



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 11:55 PM UTC

PDB ID : 2ICW / pdb_00002icw
Title : Crystal structure of a complete ternary complex between TCR, superantigen, and peptide-MHC class II molecule
Authors : Wang, L.; Zhao, Y.; Li, H.
Deposited on : 2006-09-13
Resolution : 2.41 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

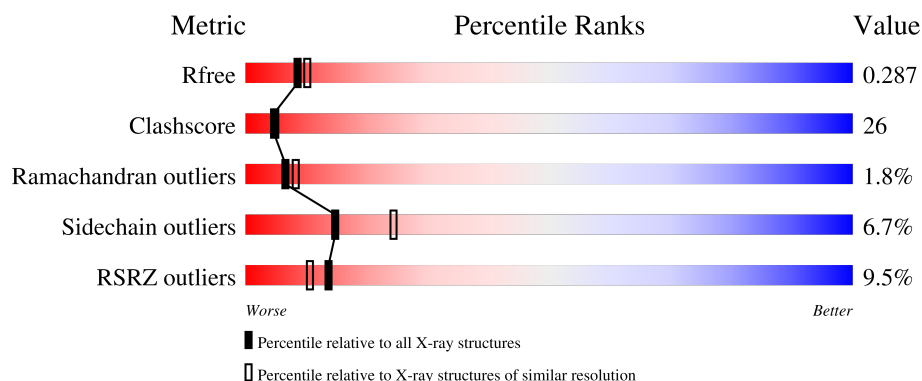
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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))
R_{free}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	179	56% 39% .
1	D	179	60% 34% 6%
2	B	190	12% 53% 38% 5% .
2	E	190	8% 53% 39% 5% .
3	C	13	62% 38%

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Mol	Chain	Length	Quality of chain
3	F	13	85% 15%
4	G	213	9% 50% 46%
4	H	213	3% 54% 40% 5%
5	I	110	35% 45% 51% 5%
5	K	110	32% 45% 51%
6	J	113	4% 57% 34% 10%
6	L	113	7% 54% 36% 8%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13464 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	Se	0	0	0
			1474	954	239	276	2	3			
1	D	179	Total	C	N	O	S	Se	0	0	0
			1474	954	239	276	2	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MSE	MET	modified residue	UNP P01903
A	36	MSE	MET	modified residue	UNP P01903
A	73	MSE	MET	modified residue	UNP P01903
D	23	MSE	MET	modified residue	UNP P01903
D	36	MSE	MET	modified residue	UNP P01903
D	73	MSE	MET	modified residue	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	184	Total	C	N	O	S		0	0	0
			1504	946	267	285	6				
2	E	185	Total	C	N	O	S		0	0	0
			1513	951	269	287	6				

- Molecule 3 is a protein called haemagglutinin peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			106	69	18	19			
3	F	13	Total	C	N	O	0	0	0
			106	69	18	19			

- Molecule 4 is a protein called Mycoplasma arthritidis mitogen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	213	Total	C	N	O	S	0	0	0
			1786	1154	301	326	5			
4	H	213	Total	C	N	O	S	0	0	0
			1786	1154	301	326	5			

- Molecule 5 is a protein called T-cell receptor alpha chain V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	110	Total	C	N	O	S	0	1	0
			863	557	144	160	2			
5	K	109	Total	C	N	O	S	0	0	0
			847	545	142	158	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	43	PRO	LEU	engineered mutation	UNP P01738
I	82	ARG	TRP	engineered mutation	UNP P01738
K	43	PRO	LEU	engineered mutation	UNP P01738
K	82	ARG	TRP	engineered mutation	UNP P01738

- Molecule 6 is a protein called T-cell receptor beta chain V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	J	113	Total	C	N	O	S	0	0	0
			857	528	151	175	3			
6	L	111	Total	C	N	O	S	0	0	0
			843	520	149	171	3			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	10	ASN	SER	SEE REMARK 999	UNP P04213
J	17	GLU	GLY	engineered mutation	UNP P04213
J	24	ASN	HIS	SEE REMARK 999	UNP P04213
J	30	ASN	ASP	SEE REMARK 999	UNP P04213
J	31	ASN	TYR	SEE REMARK 999	UNP P04213
J	42	GLU	GLY	engineered mutation	UNP P04213
J	51	GLY	VAL	SEE REMARK 999	UNP P04213
J	53	GLY	ASP	SEE REMARK 999	UNP P04213
J	80	SER	LEU	engineered mutation	UNP P04213
J	81	ALA	-	SEE REMARK 999	UNP P04213
J	82	THR	-	SEE REMARK 999	UNP P04213

