atoms, of which 520 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called FIBRILLIN.

Mol	Chain	Residues	Atoms						Trace
1	A	82	Total	C	H	N	O	S	0
			1118	356	520	96	131	15	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2158	ILE	THR	CONFLICT	UNP P35555

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

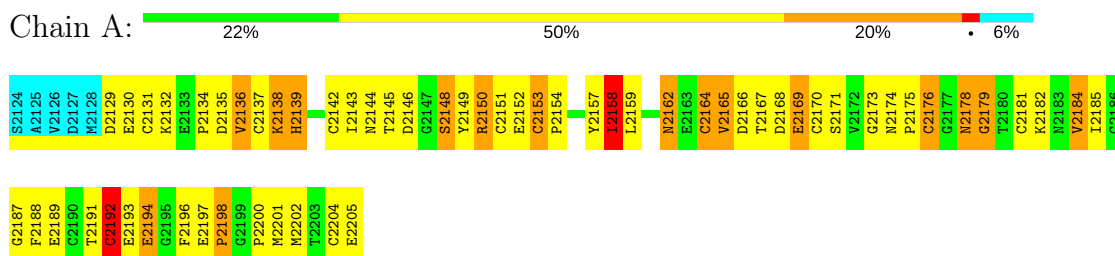
Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

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: FIBRILLIN

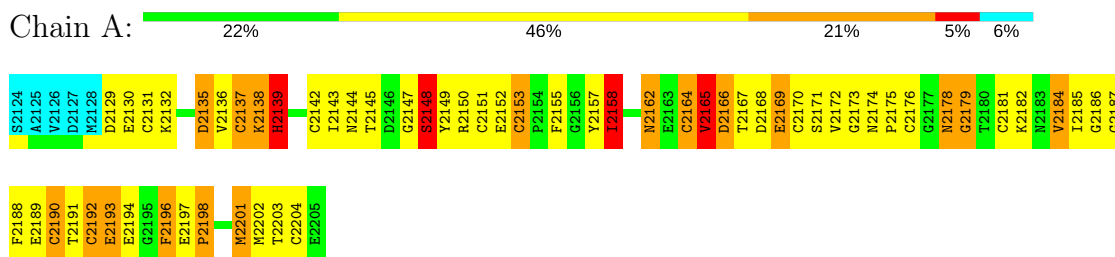


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

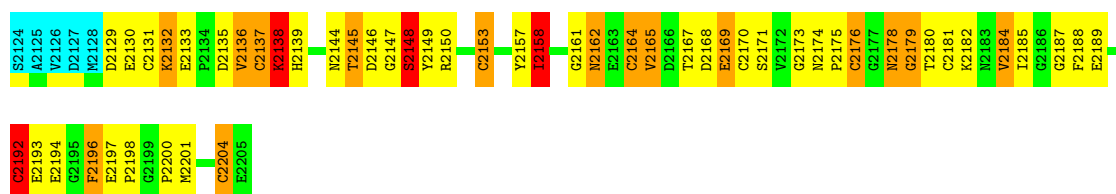
• Molecule 1: FIBRILLIN



4.2.2 Score per residue for model 2

• Molecule 1: FIBRILLIN

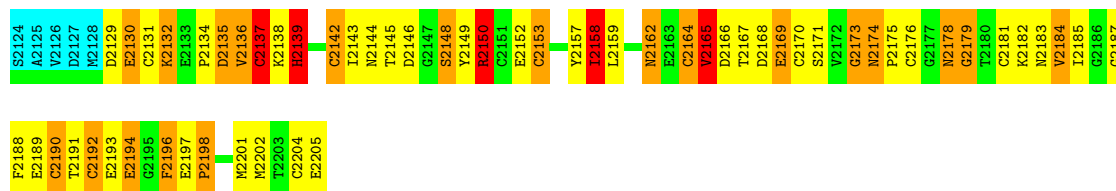




4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: FIBRILLIN

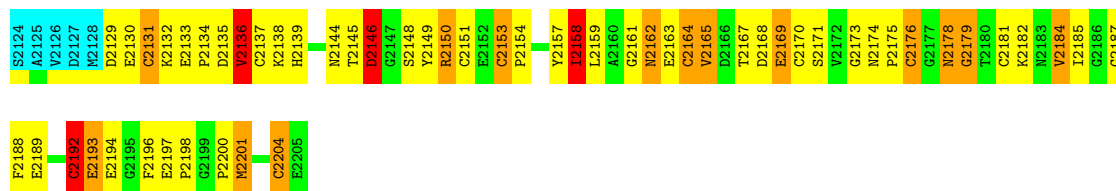
Chain A: 23% 40% 24% 6% 6%



4.2.4 Score per residue for model 4

- Molecule 1: FIBRILLIN

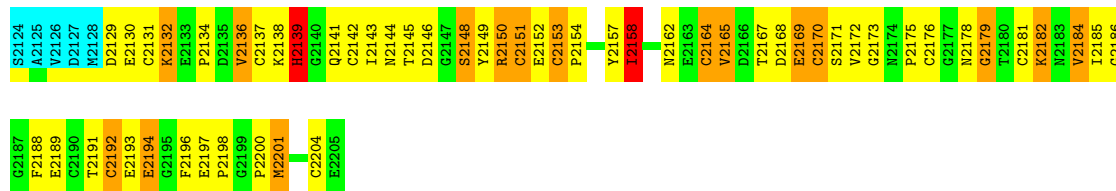
Chain A: 27% 45% 17% 5% 6%



4.2.5 Score per residue for model 5

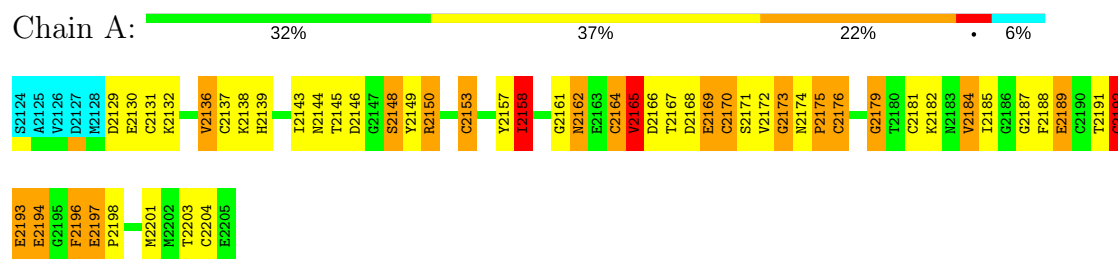
- Molecule 1: FIBRILLIN

Chain A: 27% 45% 20% 6%



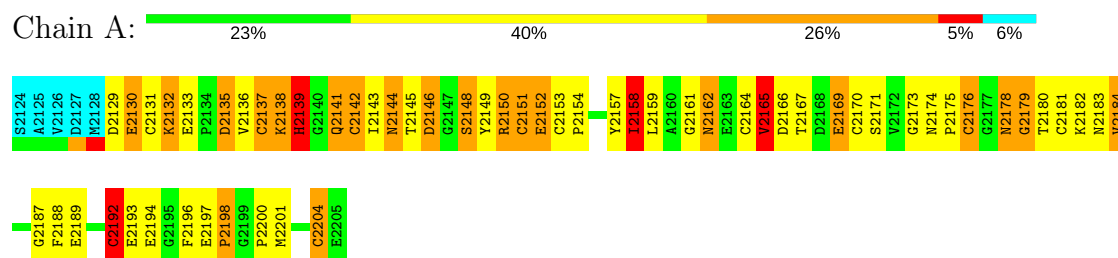
4.2.6 Score per residue for model 6

- Molecule 1: FIBRILLIN



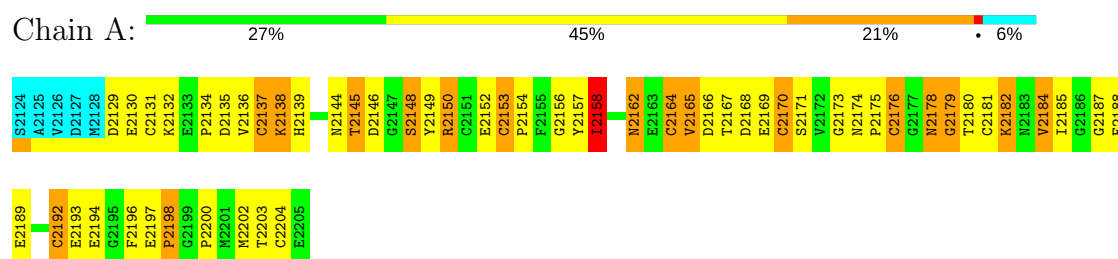
4.2.7 Score per residue for model 7

- Molecule 1: FIBRILLIN



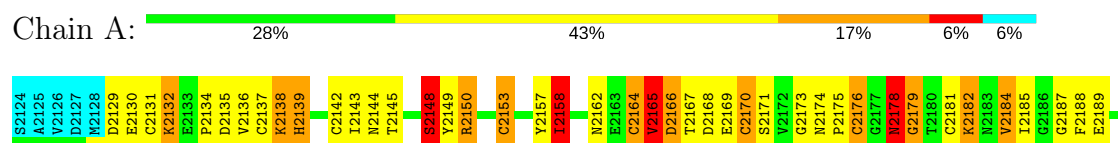
4.2.8 Score per residue for model 8

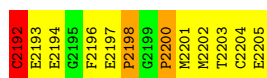
- Molecule 1: FIBRILLIN



4.2.9 Score per residue for model 9

- Molecule 1: FIBRILLIN





4.2.10 Score per residue for model 10

- Molecule 1: FIBRILLIN

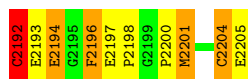
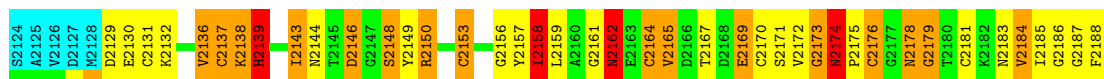
Chain A: 26% 43% 22% 6%



