



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:14 PM UTC

PDB ID : 1G6R / pdb_00001g6r
Title : A FUNCTIONAL HOT SPOT FOR ANTIGEN RECOGNITION IN A SUPERAGONIST TCR/MHC COMPLEX
Authors : Degano, M.; Garcia, K.C.; Apostolopoulos, V.; Rudolph, M.G.; Teyton, L.; Wilson, I.A.
Deposited on : 2000-11-07
Resolution : 2.80 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

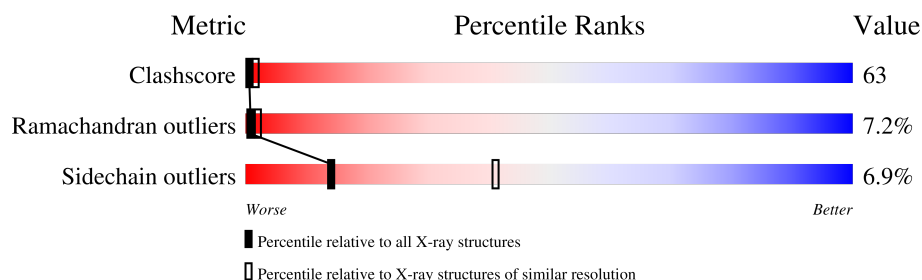
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

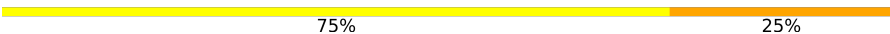
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	202	24% 61% 15%
1	C	202	21% 66% 13%
2	B	237	25% 58% 15% .
2	D	237	28% 61% 11%
3	H	274	27% 62% 11% .
3	I	274	26% 63% 11%
4	L	99	22% 65% 13%
4	M	99	22% 65% 13%

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Mol	Chain	Length	Quality of chain
5	P	8	 12% 62% 12% 12%
5	Q	8	 75% 25%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13100 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 ALPHA T CELL RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1570	999	253	310	8			
1	C	202	Total	C	N	O	S	0	0	0
			1570	999	253	310	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	ALA	GLN	conflict	UNP P01738
A	165	ALA	LYS	conflict	UNP P01738
C	127	ALA	GLN	conflict	UNP P01738
C	165	ALA	LYS	conflict	UNP P01738

- Molecule 2 is a protein called BETA T CELL RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	237	Total	C	N	O	S	0	0	0
			1853	1160	331	355	7			
2	D	237	Total	C	N	O	S	0	0	0
			1853	1160	331	355	7			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	97	GLY	GLN	conflict	UNP P01852
B	105	THR	ARG	conflict	UNP P01852
B	11	LYS	ALA	conflict	UNP P01852
B	107	TYR	GLU	conflict	UNP P01852
B	108	PHE	GLN	conflict	UNP P01852
B	109	GLY	PHE	conflict	UNP P01852
B	110	ALA	PHE	conflict	UNP P01852
B	?	-	PRO	deletion	UNP P01852

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLY	deletion	UNP P01852
B	115	SER	THR	conflict	UNP P01852
D	97	GLY	GLN	conflict	UNP P01852
D	105	THR	ARG	conflict	UNP P01852
D	11	LYS	ALA	conflict	UNP P01852
D	107	TYR	GLU	conflict	UNP P01852
D	108	PHE	GLN	conflict	UNP P01852
D	109	GLY	PHE	conflict	UNP P01852
D	110	ALA	PHE	conflict	UNP P01852
D	?	-	PRO	deletion	UNP P01852
D	?	-	GLY	deletion	UNP P01852
D	115	SER	THR	conflict	UNP P01852

- Molecule 3 is a protein called MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	274	Total	C	N	O	S	0	0	0
			2232	1408	393	422	9			
3	I	274	Total	C	N	O	S	0	0	0
			2232	1408	393	422	9			

- Molecule 4 is a protein called BETA-2 MICROGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			
4	M	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			

- Molecule 5 is a protein called SIYR PEPTIDE.