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Chain	Residue	Modelled	Actual	Comment	Reference
J	83	PRO	-	SEE REMARK 999	UNP P04213
J	84	SER	-	SEE REMARK 999	UNP P04213
J	85	GLN	-	SEE REMARK 999	UNP P04213
J	86	THR	-	SEE REMARK 999	UNP P04213
J	87	SER	-	SEE REMARK 999	UNP P04213
J	88	VAL	-	SEE REMARK 999	UNP P04213
J	89	TYR	-	SEE REMARK 999	UNP P04213
J	90	PHE	-	SEE REMARK 999	UNP P04213
J	91	CYS	-	SEE REMARK 999	UNP P04213
J	92	ALA	-	SEE REMARK 999	UNP P04213
J	93	SER	-	SEE REMARK 999	UNP P04213
J	94	GLY	-	SEE REMARK 999	UNP P04213
J	95	GLY	-	SEE REMARK 999	UNP P04213
J	96	GLY	-	SEE REMARK 999	UNP P04213
J	97	GLY	-	SEE REMARK 999	UNP P04213
J	98	THR	-	SEE REMARK 999	UNP P04213
J	100	TYR	-	SEE REMARK 999	UNP P04213
J	101	PHE	-	SEE REMARK 999	UNP P04213
J	102	GLY	-	SEE REMARK 999	UNP P04213
J	103	ALA	-	SEE REMARK 999	UNP P04213
J	104	GLY	-	SEE REMARK 999	UNP P04213
J	105	THR	-	SEE REMARK 999	UNP P04213
J	106	ARG	-	SEE REMARK 999	UNP P04213
J	107	LEU	-	SEE REMARK 999	UNP P04213
J	108	SER	-	SEE REMARK 999	UNP P04213
J	109	VAL	-	SEE REMARK 999	UNP P04213
J	110	LEU	-	SEE REMARK 999	UNP P04213
J	111	SER	-	cloning artifact	UNP P04213
J	112	SER	-	cloning artifact	UNP P04213
J	113	ALA	-	cloning artifact	UNP P04213
L	10	ASN	SER	SEE REMARK 999	UNP P04213
L	17	GLU	GLY	engineered mutation	UNP P04213
L	24	ASN	HIS	SEE REMARK 999	UNP P04213
L	30	ASN	ASP	SEE REMARK 999	UNP P04213
L	31	ASN	TYR	SEE REMARK 999	UNP P04213
L	42	GLU	GLY	engineered mutation	UNP P04213
L	51	GLY	VAL	SEE REMARK 999	UNP P04213
L	53	GLY	ASP	SEE REMARK 999	UNP P04213
L	80	SER	LEU	engineered mutation	UNP P04213
L	81	ALA	-	SEE REMARK 999	UNP P04213
L	82	THR	-	SEE REMARK 999	UNP P04213
L	83	PRO	-	SEE REMARK 999	UNP P04213

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Chain	Residue	Modelled	Actual	Comment	Reference
L	84	SER	-	SEE REMARK 999	UNP P04213
L	85	GLN	-	SEE REMARK 999	UNP P04213
L	86	THR	-	SEE REMARK 999	UNP P04213
L	87	SER	-	SEE REMARK 999	UNP P04213
L	88	VAL	-	SEE REMARK 999	UNP P04213
L	89	TYR	-	SEE REMARK 999	UNP P04213
L	90	PHE	-	SEE REMARK 999	UNP P04213
L	91	CYS	-	SEE REMARK 999	UNP P04213
L	92	ALA	-	SEE REMARK 999	UNP P04213
L	93	SER	-	SEE REMARK 999	UNP P04213
L	94	GLY	-	SEE REMARK 999	UNP P04213
L	95	GLY	-	SEE REMARK 999	UNP P04213
L	96	GLY	-	SEE REMARK 999	UNP P04213
L	97	GLY	-	SEE REMARK 999	UNP P04213
L	98	THR	-	SEE REMARK 999	UNP P04213
L	100	TYR	-	SEE REMARK 999	UNP P04213
L	101	PHE	-	SEE REMARK 999	UNP P04213
L	102	GLY	-	SEE REMARK 999	UNP P04213
L	103	ALA	-	SEE REMARK 999	UNP P04213
L	104	GLY	-	SEE REMARK 999	UNP P04213
L	105	THR	-	SEE REMARK 999	UNP P04213
L	106	ARG	-	SEE REMARK 999	UNP P04213
L	107	LEU	-	SEE REMARK 999	UNP P04213
L	108	SER	-	SEE REMARK 999	UNP P04213
L	109	VAL	-	SEE REMARK 999	UNP P04213
L	110	LEU	-	SEE REMARK 999	UNP P04213
L	111	SER	-	cloning artifact	UNP P04213
L	112	SER	-	cloning artifact	UNP P04213
L	113	ALA	-	cloning artifact	UNP P04213

