



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 12:08 AM BST

PDB ID : 2KZ1  
Title : Inter-molecular interactions in a 44 kDa interferon-receptor complex detected by asymmetric back-protonation and 2D NOESY  
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Deposited on : 2010-06-10

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  
<http://wwpdb.org/validation/2016/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  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

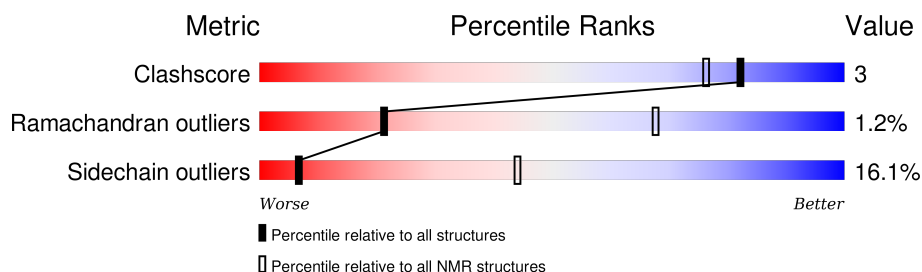
# 1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	165	 81% 13% • 5%
2	B	212	 71% 20% • 8%

## 2 Ensemble composition and analysis

This entry contains 10 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:1-A:156, B:11-B:206 (352)	0.36	6

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 3 single-model clusters were found.

Cluster number	Models
1	4, 9, 10
2	3, 6
3	2, 8
Single-model clusters	1; 5; 7

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

There are 2 unique types of molecules in this entry. The entry contains 5823 atoms, of which 2896 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Interferon alpha-2.

Mol	Chain	Residues	Atoms						Trace
1	A	165	Total	C	H	N	O	S	0
			2699	860	1348	227	255	9	

- Molecule 2 is a protein called Soluble IFN alpha/beta receptor.

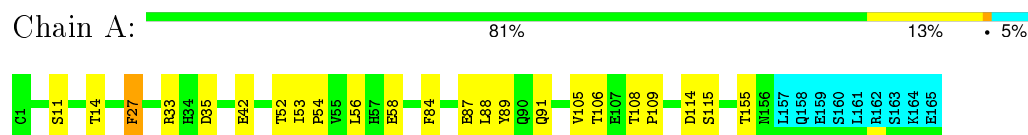
Mol	Chain	Residues	Atoms						Trace
2	B	196	Total	C	H	N	O	S	0
			3124	1014	1548	253	299	10	

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

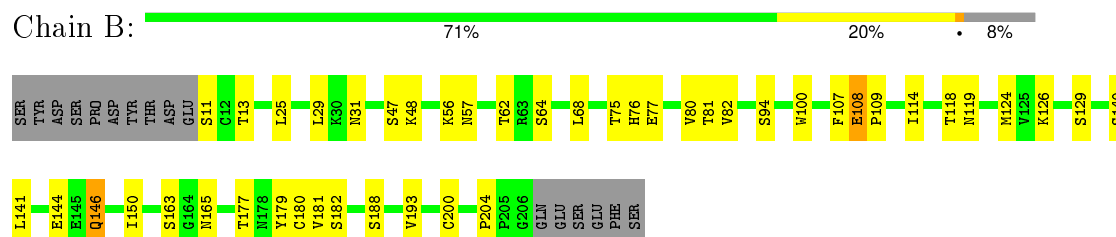
### 4.1 Average score per residue in the NMR ensemble

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: Interferon alpha-2



- Molecule 2: Soluble IFN alpha/beta receptor

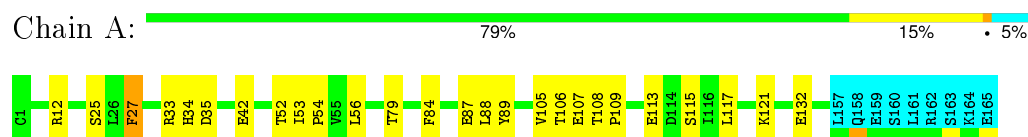


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

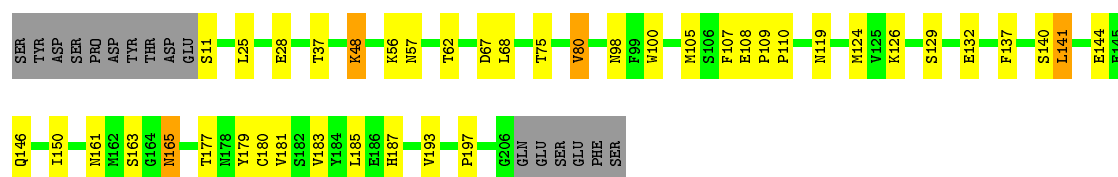
#### 4.2.1 Score per residue for model 1