4.2.11 Score per residue for model 11

- Molecule 1: FIBRILLIN

Chain A: 32% 32% 24% 6% 6%



4.2.12 Score per residue for model 12

- Molecule 1: FIBRILLIN

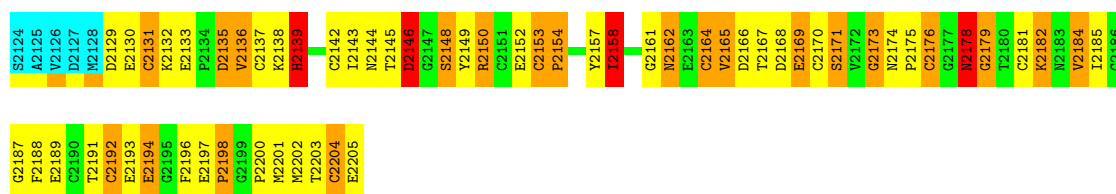
Chain A: 24% 40% 24% 5% 6%



4.2.13 Score per residue for model 13

- Molecule 1: FIBRILLIN

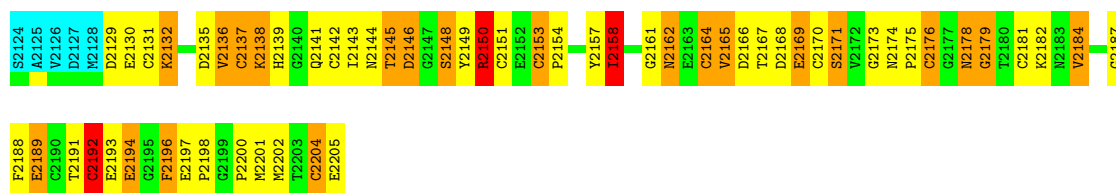
Chain A: 22% 41% 26% 5% 6%



4.2.14 Score per residue for model 14

- Molecule 1: FIBRILLIN

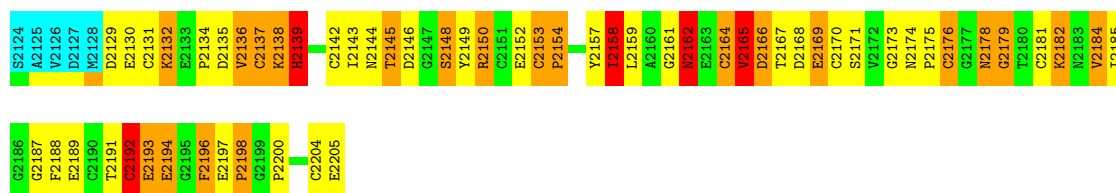
Chain A: 24% 40% 26% 6%



4.2.15 Score per residue for model 15

- Molecule 1: FIBRILLIN

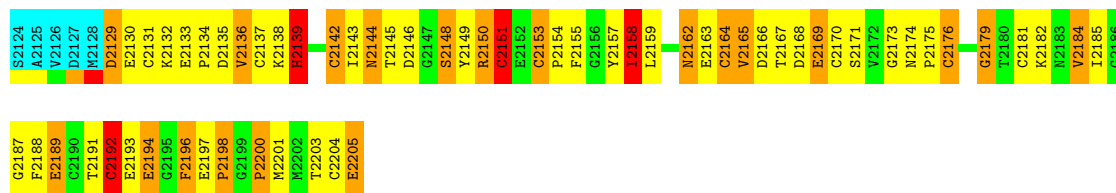
Chain A: 24% 38% 26% 6% 6%



4.2.16 Score per residue for model 16

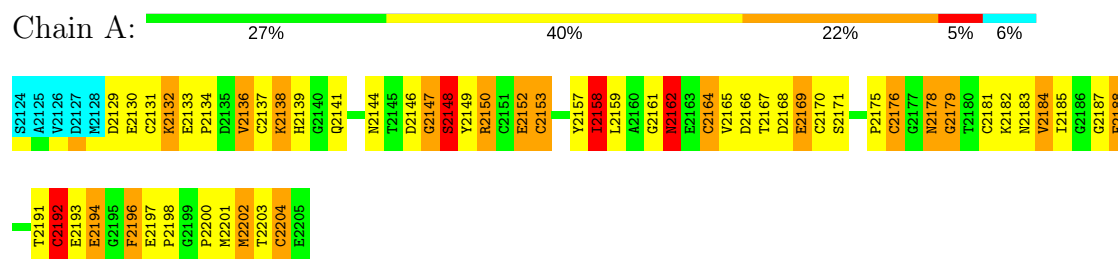
- Molecule 1: FIBRILLIN

Chain A: 21% 44% 24% 5% 6%



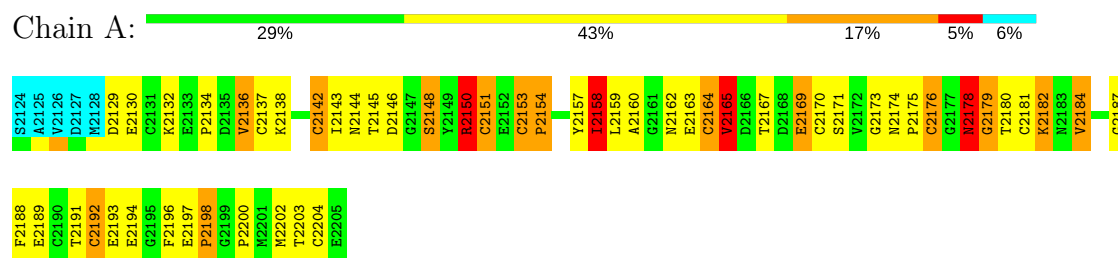
4.2.17 Score per residue for model 17

• Molecule 1: FIBRILLIN



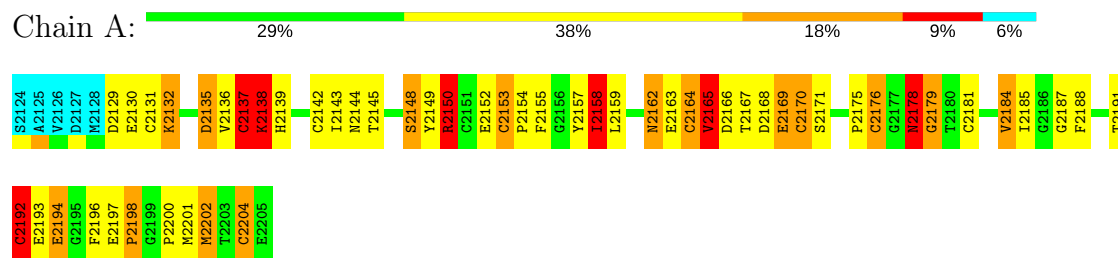
4.2.18 Score per residue for model 18

• Molecule 1: FIBRILLIN



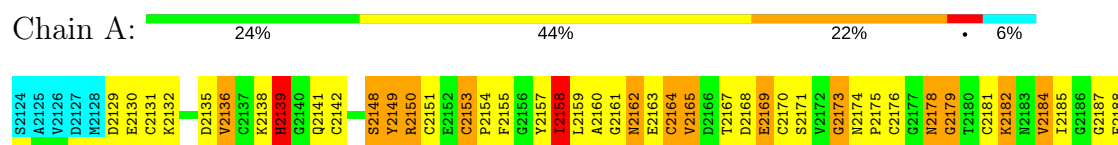
4.2.19 Score per residue for model 19

• Molecule 1: FIBRILLIN



4.2.20 Score per residue for model 20

• Molecule 1: FIBRILLIN





4.2.21 Score per residue for model 21

- Molecule 1: FIBRILLIN

Chain A: 24% 37% 26% 7% 6%



4.2.22 Score per residue for model 22

- Molecule 1: FIBRILLIN

Chain A: 26% 44% 20% 5% 6%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 200 calculated structures, 22 were deposited, based on the following criterion: $F(NOE) < 165 \text{ KJ MOL}^{-1}$ *TORSION ANGLE CONSTRAINTS VIOLATED BY* $> 3 \text{ DEGREES}$.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR	structure solution	

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

Bond lengths and bond angles in the following residue types are not validated in this section:
CA

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

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.0±0.0
All	All	0	22

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	2150	ARG	Sidechain	22

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	486	486	92±6
All	All	12452	10692	10692	2021