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	59	Total O 59 59	0	0
7	B	38	Total O 38 38	0	0
7	C	8	Total O 8 8	0	0
7	D	67	Total O 67 67	0	0
7	E	34	Total O 34 34	0	0

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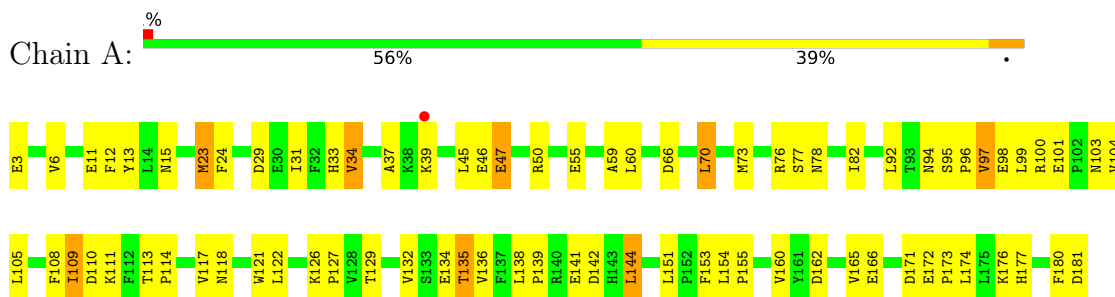
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	F	8	Total 8	O 8	0	0
7	G	32	Total 32	O 32	0	0
7	H	38	Total 38	O 38	0	0
7	I	1	Total 1	O 1	0	0
7	J	8	Total 8	O 8	0	0
7	K	4	Total 4	O 4	0	0
7	L	8	Total 8	O 8	0	0

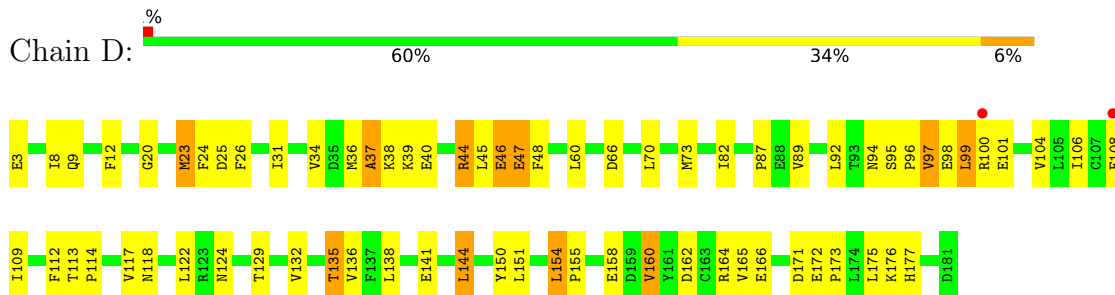
3 Residue-property plots

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 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.

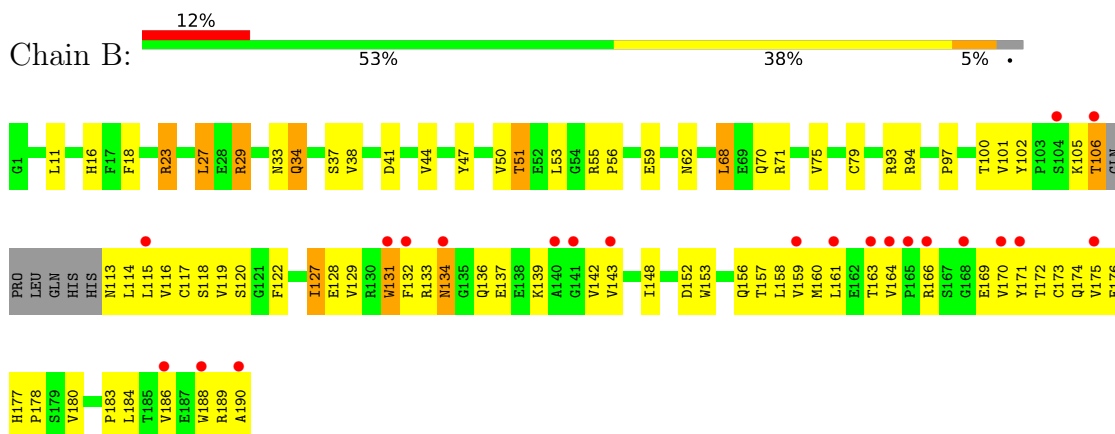
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