- Molecule 1: Interferon alpha-2



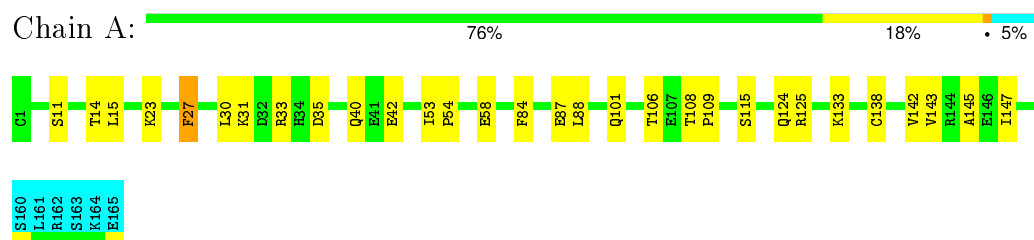
- Molecule 2: Soluble IFN alpha/beta receptor



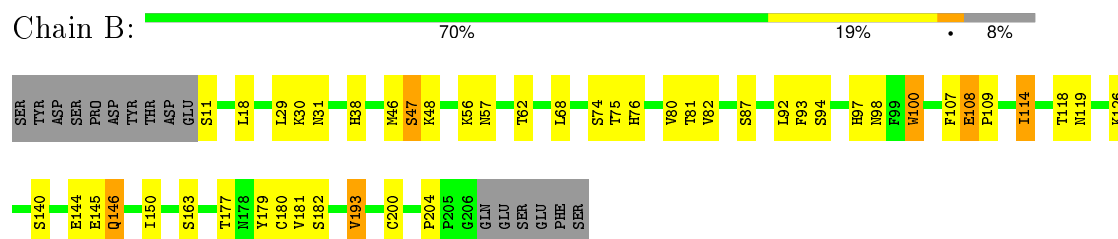


#### 4.2.2 Score per residue for model 2

- Molecule 1: Interferon alpha-2

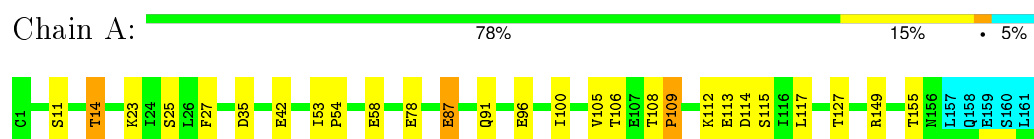


- Molecule 2: Soluble IFN alpha/beta receptor

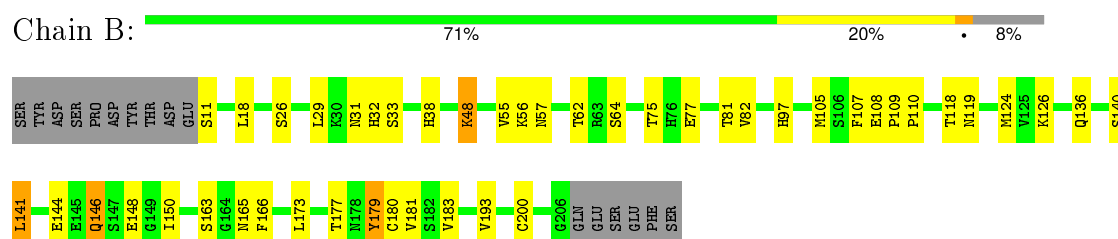


#### 4.2.3 Score per residue for model 3

- Molecule 1: Interferon alpha-2

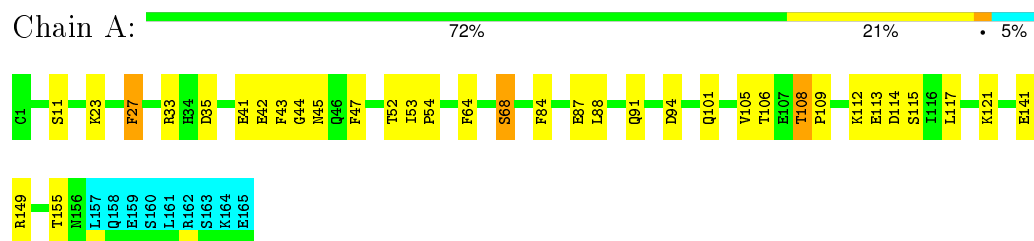


- Molecule 2: Soluble IFN alpha/beta receptor