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 87.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2158:ILE:HD11	1:A:2165:VAL:HG23	0.91	1.40	11	9
1:A:2136:VAL:HG23	1:A:2149:TYR:CE1	0.89	2.02	4	1
1:A:2142:CYS:C	1:A:2143:ILE:HD13	0.86	1.90	19	2
1:A:2136:VAL:HG12	1:A:2151:CYS:SG	0.84	2.12	16	1
1:A:2136:VAL:HG11	1:A:2149:TYR:CE1	0.84	2.07	3	2
1:A:2142:CYS:O	1:A:2143:ILE:HD13	0.83	1.72	19	2
1:A:2167:THR:HG23	1:A:2169:GLU:OE1	0.82	1.73	20	15
1:A:2164:CYS:O	1:A:2165:VAL:HG13	0.82	1.75	18	21
1:A:2184:VAL:HG12	1:A:2188:PHE:N	0.82	1.88	22	22
1:A:2142:CYS:C	1:A:2143:ILE:HD12	0.79	1.98	15	10
1:A:2184:VAL:HG12	1:A:2188:PHE:CA	0.77	2.09	15	22
1:A:2135:ASP:OD1	1:A:2136:VAL:HG23	0.74	1.82	14	2
1:A:2133:GLU:HB2	1:A:2136:VAL:HG23	0.74	1.60	13	3
1:A:2130:GLU:O	1:A:2136:VAL:HG21	0.72	1.84	15	16
1:A:2158:ILE:HD13	1:A:2158:ILE:N	0.71	2.01	16	11
1:A:2158:ILE:N	1:A:2158:ILE:HD13	0.71	2.01	5	11
1:A:2184:VAL:HG13	1:A:2185:ILE:N	0.70	2.00	1	13
1:A:2136:VAL:HG22	1:A:2137:CYS:N	0.70	2.01	4	1
1:A:2158:ILE:HD13	1:A:2158:ILE:H	0.69	1.46	16	10
1:A:2136:VAL:HG12	1:A:2137:CYS:N	0.69	2.02	22	10
1:A:2196:PHE:CZ	1:A:2198:PRO:CG	0.69	2.76	19	22
1:A:2157:TYR:OH	1:A:2185:ILE:HG23	0.67	1.89	6	10
1:A:2175:PRO:CB	1:A:2188:PHE:CD1	0.66	2.78	5	2
1:A:2192:CYS:N	1:A:2196:PHE:CZ	0.65	2.64	20	1
1:A:2175:PRO:CB	1:A:2188:PHE:CE2	0.65	2.80	19	7
1:A:2159:LEU:HD12	1:A:2163:GLU:O	0.64	1.92	16	4
1:A:2136:VAL:CG1	1:A:2149:TYR:CE1	0.64	2.81	9	5
1:A:2196:PHE:CZ	1:A:2198:PRO:CD	0.64	2.81	14	22
1:A:2184:VAL:HG12	1:A:2188:PHE:HA	0.64	1.69	15	19
1:A:2136:VAL:HG13	1:A:2149:TYR:CE2	0.64	2.27	10	2
1:A:2136:VAL:CG1	1:A:2149:TYR:CE2	0.64	2.80	19	7
1:A:2130:GLU:CB	1:A:2149:TYR:CD2	0.64	2.80	15	2
1:A:2175:PRO:CB	1:A:2188:PHE:CE1	0.64	2.81	21	5
1:A:2130:GLU:CB	1:A:2149:TYR:CD1	0.63	2.81	14	5
1:A:2196:PHE:CE2	1:A:2198:PRO:CD	0.63	2.81	20	1
1:A:2136:VAL:CG2	1:A:2149:TYR:CE1	0.63	2.82	4	1
1:A:2158:ILE:HD12	1:A:2167:THR:HB	0.62	1.70	18	2
1:A:2130:GLU:O	1:A:2136:VAL:HG11	0.62	1.94	4	4
1:A:2136:VAL:HG12	1:A:2137:CYS:SG	0.61	2.35	10	1
1:A:2158:ILE:H	1:A:2158:ILE:HD13	0.61	1.56	13	12
1:A:2136:VAL:HG22	1:A:2137:CYS:SG	0.61	2.36	4	1
1:A:2158:ILE:CD1	1:A:2158:ILE:N	0.61	2.64	14	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2143:ILE:O	1:A:2145:THR:HG23	0.60	1.95	5	3
1:A:2169:GLU:O	1:A:2172:VAL:HG23	0.60	1.96	1	5
1:A:2188:PHE:CD1	1:A:2188:PHE:N	0.59	2.69	11	8
1:A:2131:CYS:HA	1:A:2136:VAL:HG11	0.59	1.73	12	2
1:A:2158:ILE:N	1:A:2158:ILE:CD1	0.59	2.66	5	12
1:A:2184:VAL:CG1	1:A:2188:PHE:CA	0.59	2.81	12	15
1:A:2196:PHE:CG	1:A:2197:GLU:N	0.58	2.71	14	22
1:A:2130:GLU:HB3	1:A:2149:TYR:CD1	0.58	2.33	14	10
1:A:2196:PHE:CD2	1:A:2204:CYS:SG	0.58	2.97	17	20
1:A:2184:VAL:CG1	1:A:2188:PHE:N	0.58	2.66	16	11
1:A:2175:PRO:HB3	1:A:2188:PHE:CE1	0.58	2.32	21	2
1:A:2135:ASP:O	1:A:2136:VAL:C	0.58	2.41	4	1
1:A:2143:ILE:N	1:A:2143:ILE:HD12	0.58	2.13	16	4
1:A:2138:LYS:O	1:A:2139:HIS:CG	0.58	2.56	15	4
1:A:2196:PHE:CE2	1:A:2198:PRO:HD3	0.58	2.34	20	1
1:A:2196:PHE:CD2	1:A:2204:CYS:HB2	0.58	2.34	20	1
1:A:2196:PHE:CZ	1:A:2198:PRO:HD3	0.58	2.34	7	22
1:A:2143:ILE:HD12	1:A:2143:ILE:N	0.58	2.13	7	1
1:A:2136:VAL:HG11	1:A:2149:TYR:CE2	0.58	2.34	14	3
1:A:2184:VAL:HG12	1:A:2187:GLY:C	0.58	2.19	8	17
1:A:2196:PHE:CZ	1:A:2198:PRO:HG3	0.57	2.34	12	22
1:A:2129:ASP:O	1:A:2130:GLU:HB2	0.57	1.97	16	19
1:A:2169:GLU:CB	1:A:2188:PHE:CD1	0.57	2.88	15	17
1:A:2175:PRO:HB3	1:A:2188:PHE:CE2	0.57	2.34	12	3
1:A:2196:PHE:CE2	1:A:2204:CYS:SG	0.56	2.98	2	15
1:A:2192:CYS:HB2	1:A:2196:PHE:CD2	0.56	2.34	20	22
1:A:2130:GLU:HB3	1:A:2149:TYR:CD2	0.56	2.36	15	6
1:A:2182:LYS:CB	1:A:2189:GLU:O	0.56	2.54	22	7
1:A:2156:GLY:O	1:A:2167:THR:HG22	0.56	2.00	11	1
1:A:2158:ILE:HD13	1:A:2165:VAL:O	0.56	2.01	18	13
1:A:2196:PHE:CD2	1:A:2197:GLU:N	0.56	2.74	20	19
1:A:2136:VAL:HG13	1:A:2149:TYR:CE1	0.56	2.36	9	1
1:A:2149:TYR:N	1:A:2149:TYR:CD1	0.55	2.73	1	3
1:A:2159:LEU:HD11	1:A:2162:ASN:O	0.55	2.00	15	2