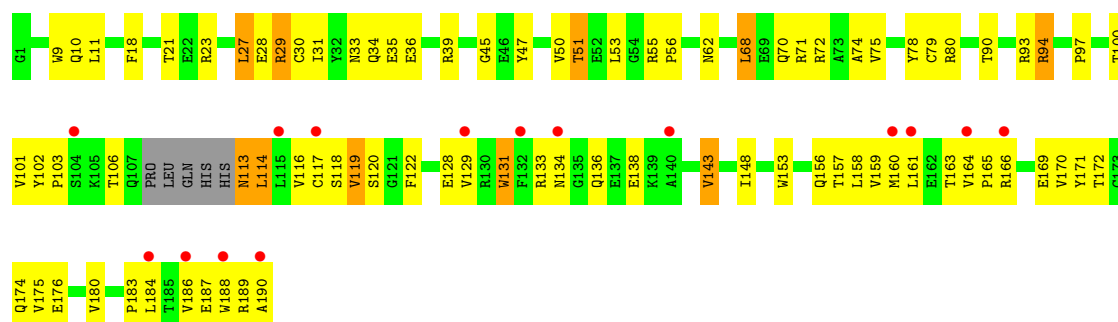


- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

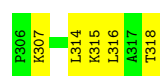


- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

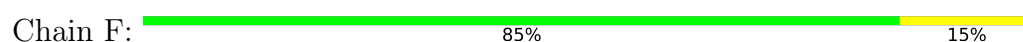




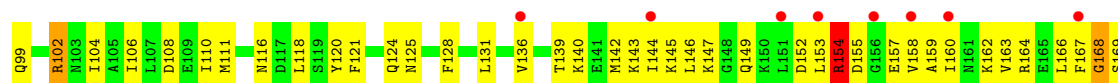
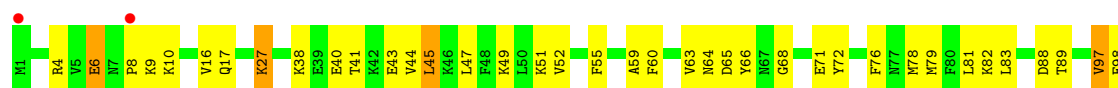
- Molecule 3: haemagglutinin peptide



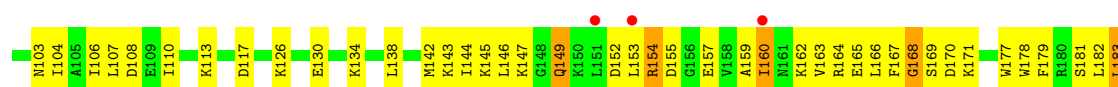
- Molecule 3: haemagglutinin peptide

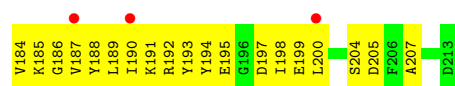


- Molecule 4: Mycoplasma arthritidis mitogen

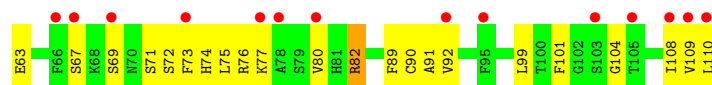
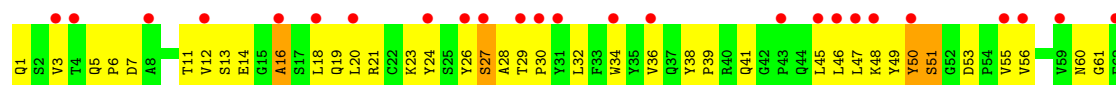
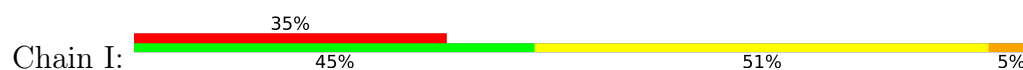


