



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 20, 2018 – 09:41 pm GMT

PDB ID : 1D00  
Title : STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COM-  
PLEX WITH A 5-RESIDUE CD40 PEPTIDE  
Authors : Ye, H.; Park, Y.C.; Kreishman, M.; Kieff, E.; Wu, H.  
Deposited on : 1999-09-07  
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

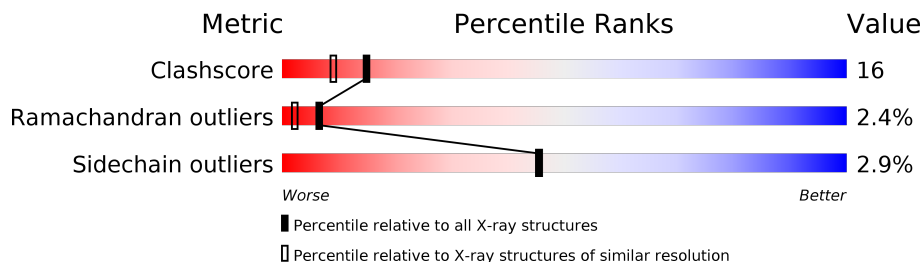
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	122078	8264 (2.00-2.00)
Ramachandran outliers	120005	8163 (2.00-2.00)
Sidechain outliers	119972	8162 (2.00-2.00)



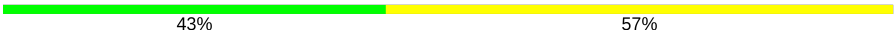






The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	168	
1	B	168	
1	C	168	
1	D	168	
1	E	168	
1	F	168	
1	G	168	

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Mol	Chain	Length	Quality of chain
1	H	168	 68% 29%
2	I	7	 71% 14% 14%
2	J	7	 43% 57%
2	K	7	 57% 43%
2	L	7	 71% 29%
2	M	7	 71% 29%
2	N	7	 71% 29%
2	O	7	 71% 14% 14%
2	P	7	 57% 43%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10670 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	B	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	C	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	D	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	E	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	F	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	G	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			
1	H	168	Total	C	N	O	S	0	0	0
			1282	825	217	231	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	362	ALA	PRO	CONFLICT	GB 1363002
A	365	ARG	LEU	CONFLICT	GB 1363002
B	362	ALA	PRO	CONFLICT	GB 1363002
B	365	ARG	LEU	CONFLICT	GB 1363002
C	362	ALA	PRO	CONFLICT	GB 1363002
C	365	ARG	LEU	CONFLICT	GB 1363002
D	362	ALA	PRO	CONFLICT	GB 1363002
D	365	ARG	LEU	CONFLICT	GB 1363002
E	362	ALA	PRO	CONFLICT	GB 1363002
E	365	ARG	LEU	CONFLICT	GB 1363002
F	362	ALA	PRO	CONFLICT	GB 1363002
F	365	ARG	LEU	CONFLICT	GB 1363002

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Chain	Residue	Modelled	Actual	Comment	Reference
G	362	ALA	PRO	CONFLICT	GB 1363002
G	365	ARG	LEU	CONFLICT	GB 1363002
H	362	ALA	PRO	CONFLICT	GB 1363002
H	365	ARG	LEU	CONFLICT	GB 1363002

- Molecule 2 is a protein called B-CELL SURFACE ANTIGEN CD40.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	J	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	K	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	L	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	M	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	N	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	O	7	Total	C	N	O	0	0	1
			43	26	7	10			
2	P	7	Total	C	N	O	0	0	1
			43	26	7	10			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total	O	0	0
			12	12		
3	B	3	Total	O	0	0
			3	3		
3	C	11	Total	O	0	0
			11	11		
3	D	7	Total	O	0	0
			7	7		
3	E	5	Total	O	0	0
			5	5		
3	F	9	Total	O	0	0
			9	9		
3	G	8	Total	O	0	0
			8	8		