1:A:2187:GLY:C	1:A:2188:PHE:CD1	0.55	2.80	17	14
1:A:2192:CYS:HB2	1:A:2196:PHE:CE1	0.55	2.37	1	21
1:A:2158:ILE:CG2	1:A:2167:THR:HB	0.55	2.32	14	21
1:A:2129:ASP:O	1:A:2144:ASN:ND2	0.55	2.40	19	7
1:A:2167:THR:CG2	1:A:2169:GLU:OE1	0.55	2.55	6	17
1:A:2193:GLU:O	1:A:2194:GLU:C	0.55	2.45	19	22
1:A:2157:TYR:CD2	1:A:2165:VAL:C	0.55	2.80	19	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2175:PRO:HG2	1:A:2188:PHE:CD2	0.55	2.37	13	14
1:A:2150:ARG:O	1:A:2151:CYS:C	0.55	2.45	18	2
1:A:2158:ILE:CD1	1:A:2165:VAL:HG23	0.55	2.25	7	2
1:A:2136:VAL:CG2	1:A:2149:TYR:CZ	0.55	2.90	4	1
1:A:2175:PRO:HG2	1:A:2188:PHE:CE2	0.55	2.37	3	3
1:A:2130:GLU:O	1:A:2136:VAL:CG2	0.55	2.55	21	9
1:A:2192:CYS:HB2	1:A:2196:PHE:CD1	0.55	2.37	1	21
1:A:2137:CYS:CA	1:A:2162:ASN:O	0.54	2.55	7	2
1:A:2138:LYS:O	1:A:2139:HIS:CB	0.54	2.56	11	13
1:A:2157:TYR:OH	1:A:2185:ILE:CG2	0.54	2.56	10	17
1:A:2132:LYS:CG	1:A:2132:LYS:O	0.54	2.56	12	1
1:A:2182:LYS:N	1:A:2189:GLU:O	0.54	2.40	18	7
1:A:2175:PRO:CG	1:A:2188:PHE:CE2	0.54	2.91	15	6
1:A:2129:ASP:O	1:A:2130:GLU:CB	0.53	2.55	12	17
1:A:2192:CYS:HB2	1:A:2196:PHE:CZ	0.53	2.38	3	21
1:A:2130:GLU:O	1:A:2136:VAL:CB	0.53	2.56	1	8
1:A:2149:TYR:O	1:A:2150:ARG:CG	0.53	2.57	13	4
1:A:2130:GLU:O	1:A:2136:VAL:CG1	0.53	2.56	4	1
1:A:2196:PHE:CE1	1:A:2198:PRO:HD3	0.53	2.39	13	21
1:A:2136:VAL:CG1	1:A:2149:TYR:CZ	0.53	2.92	9	1
1:A:2169:GLU:HB3	1:A:2188:PHE:CD1	0.53	2.38	15	15
1:A:2134:PRO:O	1:A:2138:LYS:CE	0.53	2.57	21	2
1:A:2145:THR:HG1	1:A:2148:SER:C	0.53	2.07	2	4
1:A:2158:ILE:HG21	1:A:2167:THR:HB	0.53	1.80	9	5
1:A:2130:GLU:HB2	1:A:2149:TYR:CD2	0.53	2.38	15	2
1:A:2129:ASP:OD1	1:A:2132:LYS:N	0.53	2.41	15	1
1:A:2164:CYS:O	1:A:2165:VAL:CG1	0.52	2.57	21	10
1:A:2192:CYS:HB2	1:A:2196:PHE:CE2	0.52	2.40	3	22
1:A:2188:PHE:CE2	1:A:2202:MET:O	0.52	2.61	1	5
1:A:2136:VAL:O	1:A:2162:ASN:CB	0.52	2.58	8	3
1:A:2136:VAL:CG2	1:A:2137:CYS:SG	0.52	2.97	4	1
1:A:2134:PRO:O	1:A:2138:LYS:CD	0.52	2.58	16	3
1:A:2192:CYS:N	1:A:2196:PHE:CE1	0.52	2.77	16	21
1:A:2141:GLN:O	1:A:2152:GLU:CG	0.52	2.58	12	1
1:A:2157:TYR:CD2	1:A:2165:VAL:O	0.52	2.62	6	7
1:A:2192:CYS:HB2	1:A:2196:PHE:CG	0.52	2.39	3	21
1:A:2135:ASP:O	1:A:2162:ASN:ND2	0.52	2.43	1	5
1:A:2149:TYR:CD1	1:A:2149:TYR:N	0.52	2.77	10	2
1:A:2136:VAL:O	1:A:2138:LYS:N	0.52	2.43	3	2
1:A:2196:PHE:CE2	1:A:2204:CYS:HB2	0.52	2.40	20	2
1:A:2190:CYS:SG	1:A:2191:THR:N	0.51	2.83	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2136:VAL:CG2	1:A:2137:CYS:N	0.51	2.72	4	1
1:A:2175:PRO:CD	1:A:2181:CYS:HB3	0.51	2.35	6	18
1:A:2137:CYS:O	1:A:2164:CYS:N	0.51	2.43	19	1
1:A:2169:GLU:OE1	1:A:2169:GLU:N	0.51	2.43	16	2
1:A:2158:ILE:HD12	1:A:2167:THR:N	0.51	2.20	18	1
1:A:2175:PRO:HB2	1:A:2188:PHE:CE1	0.51	2.41	5	2
1:A:2176:CYS:O	1:A:2204:CYS:CB	0.51	2.59	18	4
1:A:2136:VAL:O	1:A:2162:ASN:CA	0.51	2.59	4	1
1:A:2176:CYS:SG	1:A:2204:CYS:CB	0.51	2.99	14	7
1:A:2158:ILE:HG23	1:A:2167:THR:HB	0.51	1.81	16	6
1:A:2131:CYS:SG	1:A:2132:LYS:N	0.51	2.84	14	4
1:A:2157:TYR:O	1:A:2158:ILE:CG2	0.51	2.59	14	18
1:A:2196:PHE:CE2	1:A:2198:PRO:N	0.51	2.79	7	22
1:A:2134:PRO:HA	1:A:2138:LYS:CG	0.51	2.36	8	4
1:A:2161:GLY:O	1:A:2162:ASN:CB	0.51	2.59	15	8
1:A:2178:ASN:O	1:A:2179:GLY:O	0.50	2.29	2	10
1:A:2174:ASN:OD1	1:A:2178:ASN:N	0.50	2.43	20	1
1:A:2191:THR:HG22	1:A:2191:THR:O	0.50	2.04	1	2
1:A:2133:GLU:CB	1:A:2134:PRO:HD2	0.50	2.36	4	2
1:A:2188:PHE:N	1:A:2188:PHE:CD1	0.50	2.80	15	5
1:A:2129:ASP:O	1:A:2130:GLU:OE1	0.50	2.30	9	15
1:A:2182:LYS:HB3	1:A:2189:GLU:HB3	0.50	1.83	9	13
1:A:2137:CYS:N	1:A:2151:CYS:SG	0.50	2.84	16	1
1:A:2175:PRO:HG2	1:A:2188:PHE:CD1	0.50	2.42	8	2
1:A:2169:GLU:HB2	1:A:2188:PHE:HB3	0.50	1.83	8	17
1:A:2176:CYS:O	1:A:2204:CYS:HB2	0.50	2.06	15	8
1:A:2169:GLU:OE2	1:A:2187:GLY:CA	0.50	2.60	11	1
1:A:2149:TYR:O	1:A:2150:ARG:CD	0.50	2.59	19	2
1:A:2184:VAL:HG21	1:A:2189:GLU:OE1	0.49	2.06	20	2
1:A:2142:CYS:SG	1:A:2143:ILE:N	0.49	2.85	14	1
1:A:2130:GLU:OE2	1:A:2148:SER:N	0.49	2.45	11	2
1:A:2130:GLU:HB2	1:A:2149:TYR:CD1	0.49	2.42	14	1