- Molecule 4: Mycoplasma arthritidis mitogen

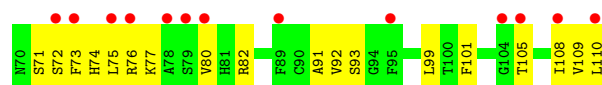
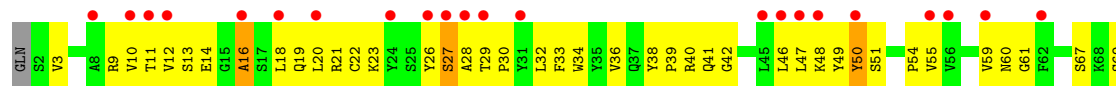




• Molecule 5: T-cell receptor alpha chain V



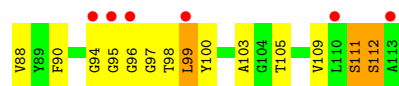
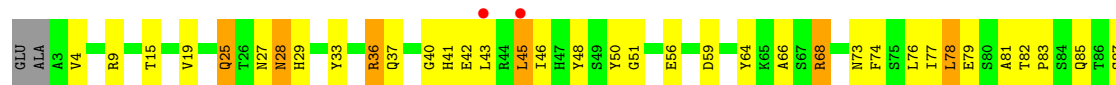
• Molecule 5: T-cell receptor alpha chain V



• Molecule 6: T-cell receptor beta chain V



• Molecule 6: T-cell receptor beta chain V



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.52Å 86.82Å 116.98Å 110.27° 92.32° 107.87°	Depositor
Resolution (Å)	47.79 – 2.41 47.79 – 2.41	Depositor EDS
% Data completeness (in resolution range)	95.0 (47.79-2.41) 95.1 (47.79-2.41)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.42Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.242 , 0.288 0.241 , 0.287	Depositor DCC
R_{free} test set	3944 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	43.7	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13464	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.49	0/1516	0.97	7/2061 (0.3%)
1	D	0.47	0/1516	0.97	7/2061 (0.3%)
2	B	0.44	0/1540	0.94	2/2088 (0.1%)
2	E	0.45	0/1549	0.93	1/2100 (0.0%)
3	C	0.47	0/107	0.94	0/141
3	F	0.51	0/107	0.94	0/141
4	G	0.42	0/1816	0.89	3/2431 (0.1%)
4	H	0.44	0/1816	0.90	5/2431 (0.2%)
5	I	0.33	0/891	0.83	0/1209
5	K	0.34	0/870	0.85	0/1181
6	J	0.40	0/875	0.88	3/1185 (0.3%)
6	L	0.44	0/861	0.88	3/1166 (0.3%)
All	All	0.43	0/13464	0.91	31/18195 (0.2%)

There are no bond length outliers.

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	6	GLU	N-CA-C	7.14	118.71	111.07
4	H	97	VAL	N-CA-C	6.30	116.98	110.36
4	G	6	GLU	N-CA-C	6.18	118.53	111.11
1	D	31	ILE	N-CA-C	-5.89	105.33	111.58
2	E	120	SER	N-CA-C	5.84	118.57	109.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1474	0	1407	61	0
1	D	1474	0	1407	60	0
2	B	1504	0	1439	88	0
2	E	1513	0	1447	79	0
3	C	106	0	119	6	0
3	F	106	0	119	2	0
4	G	1786	0	1831	105	0
4	H	1786	0	1831	110	0
5	I	863	0	839	64	0
5	K	847	0	823	58	0
6	J	857	0	811	56	0
6	L	843	0	797	44	0
7	A	59	0	0	3	0
7	B	38	0	0	0	0
7	C	8	0	0	0	0
7	D	67	0	0	1	0
7	E	34	0	0	1	0
7	F	8	0	0	0	0
7	G	32	0	0	3	0
7	H	38	0	0	1	0
7	I	1	0	0	0	0
7	J	8	0	0	0	0
7	K	4	0	0	0	0
7	L	8	0	0	0	0
All	All	13464	0	12870	672	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 26.