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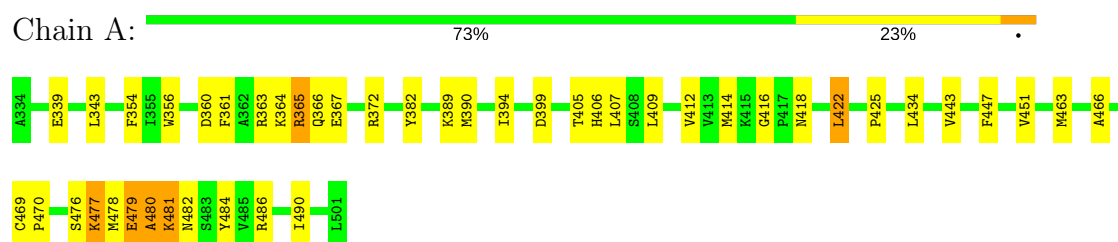
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	13	Total 13	O 13	0	0
3	K	1	Total 1	O 1	0	0
3	L	1	Total 1	O 1	0	0

### 3 Residue-property plots

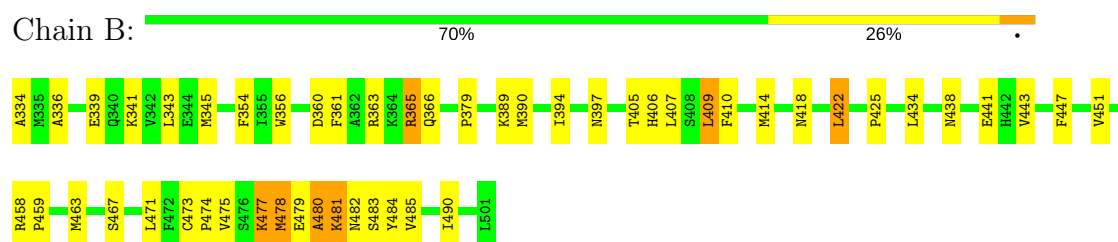
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

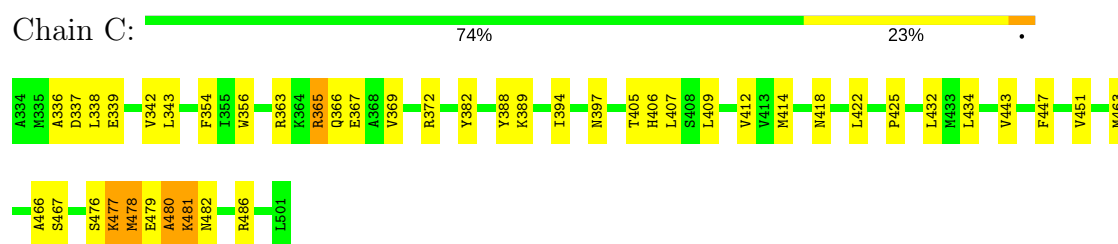
#### • Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2



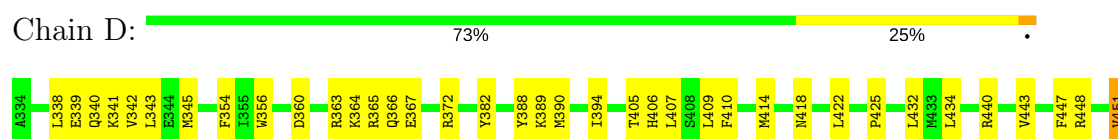
#### • Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2



#### • Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2



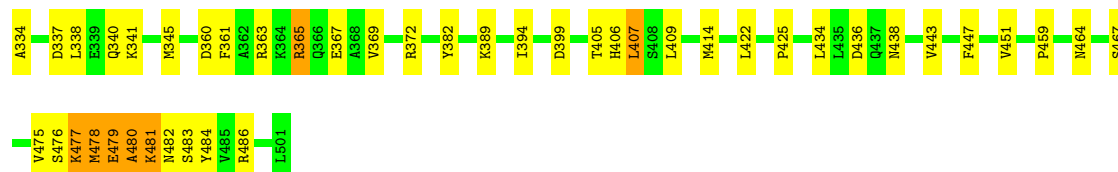
#### • Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2





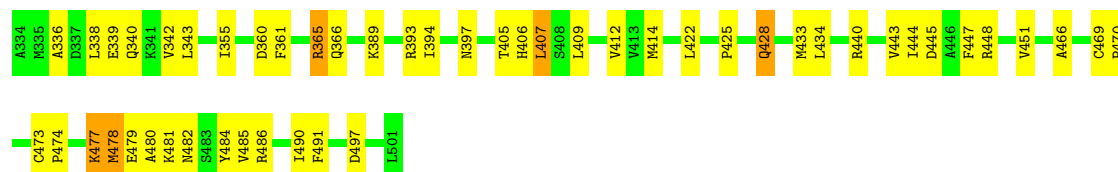
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2

Chain E: 74% 22% .