1:A:2137:CYS:CB	1:A:2142:CYS:SG	0.49	3.00	7	2
1:A:2137:CYS:N	1:A:2162:ASN:O	0.49	2.45	7	2
1:A:2184:VAL:CG1	1:A:2185:ILE:N	0.49	2.71	1	4
1:A:2170:CYS:O	1:A:2181:CYS:SG	0.49	2.71	13	16
1:A:2176:CYS:SG	1:A:2192:CYS:N	0.49	2.86	19	7
1:A:2133:GLU:OE1	1:A:2136:VAL:HG21	0.49	2.07	2	1
1:A:2157:TYR:CE1	1:A:2166:ASP:OD1	0.49	2.66	15	2
1:A:2150:ARG:CB	1:A:2150:ARG:CZ	0.49	2.88	3	1
1:A:2162:ASN:CG	1:A:2163:GLU:N	0.49	2.66	22	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2130:GLU:OE1	1:A:2148:SER:O	0.49	2.31	15	10
1:A:2182:LYS:HB3	1:A:2189:GLU:O	0.49	2.07	6	7
1:A:2143:ILE:O	1:A:2143:ILE:HG22	0.49	2.07	11	1
1:A:2169:GLU:HB3	1:A:2188:PHE:CD2	0.49	2.43	5	5
1:A:2175:PRO:O	1:A:2203:THR:OG1	0.49	2.31	16	9
1:A:2129:ASP:HA	1:A:2144:ASN:ND2	0.49	2.23	15	12
1:A:2143:ILE:N	1:A:2143:ILE:HD13	0.49	2.22	19	1
1:A:2131:CYS:O	1:A:2136:VAL:O	0.49	2.30	9	1
1:A:2176:CYS:SG	1:A:2190:CYS:O	0.48	2.71	20	1
1:A:2151:CYS:HB2	1:A:2159:LEU:HD22	0.48	1.84	7	1
1:A:2153:CYS:SG	1:A:2157:TYR:HB3	0.48	2.48	8	21
1:A:2191:THR:O	1:A:2192:CYS:O	0.48	2.30	16	14
1:A:2175:PRO:HB2	1:A:2188:PHE:CE2	0.48	2.43	19	3
1:A:2147:GLY:O	1:A:2148:SER:CB	0.48	2.62	2	2
1:A:2136:VAL:HG23	1:A:2149:TYR:CZ	0.48	2.41	4	1
1:A:2196:PHE:CZ	1:A:2198:PRO:CB	0.48	2.97	19	21
1:A:2179:GLY:HA3	1:A:2192:CYS:HA	0.48	1.85	6	22
1:A:2138:LYS:O	1:A:2139:HIS:CD2	0.48	2.67	11	3
1:A:2169:GLU:OE1	1:A:2187:GLY:O	0.48	2.32	9	2
1:A:2136:VAL:O	1:A:2162:ASN:O	0.48	2.32	15	9
1:A:2157:TYR:C	1:A:2158:ILE:CG2	0.48	2.82	19	20
1:A:2139:HIS:CB	1:A:2164:CYS:O	0.48	2.62	16	3
1:A:2185:ILE:O	1:A:2201:MET:SD	0.48	2.72	4	2
1:A:2129:ASP:OD1	1:A:2131:CYS:SG	0.48	2.71	3	13
1:A:2169:GLU:N	1:A:2169:GLU:OE1	0.48	2.47	19	2
1:A:2178:ASN:CG	1:A:2179:GLY:N	0.48	2.67	2	1
1:A:2187:GLY:C	1:A:2188:PHE:CD2	0.48	2.87	2	1
1:A:2145:THR:HG23	1:A:2149:TYR:HA	0.47	1.85	7	1
1:A:2175:PRO:CD	1:A:2181:CYS:CB	0.47	2.92	21	2
1:A:2157:TYR:CB	1:A:2165:VAL:O	0.47	2.63	7	7
1:A:2129:ASP:O	1:A:2129:ASP:OD1	0.47	2.32	16	3
1:A:2169:GLU:OE2	1:A:2187:GLY:O	0.47	2.32	11	7
1:A:2138:LYS:C	1:A:2139:HIS:CG	0.47	2.87	8	2
1:A:2149:TYR:C	1:A:2150:ARG:CG	0.47	2.83	7	2
1:A:2158:ILE:HD12	1:A:2167:THR:CB	0.47	2.38	18	1
1:A:2158:ILE:O	1:A:2164:CYS:SG	0.47	2.72	7	18
1:A:2170:CYS:O	1:A:2170:CYS:SG	0.47	2.73	13	8
1:A:2175:PRO:HB2	1:A:2188:PHE:CD1	0.47	2.44	5	2
1:A:2176:CYS:SG	1:A:2204:CYS:HB2	0.47	2.49	14	9
1:A:2153:CYS:SG	1:A:2158:ILE:O	0.47	2.73	7	11
1:A:2167:THR:O	1:A:2183:ASN:OD1	0.47	2.32	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2149:TYR:C	1:A:2149:TYR:CD1	0.47	2.88	4	1
1:A:2145:THR:OG1	1:A:2148:SER:O	0.47	2.31	16	3
1:A:2166:ASP:OD2	1:A:2184:VAL:O	0.47	2.33	3	8
1:A:2135:ASP:OD1	1:A:2136:VAL:CG2	0.47	2.62	3	1
1:A:2136:VAL:HG13	1:A:2149:TYR:CZ	0.47	2.44	9	1
1:A:2137:CYS:O	1:A:2138:LYS:HB2	0.47	2.09	1	11
1:A:2197:GLU:CG	1:A:2197:GLU:O	0.47	2.62	6	1
1:A:2158:ILE:CD1	1:A:2165:VAL:O	0.47	2.62	10	3
1:A:2157:TYR:C	1:A:2158:ILE:HG23	0.47	2.29	14	17
1:A:2196:PHE:CE2	1:A:2198:PRO:CA	0.47	2.98	7	21
1:A:2174:ASN:ND2	1:A:2179:GLY:C	0.47	2.68	6	2
1:A:2131:CYS:O	1:A:2137:CYS:O	0.47	2.33	4	2
1:A:2173:GLY:O	1:A:2181:CYS:SG	0.47	2.73	10	3
1:A:2188:PHE:CE1	1:A:2202:MET:O	0.46	2.68	21	2
1:A:2133:GLU:HB2	1:A:2136:VAL:CG2	0.46	2.40	10	1
1:A:2173:GLY:O	1:A:2174:ASN:OD1	0.46	2.34	3	1
1:A:2174:ASN:O	1:A:2174:ASN:CG	0.46	2.54	9	10
1:A:2174:ASN:HA	1:A:2181:CYS:HB3	0.46	1.86	3	9
1:A:2156:GLY:O	1:A:2166:ASP:OD1	0.46	2.34	8	1
1:A:2173:GLY:O	1:A:2174:ASN:C	0.46	2.54	8	11
1:A:2145:THR:OG1	1:A:2149:TYR:HA	0.46	2.11	22	3
1:A:2176:CYS:HA	1:A:2204:CYS:HB3	0.46	1.88	2	9
1:A:2204:CYS:O	1:A:2204:CYS:SG	0.46	2.73	20	1
1:A:2174:ASN:O	1:A:2174:ASN:OD1	0.46	2.34	1	1
1:A:2137:CYS:SG	1:A:2142:CYS:SG	0.46	3.14	16	3
1:A:2175:PRO:HD2	1:A:2181:CYS:HB3	0.46	1.86	12	6
1:A:2129:ASP:O	1:A:2144:ASN:OD1	0.46	2.34	16	1
1:A:2139:HIS:O	1:A:2164:CYS:SG	0.46	2.74	7	1
1:A:2175:PRO:HB3	1:A:2188:PHE:CD1	0.46	2.46	21	2
1:A:2170:CYS:SG	1:A:2170:CYS:O	0.46	2.74	14	9
1:A:2146:ASP:OD1	1:A:2146:ASP:O	0.46	2.33	17	1