The worst 5 of 672 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)
4:H:160:ILE:HD13	4:H:160:ILE:H	1.15	1.09
4:G:154:ARG:H	4:G:154:ARG:HD3	1.21	1.00
2:B:116:VAL:HG12	2:B:160:MET:HG2	1.40	0.99
5:K:99:LEU:HG	6:L:99:LEU:HD23	1.47	0.96
4:H:51:LYS:HG3	4:H:104:ILE:HG23	1.47	0.96

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	177/179 (99%)	168 (95%)	9 (5%)	0	100	100
1	D	177/179 (99%)	169 (96%)	8 (4%)	0	100	100
2	B	180/190 (95%)	167 (93%)	10 (6%)	3 (2%)	7	9
2	E	181/190 (95%)	169 (93%)	12 (7%)	0	100	100
3	C	11/13 (85%)	11 (100%)	0	0	100	100
3	F	11/13 (85%)	11 (100%)	0	0	100	100
4	G	211/213 (99%)	194 (92%)	14 (7%)	3 (1%)	9	12
4	H	211/213 (99%)	196 (93%)	12 (6%)	3 (1%)	9	12
5	I	109/110 (99%)	91 (84%)	12 (11%)	6 (6%)	1	1
5	K	107/110 (97%)	88 (82%)	14 (13%)	5 (5%)	2	1
6	J	111/113 (98%)	104 (94%)	3 (3%)	4 (4%)	2	2
6	L	109/113 (96%)	102 (94%)	3 (3%)	4 (4%)	2	2
All	All	1595/1636 (98%)	1470 (92%)	97 (6%)	28 (2%)	6	8

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	G	154	ARG
4	H	154	ARG
6	J	97	GLY
6	L	97	GLY
4	G	145	LYS

5.3.2 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 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	164/161 (102%)	152 (93%)	12 (7%)	13	21
1	D	164/161 (102%)	151 (92%)	13 (8%)	11	18
2	B	165/171 (96%)	154 (93%)	11 (7%)	15	24
2	E	166/171 (97%)	153 (92%)	13 (8%)	11	18
3	C	12/12 (100%)	12 (100%)	0	100	100
3	F	12/12 (100%)	12 (100%)	0	100	100
4	G	196/196 (100%)	185 (94%)	11 (6%)	19	31
4	H	196/196 (100%)	185 (94%)	11 (6%)	19	31
5	I	94/93 (101%)	91 (97%)	3 (3%)	34	54
5	K	92/93 (99%)	90 (98%)	2 (2%)	45	66
6	J	92/92 (100%)	81 (88%)	11 (12%)	5	6
6	L	91/92 (99%)	82 (90%)	9 (10%)	7	11
All	All	1444/1450 (100%)	1348 (93%)	96 (7%)	15	25

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	G	187	VAL
5	I	1	GLN
4	G	194	TYR
4	H	47	LEU
6	J	25	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
4	H	90	GLN
5	I	44	GLN
6	L	25	GLN
4	H	99	GLN
5	I	19	GLN

5.3.3 RNA ⓘ

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	176/179 (98%)	0.04	1 (0%) 85 84	22, 44, 73, 88	0
1	D	176/179 (98%)	0.11	2 (1%) 78 75	25, 44, 74, 87	0
2	B	184/190 (96%)	0.58	22 (11%) 9 6	25, 54, 107, 112	0
2	E	185/190 (97%)	0.47	15 (8%) 18 14	26, 52, 106, 112	0
3	C	13/13 (100%)	0.12	0 100 100	35, 40, 52, 55	0
3	F	13/13 (100%)	-0.21	0 100 100	33, 38, 48, 54	0
4	G	213/213 (100%)	0.61	19 (8%) 15 12	33, 59, 102, 110	0
4	H	213/213 (100%)	0.42	7 (3%) 49 45	32, 55, 99, 108	0
5	I	110/110 (100%)	1.84	39 (35%) 1 0	46, 108, 118, 121	1 (0%)
5	K	109/110 (99%)	1.85	35 (32%) 1 1	65, 107, 117, 119	0
6	J	113/113 (100%)	0.50	5 (4%) 39 34	41, 58, 80, 103	0
6	L	111/113 (98%)	0.55	8 (7%) 21 18	40, 56, 79, 102	0
All	All	1616/1636 (98%)	0.59	153 (9%) 14 10	22, 57, 110, 121	1 (0%)

The worst 5 of 153 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	K	56	VAL	4.9
6	L	95	GLY	4.8
5	I	26	TYR	4.4
5	I	56	VAL	4.4
5	K	28	ALA	4.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.