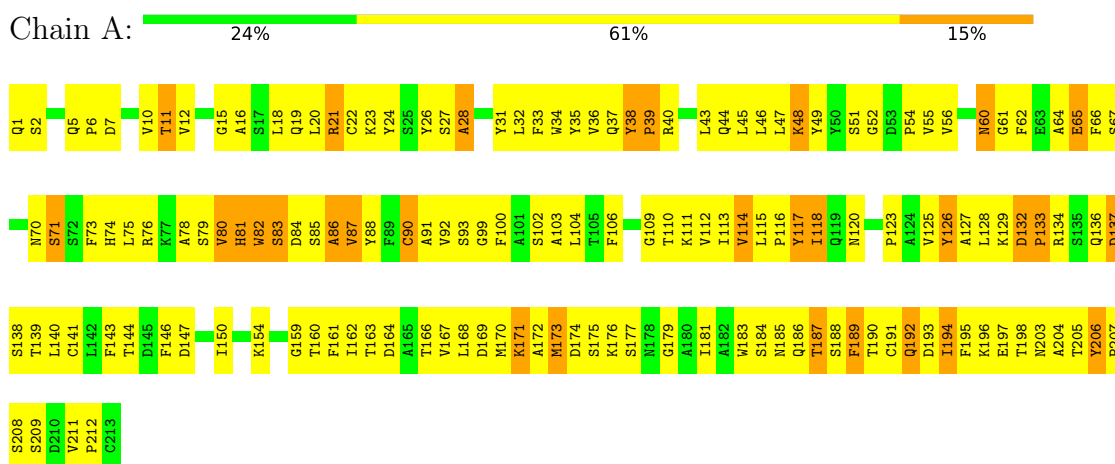
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	P	8	Total	C	N	O	0	0	0
			74	50	11	13			
5	Q	8	Total	C	N	O	0	0	0
			74	50	11	13			

3 Residue-property plots

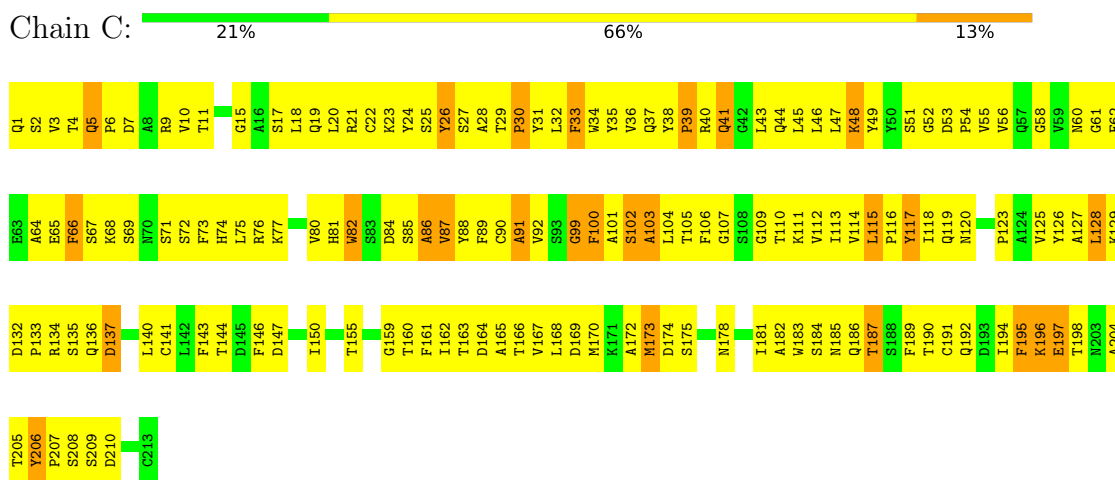
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS was not executed.