1:A:2136:VAL:O	1:A:2151:CYS:SG	0.46	2.73	4	1
1:A:2175:PRO:CG	1:A:2188:PHE:CD1	0.46	2.98	9	3
1:A:2131:CYS:O	1:A:2131:CYS:SG	0.46	2.73	16	2
1:A:2129:ASP:OD1	1:A:2129:ASP:O	0.46	2.33	13	1
1:A:2173:GLY:O	1:A:2174:ASN:O	0.46	2.34	11	2
1:A:2133:GLU:CB	1:A:2134:PRO:CD	0.46	2.94	4	2
1:A:2130:GLU:O	1:A:2136:VAL:HB	0.46	2.11	9	3
1:A:2174:ASN:CG	1:A:2174:ASN:O	0.46	2.54	13	3
1:A:2145:THR:O	1:A:2146:ASP:O	0.46	2.33	13	2
1:A:2131:CYS:HB2	1:A:2137:CYS:CB	0.46	2.41	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2136:VAL:O	1:A:2137:CYS:C	0.46	2.54	9	3
1:A:2176:CYS:CA	1:A:2204:CYS:HB2	0.46	2.40	18	5
1:A:2167:THR:HG23	1:A:2168:ASP:N	0.46	2.25	19	3
1:A:2189:GLU:OE1	1:A:2200:PRO:O	0.46	2.34	12	1
1:A:2134:PRO:CA	1:A:2138:LYS:HD3	0.46	2.41	18	1
1:A:2137:CYS:O	1:A:2162:ASN:O	0.45	2.34	22	3
1:A:2142:CYS:SG	1:A:2151:CYS:N	0.45	2.89	20	1
1:A:2150:ARG:O	1:A:2151:CYS:SG	0.45	2.74	14	1
1:A:2175:PRO:HD3	1:A:2181:CYS:HB3	0.45	1.87	9	9
1:A:2131:CYS:O	1:A:2137:CYS:HB2	0.45	2.11	14	4
1:A:2132:LYS:HG3	1:A:2132:LYS:O	0.45	2.10	12	2
1:A:2160:ALA:O	1:A:2162:ASN:N	0.45	2.49	20	1
1:A:2184:VAL:HG11	1:A:2201:MET:HG2	0.45	1.86	14	1
1:A:2145:THR:OG1	1:A:2148:SER:C	0.45	2.55	22	12
1:A:2158:ILE:HG12	1:A:2159:LEU:N	0.45	2.26	12	7
1:A:2178:ASN:OD1	1:A:2192:CYS:SG	0.45	2.74	2	1
1:A:2133:GLU:HB2	1:A:2136:VAL:CG1	0.45	2.41	4	1
1:A:2130:GLU:OE1	1:A:2144:ASN:ND2	0.45	2.49	4	2
1:A:2131:CYS:HA	1:A:2136:VAL:CG1	0.45	2.42	19	4
1:A:2167:THR:HG22	1:A:2169:GLU:OE1	0.45	2.11	4	3
1:A:2158:ILE:CD1	1:A:2167:THR:HB	0.45	2.41	14	2
1:A:2176:CYS:SG	1:A:2192:CYS:SG	0.45	3.15	15	3
1:A:2150:ARG:CZ	1:A:2150:ARG:CB	0.45	2.93	22	1
1:A:2173:GLY:O	1:A:2175:PRO:N	0.45	2.50	16	5
1:A:2168:ASP:OD1	1:A:2168:ASP:C	0.45	2.55	22	4
1:A:2170:CYS:HB2	1:A:2182:LYS:N	0.45	2.27	12	3
1:A:2182:LYS:HG3	1:A:2183:ASN:N	0.45	2.27	17	3
1:A:2149:TYR:O	1:A:2150:ARG:HG2	0.45	2.12	8	2
1:A:2148:SER:C	1:A:2149:TYR:CD2	0.45	2.89	20	1
1:A:2146:ASP:O	1:A:2146:ASP:OD1	0.45	2.35	22	1
1:A:2193:GLU:O	1:A:2193:GLU:OE1	0.45	2.35	4	1
1:A:2193:GLU:OE1	1:A:2193:GLU:O	0.45	2.35	1	1
1:A:2135:ASP:O	1:A:2162:ASN:HB3	0.45	2.12	20	3
1:A:2176:CYS:SG	1:A:2204:CYS:HB3	0.45	2.52	20	1
1:A:2137:CYS:CB	1:A:2142:CYS:HB3	0.45	2.42	18	1
1:A:2129:ASP:HB3	1:A:2132:LYS:CG	0.45	2.42	22	1
1:A:2169:GLU:CB	1:A:2188:PHE:HB3	0.44	2.42	21	1
1:A:2176:CYS:CA	1:A:2204:CYS:HB3	0.44	2.42	2	7
1:A:2138:LYS:CE	1:A:2163:GLU:OE2	0.44	2.65	18	1
1:A:2166:ASP:OD2	1:A:2167:THR:O	0.44	2.35	17	1
1:A:2136:VAL:CG1	1:A:2137:CYS:N	0.44	2.71	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2158:ILE:HD11	1:A:2165:VAL:CG2	0.44	2.30	11	1
1:A:2176:CYS:O	1:A:2204:CYS:HB3	0.44	2.12	17	5
1:A:2131:CYS:HB3	1:A:2149:TYR:CD2	0.44	2.46	12	1
1:A:2193:GLU:OE2	1:A:2194:GLU:O	0.44	2.35	9	1
1:A:2129:ASP:C	1:A:2129:ASP:OD1	0.44	2.56	8	4
1:A:2141:GLN:O	1:A:2152:GLU:HB2	0.44	2.12	7	1
1:A:2136:VAL:O	1:A:2162:ASN:HA	0.44	2.12	4	1
1:A:2169:GLU:CB	1:A:2188:PHE:CD2	0.44	3.00	2	1
1:A:2134:PRO:O	1:A:2138:LYS:HD2	0.44	2.11	21	2
1:A:2137:CYS:O	1:A:2138:LYS:CB	0.44	2.64	14	3
1:A:2168:ASP:C	1:A:2168:ASP:OD1	0.44	2.56	15	12
1:A:2186:GLY:O	1:A:2201:MET:SD	0.44	2.76	11	3
1:A:2201:MET:O	1:A:2201:MET:SD	0.44	2.76	22	1
1:A:2129:ASP:OD2	1:A:2132:LYS:HB3	0.43	2.12	15	1
1:A:2142:CYS:HA	1:A:2150:ARG:O	0.43	2.13	21	2
1:A:2197:GLU:O	1:A:2205:GLU:HG3	0.43	2.13	21	1
1:A:2173:GLY:O	1:A:2175:PRO:HD3	0.43	2.13	8	9
1:A:2129:ASP:O	1:A:2144:ASN:HB2	0.43	2.13	16	1
1:A:2142:CYS:SG	1:A:2150:ARG:C	0.43	2.96	20	1
1:A:2136:VAL:O	1:A:2162:ASN:C	0.43	2.57	12	3
1:A:2143:ILE:O	1:A:2144:ASN:C	0.43	2.57	14	1
1:A:2139:HIS:HB2	1:A:2164:CYS:O	0.43	2.13	11	3
1:A:2129:ASP:OD1	1:A:2129:ASP:C	0.43	2.57	13	1
1:A:2136:VAL:O	1:A:2137:CYS:HB2	0.43	2.14	19	1
1:A:2197:GLU:O	1:A:2205:GLU:O	0.43	2.36	16	1
1:A:2184:VAL:HG22	1:A:2185:ILE:H	0.43	1.74	15	1
1:A:2170:CYS:HA	1:A:2181:CYS:HB2	0.43	1.91	20	4
1:A:2146:ASP:OD1	1:A:2146:ASP:N	0.43	2.51	12	1
1:A:2151:CYS:SG	1:A:2159:LEU:HD13	0.43	2.54	22	1