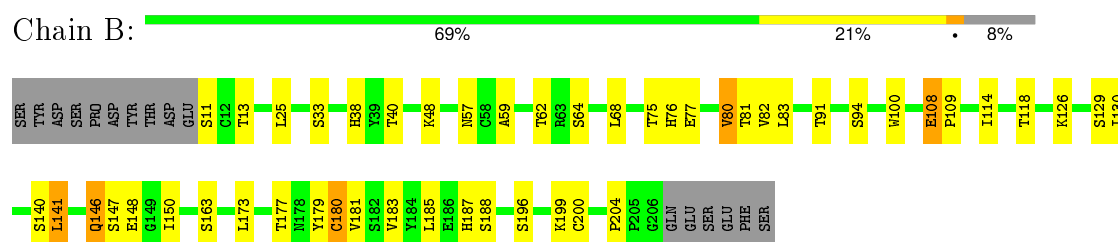


#### 4.2.4 Score per residue for model 4

- Molecule 1: Interferon alpha-2

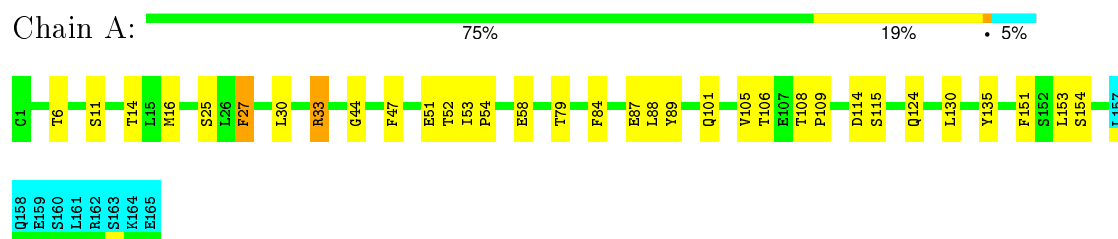


- Molecule 2: Soluble IFN alpha/beta receptor

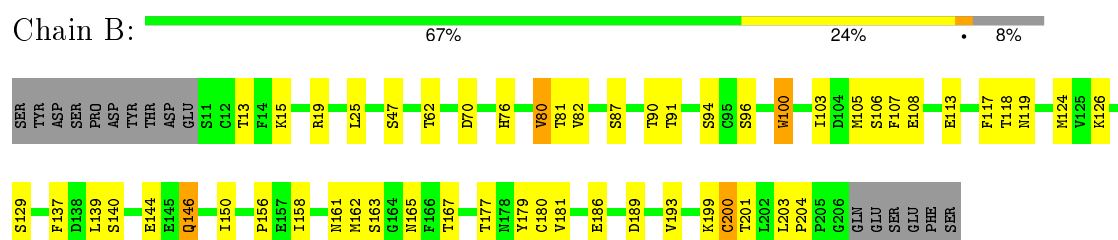


#### 4.2.5 Score per residue for model 5

- Molecule 1: Interferon alpha-2

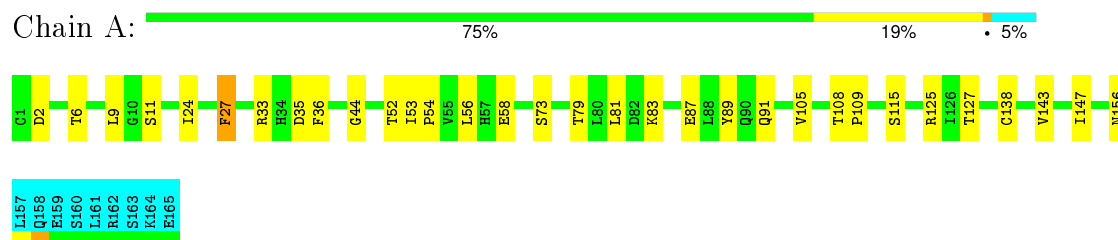


- Molecule 2: Soluble IFN alpha/beta receptor

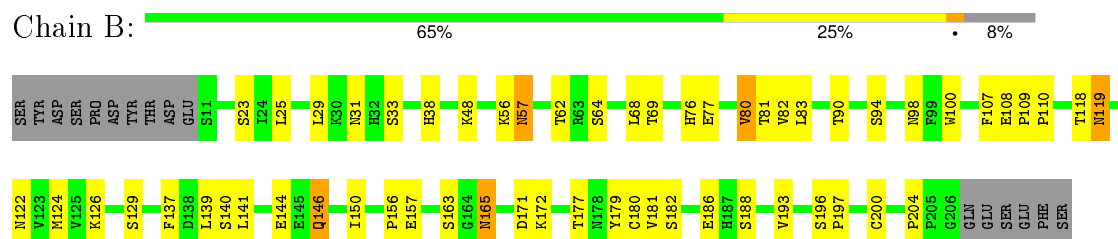


#### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Interferon alpha-2

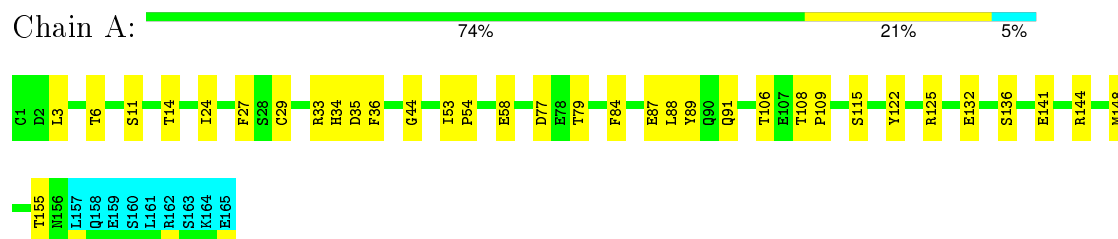