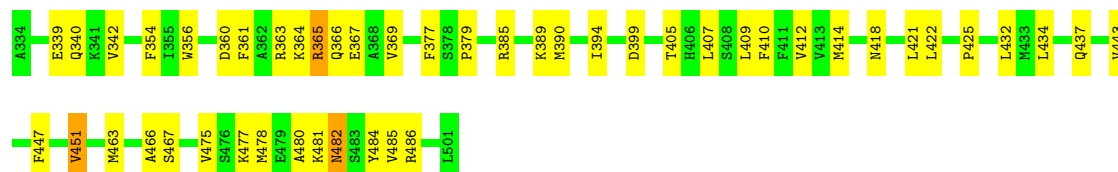
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2

Chain F: 70% 27% .



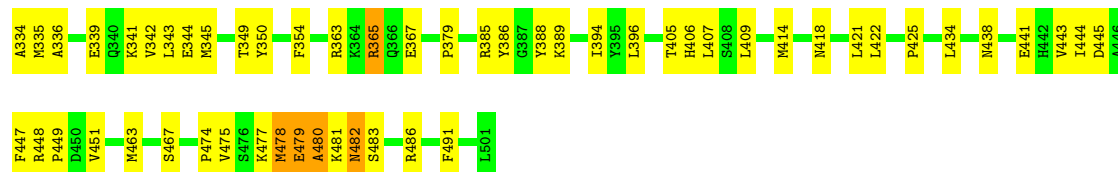
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2

Chain G: 71% 27% .



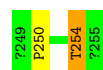
• Molecule 1: TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED PROTEIN 2

Chain H: 68% 29% .



• Molecule 2: B-CELL SURFACE ANTIGEN CD40

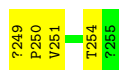
Chain I: 71% 14% 14%



• Molecule 2: B-CELL SURFACE ANTIGEN CD40



Chain J:  43% 57%



- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain K:  57% 43%



- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain L:  71% 29%



- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain M:  71% 29%



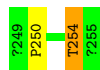
- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain N:  71% 29%



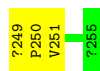
- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain O:  71% 14% 14%



- Molecule 2: B-CELL SURFACE ANTIGEN CD40

Chain P:  57% 43%



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	R 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.40Å 111.40Å 111.40Å 103.70° 103.70° 103.70°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.219 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10670	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, NH2

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.44	0/1312	0.71	0/1781
1	B	0.42	0/1312	0.71	0/1781
1	C	0.43	0/1312	0.72	0/1781
1	D	0.44	0/1312	0.71	0/1781
1	E	0.43	0/1312	0.70	1/1781 (0.1%)
1	F	0.44	0/1312	0.73	1/1781 (0.1%)
1	G	0.42	0/1312	0.71	0/1781
1	H	0.41	0/1312	0.71	0/1781
2	I	0.42	0/40	0.74	0/55
2	J	0.51	0/40	0.77	0/55
2	K	0.47	0/40	0.69	0/55
2	L	0.48	0/40	0.81	0/55
2	M	0.44	0/40	0.73	0/55
2	N	0.47	0/40	0.73	0/55
2	O	0.49	0/40	0.71	0/55
2	P	0.50	0/40	0.79	0/55
All	All	0.43	0/10816	0.71	2/14688 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	407	LEU	N-CA-C	-5.20	96.96	111.00
1	F	407	LEU	N-CA-C	-5.15	97.09	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1282	0	1242	36	0
1	B	1282	0	1242	45	0
1	C	1282	0	1242	37	0
1	D	1282	0	1242	43	0
1	E	1282	0	1242	41	0
1	F	1282	0	1242	43	0
1	G	1282	0	1242	44	0
1	H	1282	0	1242	53	0
2	I	43	0	40	3	0
2	J	43	0	40	7	0
2	K	43	0	40	6	0
2	L	43	0	40	1	0
2	M	43	0	40	3	0
2	N	43	0	40	1	0
2	O	43	0	40	4	0
2	P	43	0	40	9	0
3	A	12	0	0	1	0
3	B	3	0	0	0	0
3	C	11	0	0	0	0
3	D	7	0	0	3	0
3	E	5	0	0	1	0
3	F	9	0	0	4	0
3	G	8	0	0	0	0
3	H	13	0	0	5	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
All	All	10670	0	10256	337	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