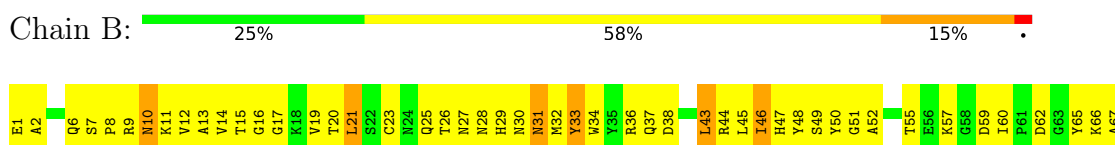
• Molecule 1: ALPHA T CELL RECEPTOR

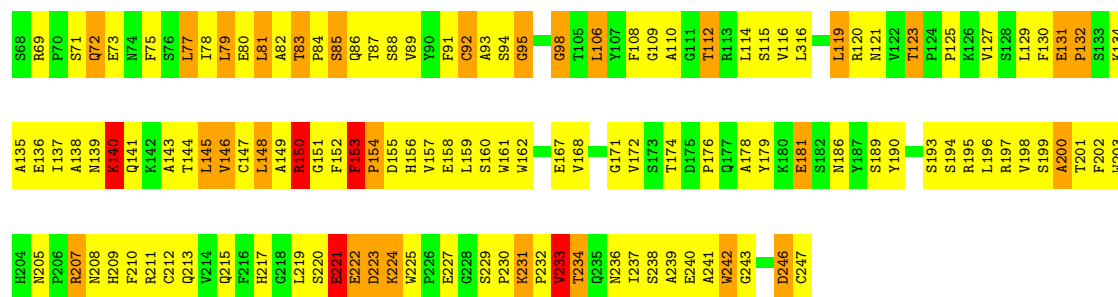


• Molecule 1: ALPHA T CELL RECEPTOR



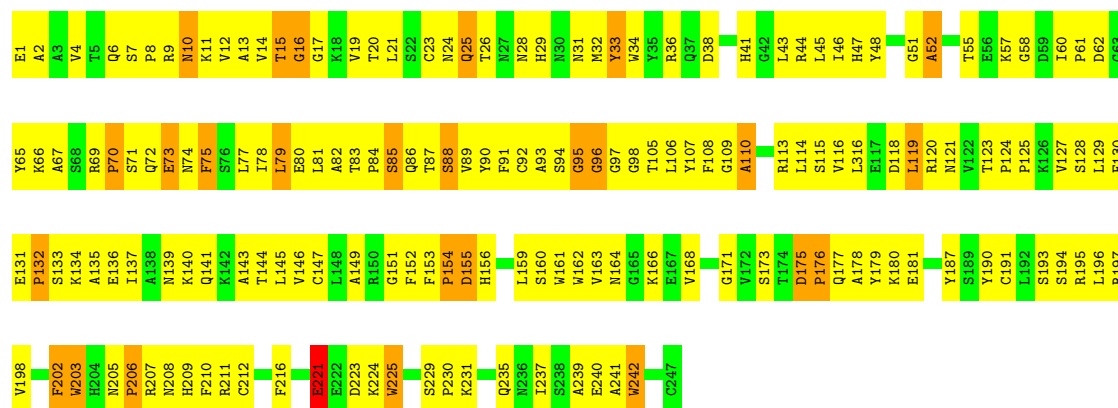
• Molecule 2: BETA T CELL RECEPTOR





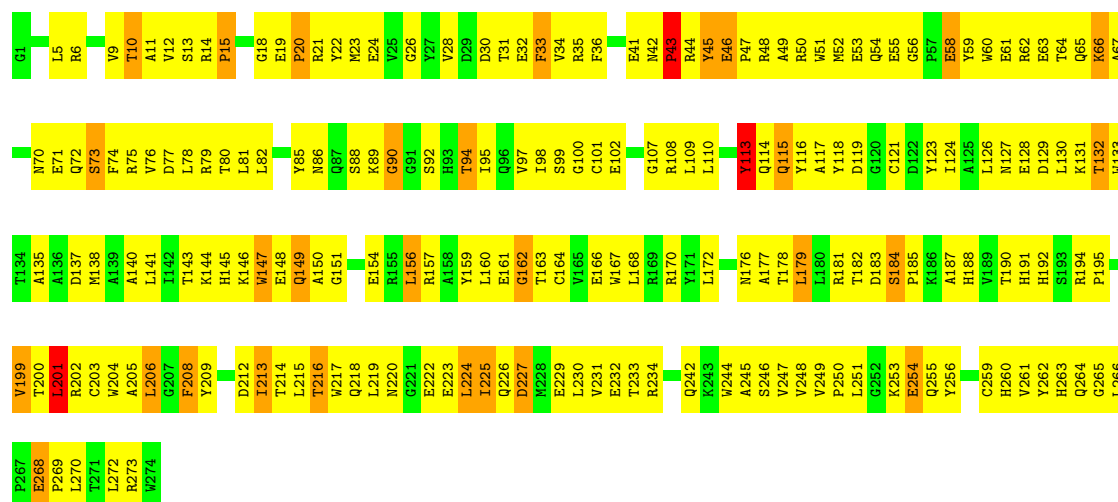
• Molecule 2: BETA T CELL RECEPTOR

Chain D: 28% 61% 11%



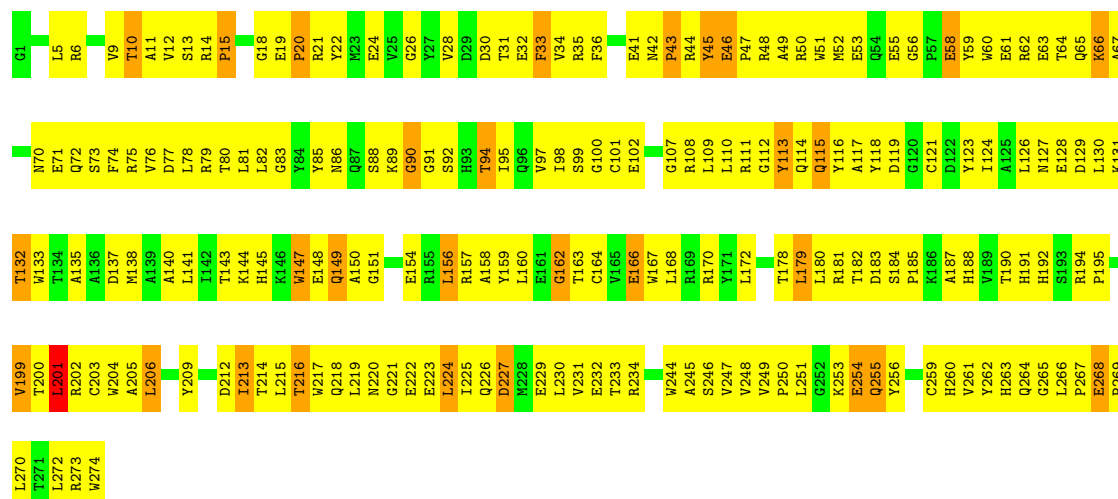
• Molecule 3: MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULE

Chain H: 27% 62% 11%

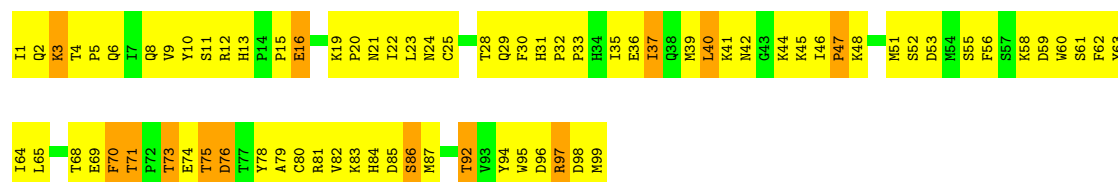


• Molecule 3: MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULE

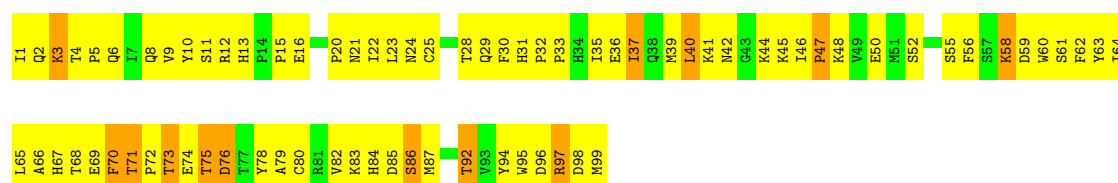
Chain I: 26% 63% 11%



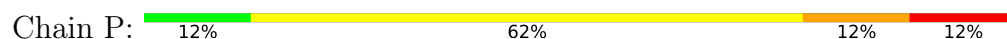
● Molecule 4: BETA-2 MICROGLOBULIN



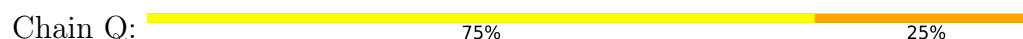
● Molecule 4: BETA-2 MICROGLOBULIN



● Molecule 5: SIYR PEPTIDE



● Molecule 5: SIYR PEPTIDE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	297.71Å 94.57Å 84.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.80)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.298 , 0.327	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	13100	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.69	0/1611	1.19	11/2193 (0.5%)
1	C	0.52	0/1611	1.07	17/2193 (0.8%)
2	B	0.67	0/1904	1.29	26/2586 (1.0%)
2	D	0.44	0/1904	0.98	8/2586 (0.3%)
3	H	0.59	1/2293 (0.0%)	1.08	14/3113 (0.4%)
3	I	0.54	0/2293	1.04	12/3113 (0.4%)
4	L	0.62	0/847	1.15	6/1148 (0.5%)
4	M	0.57	0/847	1.10	5/1148 (0.4%)
5	P	0.70	0/76	0.93	0/100
5	Q	0.63	0/76	0.85	0/100
All	All	0.58	1/13462 (0.0%)	1.11	99/18280 (0.5%)