- Molecule 2: Soluble IFN alpha/beta receptor

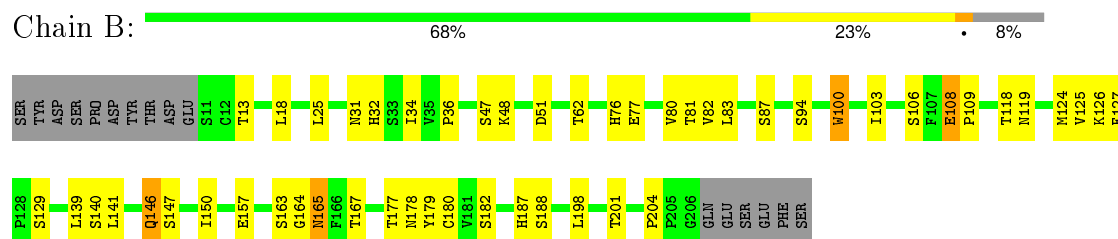


#### 4.2.7 Score per residue for model 7

- Molecule 1: Interferon alpha-2

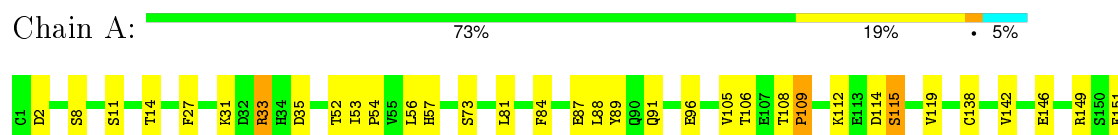


- Molecule 2: Soluble IFN alpha/beta receptor

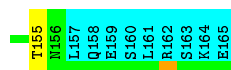


#### 4.2.8 Score per residue for model 8

- Molecule 1: Interferon alpha-2

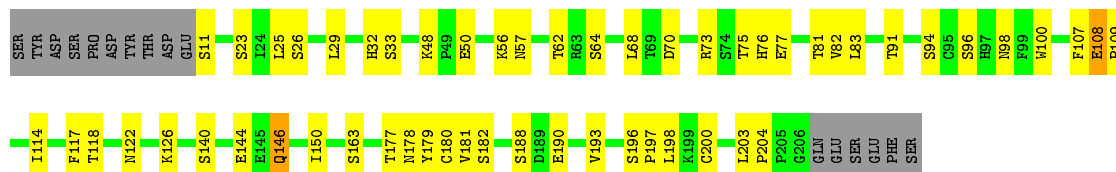






- Molecule 2: Soluble IFN alpha/beta receptor

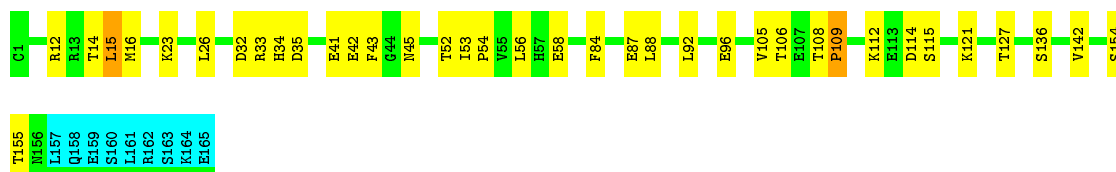
Chain B:



#### 4.2.9 Score per residue for model 9

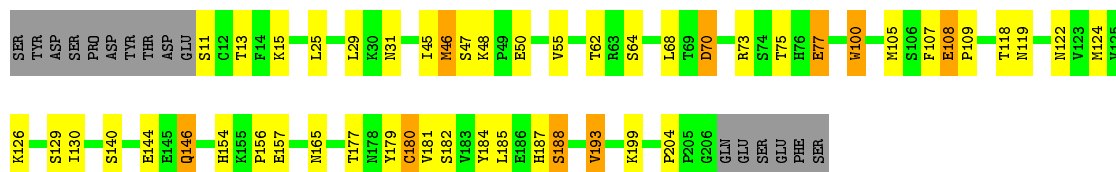
- Molecule 1: Interferon alpha-2

Chain A:



- Molecule 2: Soluble IFN alpha/beta receptor

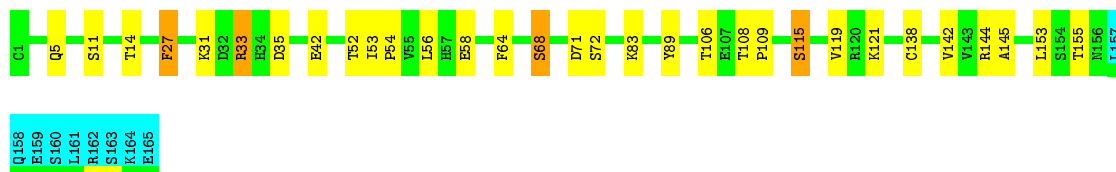
Chain B:



#### 4.2.10 Score per residue for model 10

- Molecule 1: Interferon alpha-2

Chain A:



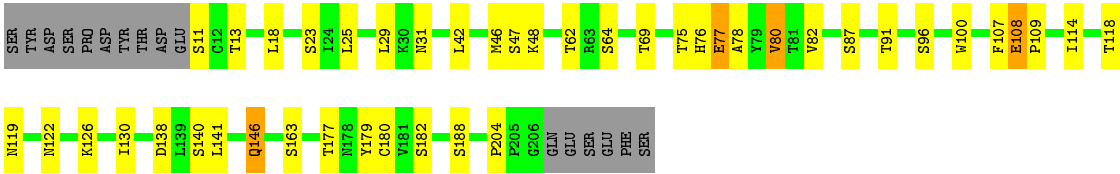
- Molecule 2: Soluble IFN alpha/beta receptor

Chain B: 

72%

19%

• 8%



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics*.

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *STRUCTURES WITH THE LOWEST ENERGY*.