1:A:2134:PRO:HA	1:A:2138:LYS:CD	0.43	2.44	9	1
1:A:2144:ASN:C	1:A:2144:ASN:OD1	0.43	2.57	12	2
1:A:2175:PRO:CG	1:A:2188:PHE:CD2	0.43	3.01	15	3
1:A:2129:ASP:C	1:A:2144:ASN:OD1	0.43	2.57	7	1
1:A:2129:ASP:OD2	1:A:2132:LYS:HB2	0.43	2.13	19	3
1:A:2157:TYR:O	1:A:2158:ILE:HG22	0.43	2.14	12	5
1:A:2130:GLU:HG2	1:A:2148:SER:O	0.43	2.14	16	2
1:A:2162:ASN:ND2	1:A:2163:GLU:N	0.43	2.67	12	1
1:A:2159:LEU:HG	1:A:2160:ALA:N	0.43	2.29	18	1
1:A:2153:CYS:SG	1:A:2154:PRO:HD2	0.43	2.54	21	8
1:A:2138:LYS:O	1:A:2139:HIS:HB2	0.43	2.14	5	9
1:A:2158:ILE:HG21	1:A:2167:THR:CB	0.43	2.44	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2135:ASP:N	1:A:2135:ASP:OD1	0.43	2.52	13	1
1:A:2136:VAL:O	1:A:2162:ASN:HB2	0.42	2.14	4	3
1:A:2201:MET:SD	1:A:2201:MET:O	0.42	2.77	20	1
1:A:2135:ASP:OD1	1:A:2135:ASP:C	0.42	2.57	2	1
1:A:2152:GLU:O	1:A:2153:CYS:C	0.42	2.58	17	1
1:A:2139:HIS:ND1	1:A:2139:HIS:N	0.42	2.66	6	1
1:A:2129:ASP:HB3	1:A:2132:LYS:CB	0.42	2.44	7	1
1:A:2139:HIS:O	1:A:2164:CYS:HB3	0.42	2.13	8	6
1:A:2205:GLU:O	1:A:2205:GLU:CG	0.42	2.67	20	1
1:A:2149:TYR:O	1:A:2150:ARG:HG3	0.42	2.14	9	2
1:A:2135:ASP:O	1:A:2162:ASN:CB	0.42	2.68	20	1
1:A:2179:GLY:HA3	1:A:2191:THR:O	0.42	2.15	20	2
1:A:2131:CYS:SG	1:A:2137:CYS:HB3	0.42	2.54	21	1
1:A:2137:CYS:O	1:A:2138:LYS:O	0.42	2.38	10	1
1:A:2136:VAL:HG13	1:A:2162:ASN:OD1	0.42	2.14	21	1
1:A:2157:TYR:HB3	1:A:2165:VAL:O	0.42	2.14	6	3
1:A:2139:HIS:CB	1:A:2164:CYS:HB3	0.42	2.44	7	1
1:A:2175:PRO:CG	1:A:2188:PHE:CE1	0.42	3.02	9	1
1:A:2160:ALA:O	1:A:2161:GLY:C	0.42	2.56	20	1
1:A:2169:GLU:OE2	1:A:2187:GLY:HA2	0.42	2.15	11	1
1:A:2130:GLU:HB3	1:A:2149:TYR:CE2	0.42	2.49	3	1
1:A:2136:VAL:HG23	1:A:2149:TYR:CD1	0.42	2.49	4	1
1:A:2182:LYS:CG	1:A:2183:ASN:N	0.42	2.82	3	2
1:A:2131:CYS:HB2	1:A:2137:CYS:SG	0.42	2.55	6	1
1:A:2132:LYS:O	1:A:2132:LYS:CG	0.42	2.68	13	1
1:A:2188:PHE:CZ	1:A:2202:MET:O	0.42	2.73	21	2
1:A:2134:PRO:O	1:A:2138:LYS:HG3	0.42	2.15	16	1
1:A:2136:VAL:HA	1:A:2162:ASN:ND2	0.41	2.30	14	4
1:A:2157:TYR:CD1	1:A:2166:ASP:OD1	0.41	2.73	15	1
1:A:2135:ASP:OD1	1:A:2135:ASP:N	0.41	2.53	8	1
1:A:2135:ASP:O	1:A:2162:ASN:CG	0.41	2.58	20	2
1:A:2175:PRO:CB	1:A:2188:PHE:CD2	0.41	3.02	11	1
1:A:2175:PRO:O	1:A:2176:CYS:C	0.41	2.57	18	2
1:A:2197:GLU:O	1:A:2205:GLU:CG	0.41	2.67	21	1
1:A:2173:GLY:C	1:A:2174:ASN:OD1	0.41	2.59	3	1
1:A:2147:GLY:O	1:A:2148:SER:HB2	0.41	2.16	2	2
1:A:2158:ILE:CG1	1:A:2167:THR:HB	0.41	2.46	14	1
1:A:2188:PHE:O	1:A:2201:MET:HA	0.41	2.15	22	1
1:A:2129:ASP:CB	1:A:2132:LYS:HB2	0.41	2.46	9	1
1:A:2157:TYR:N	1:A:2157:TYR:CD1	0.41	2.89	12	2
1:A:2184:VAL:CG1	1:A:2188:PHE:HA	0.41	2.45	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2134:PRO:O	1:A:2138:LYS:HE3	0.41	2.16	5	1
1:A:2130:GLU:HB3	1:A:2149:TYR:CE1	0.41	2.49	12	1
1:A:2169:GLU:HG2	1:A:2188:PHE:CD1	0.41	2.51	11	1
1:A:2182:LYS:HB3	1:A:2189:GLU:CB	0.41	2.45	9	2
1:A:2157:TYR:CD1	1:A:2157:TYR:N	0.41	2.89	10	3
1:A:2142:CYS:SG	1:A:2151:CYS:HA	0.41	2.56	20	1
1:A:2150:ARG:CZ	1:A:2150:ARG:HB3	0.41	2.45	3	1
1:A:2131:CYS:SG	1:A:2137:CYS:HB2	0.41	2.56	7	1
1:A:2151:CYS:HB2	1:A:2159:LEU:HD13	0.41	1.92	4	1
1:A:2161:GLY:O	1:A:2162:ASN:HB3	0.41	2.16	4	1
1:A:2130:GLU:OE1	1:A:2144:ASN:CG	0.41	2.59	16	1
1:A:2138:LYS:O	1:A:2139:HIS:C	0.41	2.59	17	1
1:A:2149:TYR:CD1	1:A:2149:TYR:C	0.41	2.95	13	1
1:A:2148:SER:O	1:A:2149:TYR:HB3	0.41	2.16	20	1
1:A:2173:GLY:O	1:A:2175:PRO:CD	0.41	2.69	16	2
1:A:2203:THR:HG23	1:A:2204:CYS:N	0.41	2.30	18	3
1:A:2138:LYS:HE2	1:A:2163:GLU:OE1	0.41	2.16	18	1
1:A:2138:LYS:O	1:A:2164:CYS:HB2	0.41	2.16	22	1
1:A:2145:THR:O	1:A:2146:ASP:C	0.41	2.58	4	1
1:A:2176:CYS:HA	1:A:2203:THR:OG1	0.40	2.16	20	1
1:A:2168:ASP:O	1:A:2171:SER:HB2	0.40	2.17	14	2
1:A:2138:LYS:O	1:A:2164:CYS:CB	0.40	2.69	9	1
1:A:2142:CYS:O	1:A:2143:ILE:HD12	0.40	2.14	14	1
1:A:2142:CYS:HB2	1:A:2150:ARG:O	0.40	2.16	14	1
1:A:2160:ALA:C	1:A:2162:ASN:N	0.40	2.75	20	1
1:A:2166:ASP:OD2	1:A:2185:ILE:HA	0.40	2.17	9	1
1:A:2136:VAL:HG12	1:A:2137:CYS:H	0.40	1.76	13	1