The worst 5 of 337 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:425:PRO:HG3	1:H:451:VAL:HG13	1.41	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:PRO:HG3	1:A:451:VAL:HG13	1.43	0.99
1:H:394:ILE:HD11	1:H:407:LEU:HD21	1.41	0.99
1:G:389:LYS:HG2	1:G:414:MET:HE3	1.46	0.95
1:E:425:PRO:HG3	1:E:451:VAL:HG13	1.51	0.93

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	166/168 (99%)	156 (94%)	6 (4%)	4 (2%)	6	2
1	B	166/168 (99%)	156 (94%)	6 (4%)	4 (2%)	6	2
1	C	166/168 (99%)	154 (93%)	7 (4%)	5 (3%)	5	1
1	D	166/168 (99%)	156 (94%)	7 (4%)	3 (2%)	9	4
1	E	166/168 (99%)	155 (93%)	5 (3%)	6 (4%)	4	1
1	F	166/168 (99%)	158 (95%)	5 (3%)	3 (2%)	9	4
1	G	166/168 (99%)	155 (93%)	9 (5%)	2 (1%)	14	7
1	H	166/168 (99%)	152 (92%)	8 (5%)	6 (4%)	4	1
2	I	5/7 (71%)	5 (100%)	0	0	100	100
2	J	5/7 (71%)	4 (80%)	1 (20%)	0	100	100
2	K	5/7 (71%)	5 (100%)	0	0	100	100
2	L	5/7 (71%)	5 (100%)	0	0	100	100
2	M	5/7 (71%)	5 (100%)	0	0	100	100
2	N	5/7 (71%)	5 (100%)	0	0	100	100
2	O	5/7 (71%)	5 (100%)	0	0	100	100
2	P	5/7 (71%)	5 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1368/1400 (98%)	1281 (94%)	54 (4%)	33 (2%)	6 2

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	477	LYS
1	A	480	ALA
1	B	477	LYS
1	B	480	ALA
1	C	477	LYS

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	132/144 (92%)	128 (97%)	4 (3%)	44 44
1	B	132/144 (92%)	127 (96%)	5 (4%)	36 33
1	C	132/144 (92%)	130 (98%)	2 (2%)	67 72
1	D	132/144 (92%)	129 (98%)	3 (2%)	53 56
1	E	132/144 (92%)	129 (98%)	3 (2%)	53 56
1	F	132/144 (92%)	126 (96%)	6 (4%)	30 26
1	G	132/144 (92%)	129 (98%)	3 (2%)	53 56
1	H	132/144 (92%)	130 (98%)	2 (2%)	67 72
2	I	5/5 (100%)	4 (80%)	1 (20%)	1 0
2	J	5/5 (100%)	5 (100%)	0	100 100
2	K	5/5 (100%)	5 (100%)	0	100 100
2	L	5/5 (100%)	4 (80%)	1 (20%)	1 0
2	M	5/5 (100%)	5 (100%)	0	100 100
2	N	5/5 (100%)	4 (80%)	1 (20%)	1 0
2	O	5/5 (100%)	4 (80%)	1 (20%)	1 0
2	P	5/5 (100%)	5 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1096/1192 (92%)	1064 (97%)	32 (3%)	45 45

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	365	ARG
1	F	360	ASP
2	L	254	THR
1	E	422	LEU
1	F	365	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	406	HIS
1	E	438	ASN
1	H	438	ASN
1	E	418	ASN
1	E	461	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.