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

Software name	Classification	Version
HADDOCK	refinement	2.0

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	1275	1270	1269	9±2
2	B	1576	1548	1547	10±2
All	All	28510	28180	28160	173

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:PHE:CE2	2:B:80:VAL:HB	0.65	2.27	4	6
2:B:146:GLN:O	2:B:179:TYR:HA	0.62	1.95	6	10
1:A:33:ARG:HD2	1:A:33:ARG:O	0.61	1.96	5	1
1:A:35:ASP:OD1	2:B:48:LYS:HE2	0.58	1.98	4	2
2:B:146:GLN:HA	2:B:150:ILE:O	0.57	2.00	6	8
2:B:141:LEU:HD11	2:B:183:VAL:HG13	0.56	1.77	4	3
2:B:179:TYR:CE2	2:B:201:THR:HB	0.55	2.36	7	2
1:A:64:PHE:O	1:A:68:SER:HB2	0.55	2.01	10	2
1:A:35:ASP:CB	2:B:48:LYS:HE2	0.53	2.33	7	2
1:A:36:PHE:HA	1:A:125:ARG:NH1	0.52	2.19	7	2
1:A:109:PRO:O	1:A:112:LYS:HG2	0.52	2.03	8	3
2:B:45:ILE:HB	2:B:77:GLU:OE2	0.52	2.05	9	1
1:A:53:ILE:N	1:A:54:PRO:HD2	0.51	2.21	6	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:109:PRO:N	2:B:110:PRO:HD2	0.51	2.21	3	3
1:A:52:THR:O	1:A:56:LEU:HG	0.51	2.06	10	5
1:A:84:PHE:O	1:A:88:LEU:HG	0.50	2.07	5	7
2:B:144:GLU:O	2:B:181:VAL:HA	0.49	2.06	8	7
2:B:83:LEU:O	2:B:94:SER:HA	0.49	2.07	4	4
2:B:124:MET:SD	2:B:165:ASN:HB2	0.49	2.48	1	6
2:B:40:THR:HG23	2:B:59:ALA:HA	0.48	1.83	4	1
1:A:15:LEU:HD11	2:B:100:TRP:CZ2	0.48	2.44	2	1
2:B:70:ASP:OD2	2:B:73:ARG:HD3	0.48	2.08	9	1
1:A:15:LEU:HD11	2:B:100:TRP:CH2	0.47	2.44	9	2
1:A:47:PHE:O	1:A:52:THR:HB	0.47	2.09	4	2
1:A:113:GLU:O	1:A:117:LEU:HG	0.47	2.09	3	3
1:A:143:VAL:O	1:A:147:ILE:HG12	0.47	2.09	2	3
1:A:144:ARG:NH1	1:A:145:ALA:HA	0.47	2.25	10	1
1:A:33:ARG:O	1:A:33:ARG:HD2	0.47	2.10	10	2
2:B:114:ILE:HD13	2:B:181:VAL:HB	0.46	1.87	2	2
2:B:108:GLU:H	2:B:109:PRO:CD	0.46	2.24	7	4
2:B:18:LEU:HD23	2:B:107:PHE:CZ	0.46	2.46	10	1
1:A:54:PRO:HD3	1:A:105:VAL:CG1	0.45	2.42	3	7
2:B:158:ILE:HG22	2:B:162:MET:HB2	0.45	1.88	5	1
2:B:56:LYS:O	2:B:57:ASN:HB3	0.45	2.11	2	4
1:A:56:LEU:HD22	1:A:154:SER:HB3	0.45	1.87	9	1
1:A:54:PRO:O	1:A:58:GLU:HG2	0.45	2.12	3	1
1:A:130:LEU:HB3	1:A:135:TYR:CE1	0.45	2.47	5	1