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 outliers	#Planarity outliers
2	B	0	1
5	P	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	225	ILE	CA-CB	5.05	1.61	1.54

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	131	GLU	CA-C-N	11.15	131.27	119.90
2	B	131	GLU	C-N-CA	11.15	131.27	119.90
2	B	221	GLU	N-CA-C	-10.04	96.20	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	153	PHE	CA-C-N	-9.97	108.42	119.98
2	B	153	PHE	C-N-CA	-9.97	108.42	119.98

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	50	TYR	Sidechain
5	P	3	TYR	Sidechain

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	1570	0	1508	214	0
1	C	1570	0	1508	216	0
2	B	1853	0	1767	254	0
2	D	1853	0	1767	247	0
3	H	2232	0	2127	272	0
3	I	2232	0	2127	257	0
4	L	821	0	798	113	0
4	M	821	0	798	110	0
5	P	74	0	72	19	0
5	Q	74	0	72	19	0
All	All	13100	0	12544	1609	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 63.

The worst 5 of 1609 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance ($\text{\AA}$)	Clash overlap ($\text{\AA}$)
1:C:85:SER:HB2	1:C:114:VAL:HG12	1.28	1.15
1:A:10:VAL:HB	1:A:112:VAL:HG12	1.27	1.14
1:A:85:SER:HB2	1:A:114:VAL:HG12	1.31	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:133:TRP:HB2	3:H:144:LYS:HE2	1.33	1.07
3:H:126:LEU:HD22	3:H:156:LEU:HD13	1.38	1.06

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	200/202 (99%)	155 (78%)	28 (14%)	17 (8%)	0	1
1	C	200/202 (99%)	148 (74%)	35 (18%)	17 (8%)	0	1
2	B	235/237 (99%)	186 (79%)	38 (16%)	11 (5%)	2	6
2	D	235/237 (99%)	178 (76%)	34 (14%)	23 (10%)	0	1
3	H	272/274 (99%)	202 (74%)	57 (21%)	13 (5%)	2	6
3	I	272/274 (99%)	205 (75%)	54 (20%)	13 (5%)	2	6
4	L	97/99 (98%)	78 (80%)	10 (10%)	9 (9%)	0	1
4	M	97/99 (98%)	79 (81%)	9 (9%)	9 (9%)	0	1
5	P	6/8 (75%)	1 (17%)	3 (50%)	2 (33%)	0	0
5	Q	6/8 (75%)	1 (17%)	3 (50%)	2 (33%)	0	0
All	All	1620/1640 (99%)	1233 (76%)	271 (17%)	116 (7%)	1	2

5 of 116 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ALA
1	A	38	TYR
1	A	61	GLY
1	A	82	TRP
1	A	173	MET

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	176/176 (100%)	164 (93%)	12 (7%)	14	42
1	C	176/176 (100%)	168 (96%)	8 (4%)	24	58
2	B	200/200 (100%)	176 (88%)	24 (12%)	5	17
2	D	200/200 (100%)	194 (97%)	6 (3%)	36	72
3	H	232/232 (100%)	213 (92%)	19 (8%)	10	33
3	I	232/232 (100%)	215 (93%)	17 (7%)	13	38
4	L	94/94 (100%)	88 (94%)	6 (6%)	16	44
4	M	94/94 (100%)	88 (94%)	6 (6%)	16	44
5	P	7/7 (100%)	7 (100%)	0	100	100
5	Q	7/7 (100%)	7 (100%)	0	100	100
All	All	1418/1418 (100%)	1320 (93%)	98 (7%)	14	41

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	58	LYS
2	D	79	LEU
4	L	73	THR
1	C	117	TYR
3	I	10	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	149	GLN
2	D	139	ASN
3	I	260	HIS
1	C	186	GLN
2	D	31	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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.