6.3 Torsion angles ⓘ

6.3.1 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 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	76/82 (93%)	46±3 (61±4%)	19±3 (25±4%)	11±1 (14±2%)	1	5
All	All	1672/1804 (93%)	1017 (61%)	414 (25%)	241 (14%)	1	5

All 23 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	2192	CYS	22
1	A	2179	GLY	22
1	A	2158	ILE	22
1	A	2162	ASN	21
1	A	2165	VAL	20
1	A	2178	ASN	18
1	A	2200	PRO	17
1	A	2136	VAL	17
1	A	2198	PRO	14
1	A	2154	PRO	11
1	A	2139	HIS	10
1	A	2173	GLY	9
1	A	2138	LYS	7
1	A	2146	ASP	7
1	A	2148	SER	6
1	A	2137	CYS	5
1	A	2151	CYS	4
1	A	2174	ASN	3
1	A	2143	ILE	2
1	A	2194	GLU	1
1	A	2142	CYS	1
1	A	2147	GLY	1
1	A	2149	TYR	1

6.3.2 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 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	65/69 (94%)	44±3 (67±5%)	21±3 (33±5%)	1	13
All	All	1430/1518 (94%)	965 (67%)	465 (33%)	1	13

All 52 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	2171	SER	22

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Mol	Chain	Res	Type	Models (Total)
1	A	2184	VAL	22
1	A	2158	ILE	22
1	A	2148	SER	21
1	A	2164	CYS	21
1	A	2153	CYS	21
1	A	2176	CYS	21
1	A	2132	LYS	20
1	A	2169	GLU	20
1	A	2201	MET	17
1	A	2192	CYS	16
1	A	2146	ASP	16
1	A	2178	ASN	15
1	A	2194	GLU	13
1	A	2139	HIS	12
1	A	2150	ARG	11
1	A	2152	GLU	11
1	A	2204	CYS	10
1	A	2196	PHE	10
1	A	2138	LYS	10
1	A	2202	MET	9
1	A	2205	GLU	9
1	A	2182	LYS	9
1	A	2165	VAL	9
1	A	2135	ASP	8
1	A	2189	GLU	8
1	A	2141	GLN	7
1	A	2137	CYS	7
1	A	2170	CYS	6
1	A	2145	THR	5
1	A	2142	CYS	5
1	A	2193	GLU	5
1	A	2180	THR	5
1	A	2155	PHE	5
1	A	2131	CYS	5
1	A	2166	ASP	4
1	A	2162	ASN	4
1	A	2151	CYS	4
1	A	2144	ASN	2
1	A	2200	PRO	2
1	A	2175	PRO	2
1	A	2190	CYS	2
1	A	2174	ASN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	2130	GLU	2
1	A	2133	GLU	1
1	A	2197	GLU	1
1	A	2188	PHE	1
1	A	2163	GLU	1
1	A	2154	PRO	1
1	A	2129	ASP	1
1	A	2149	TYR	1
1	A	2136	VAL	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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