1:A:26:LEU:HG	2:B:46:MET:O	0.45	2.11	9	1
1:A:35:ASP:HA	2:B:48:LYS:HE2	0.45	1.89	3	4
1:A:138:CYS:O	1:A:142:VAL:HG23	0.44	2.12	8	3
2:B:46:MET:HB3	2:B:77:GLU:OE1	0.44	2.12	10	1
1:A:16:MET:SD	2:B:189:ASP:HB2	0.44	2.52	5	1
1:A:35:ASP:HB2	2:B:48:LYS:NZ	0.44	2.27	10	1
2:B:108:GLU:H	2:B:109:PRO:HD2	0.44	1.73	4	3
2:B:117:PHE:O	2:B:203:LEU:HB2	0.44	2.13	8	2
2:B:180:CYS:HA	2:B:199:LYS:O	0.43	2.13	4	2
1:A:36:PHE:HB2	1:A:122:TYR:CE1	0.43	2.48	7	1
1:A:144:ARG:O	1:A:148:MET:HB2	0.43	2.14	7	1
1:A:12:ARG:HG2	2:B:187:HIS:CE1	0.43	2.49	1	1
2:B:77:GLU:HA	2:B:100:TRP:CH2	0.43	2.48	7	1
1:A:24:ILE:HD12	1:A:29:CYS:SG	0.43	2.54	7	1
2:B:147:SER:HA	2:B:178:ASN:O	0.42	2.14	7	1
2:B:34:ILE:O	2:B:36:PRO:HD3	0.42	2.14	7	1
2:B:125:VAL:O	2:B:165:ASN:HA	0.42	2.14	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:108:THR:O	1:A:112:LYS:HD3	0.42	2.14	4	1
1:A:115:SER:O	1:A:119:VAL:HG23	0.42	2.14	10	2
2:B:92:LEU:HG	2:B:93:PHE:CD2	0.42	2.49	2	1
2:B:100:TRP:HB3	2:B:103:ILE:HG22	0.42	1.90	5	1
1:A:41:GLU:O	1:A:45:ASN:HB2	0.42	2.15	9	2
2:B:70:ASP:OD1	2:B:73:ARG:HD3	0.42	2.14	8	1
2:B:154:HIS:O	2:B:156:PRO:HD3	0.42	2.14	9	1
2:B:113:GLU:OE1	2:B:199:LYS:HE2	0.42	2.15	5	1
1:A:73:SER:HA	1:A:81:LEU:HD13	0.42	1.91	6	2
2:B:46:MET:HB2	2:B:78:ALA:O	0.42	2.15	10	1
1:A:145:ALA:HB1	2:B:47:SER:HA	0.41	1.92	2	1
1:A:33:ARG:NH1	2:B:50:GLU:HB2	0.41	2.31	8	1
2:B:127:PHE:HB2	2:B:164:GLY:O	0.41	2.16	7	1
1:A:35:ASP:HB2	2:B:48:LYS:HE2	0.41	1.92	7	1
1:A:14:THR:HG23	1:A:87:GLU:HB3	0.41	1.92	3	1
1:A:16:MET:SD	2:B:188:SER:HB2	0.41	2.55	9	1
1:A:32:ASP:O	1:A:142:VAL:HG21	0.40	2.16	9	1
1:A:92:LEU:O	1:A:96:GLU:HG2	0.40	2.16	9	1
2:B:171:ASP:O	2:B:172:LYS:HB2	0.40	2.17	6	1
2:B:179:TYR:O	2:B:200:CYS:HA	0.40	2.17	5	1
1:A:96:GLU:O	1:A:100:ILE:HG13	0.40	2.17	3	1
1:A:57:HIS:CD2	1:A:96:GLU:HB3	0.40	2.52	8	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	155/165 (94%)	139±2 (90±2%)	14±2 (9±2%)	1±0 (1±0%)	29	74
2	B	194/212 (92%)	165±3 (85±1%)	26±2 (13±1%)	3±1 (1±1%)	18	63
All	All	3490/3770 (93%)	3046 (87%)	403 (12%)	41 (1%)	21	68

All 10 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	108	GLU	10
1	A	109	PRO	10
2	B	204	PRO	8
2	B	197	PRO	3
2	B	106	SER	2
2	B	193	VAL	2
1	A	31	LYS	2
2	B	156	PRO	2
2	B	188	SER	1
2	B	119	ASN	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	143/152 (94%)	125±2 (87±1%)	18±2 (13±1%)	10	52
2	B	185/201 (92%)	150±3 (81±2%)	35±3 (19±2%)	5	38
All	All	3280/3530 (93%)	2752 (84%)	528 (16%)	7	44

All 144 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	108	THR	10
2	B	126	LYS	10
2	B	180	CYS	10
2	B	140	SER	10
2	B	177	THR	10
1	A	115	SER	10
2	B	62	THR	10
2	B	118	THR	9
1	A	27	PHE	9
2	B	100	TRP	9
1	A	87	GLU	9
1	A	106	THR	9
2	B	146	GLN	9
2	B	163	SER	9
2	B	25	LEU	8

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Mol	Chain	Res	Type	Models (Total)
1	A	11	SER	8
1	A	33	ARG	8
2	B	82	VAL	8
2	B	119	ASN	8
2	B	107	PHE	7
2	B	81	THR	7
2	B	193	VAL	7
2	B	75	THR	7
2	B	11	SER	7
1	A	14	THR	7
2	B	76	HIS	7
1	A	58	GLU	6
2	B	77	GLU	6
2	B	68	LEU	6
2	B	31	ASN	6
2	B	129	SER	6
2	B	64	SER	6
2	B	29	LEU	6
2	B	80	VAL	6
1	A	89	TYR	6
1	A	42	GLU	6
2	B	200	CYS	6
2	B	141	LEU	6
2	B	182	SER	6
1	A	155	THR	6
2	B	13	THR	5
2	B	47	SER	5
1	A	114	ASP	5
2	B	188	SER	5
1	A	91	GLN	5
2	B	91	THR	4
1	A	121	LYS	4
2	B	98	ASN	4
1	A	79	THR	4
2	B	122	ASN	4
2	B	33	SER	4
2	B	105	MET	4
1	A	23	LYS	4
2	B	38	HIS	4
2	B	87	SER	4
1	A	153	LEU	3
2	B	57	ASN	3

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Mol	Chain	Res	Type	Models (Total)
2	B	114	ILE	3
2	B	196	SER	3
1	A	101	GLN	3
2	B	23	SER	3
2	B	96	SER	3
1	A	149	ARG	3
2	B	165	ASN	3
2	B	185	LEU	3
1	A	6	THR	3
2	B	157	GLU	3
2	B	187	HIS	3
2	B	18	LEU	3
1	A	127	THR	3
1	A	25	SER	3
2	B	137	PHE	3
2	B	130	ILE	3
2	B	139	LEU	3
1	A	34	HIS	3
2	B	32	HIS	3
2	B	26	SER	2
1	A	43	PHE	2
2	B	148	GLU	2
1	A	68	SER	2
1	A	2	ASP	2
2	B	94	SER	2
1	A	151	PHE	2
2	B	90	THR	2
1	A	30	LEU	2
1	A	132	GLU	2
2	B	167	THR	2
1	A	83	LYS	2
2	B	15	LYS	2
2	B	173	LEU	2
2	B	69	THR	2
2	B	46	MET	2
2	B	48	LYS	2
1	A	136	SER	2
2	B	55	VAL	2
1	A	124	GLN	2
2	B	97	HIS	2
2	B	161	ASN	2
2	B	186	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	141	GLU	2
2	B	198	LEU	2
2	B	70	ASP	2
1	A	133	LYS	1
2	B	30	LYS	1
1	A	156	ASN	1
2	B	28	GLU	1
2	B	184	TYR	1
1	A	72	SER	1
1	A	31	LYS	1
1	A	8	SER	1
1	A	138	CYS	1
1	A	78	GLU	1
1	A	15	LEU	1
2	B	190	GLU	1
2	B	178	ASN	1
1	A	40	GLN	1
1	A	24	ILE	1
1	A	77	ASP	1
2	B	74	SER	1
2	B	50	GLU	1
2	B	147	SER	1
2	B	103	ILE	1
1	A	12	ARG	1
1	A	146	GLU	1
2	B	19	ARG	1
2	B	51	ASP	1
1	A	51	GLU	1
1	A	154	SER	1
1	A	94	ASP	1
2	B	56	LYS	1
2	B	37	THR	1
2	B	145	GLU	1
1	A	3	LEU	1
2	B	67	ASP	1
2	B	42	LEU	1
2	B	132	GLU	1
1	A	107	GLU	1
1	A	71	ASP	1
1	A	5	GLN	1
2	B	166	PHE	1
2	B	138	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	9	LEU	1
2	B	179	TYR	1
1	A	125	ARG	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