



wwPDB X-ray Structure Validation Summary Report

Mar 18, 2026 – 02:14 AM UTC

PDB ID : 2OF5 / pdb_00002of5
Title : Oligomeric Death Domain complex
Authors : Park, H.H.; Logette, E.; Raunser, S.; Cuenin, S.; Walz, T.; Tschopp, J.; Wu, H.
Deposited on : 2007-01-02
Resolution : 3.20 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) : 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

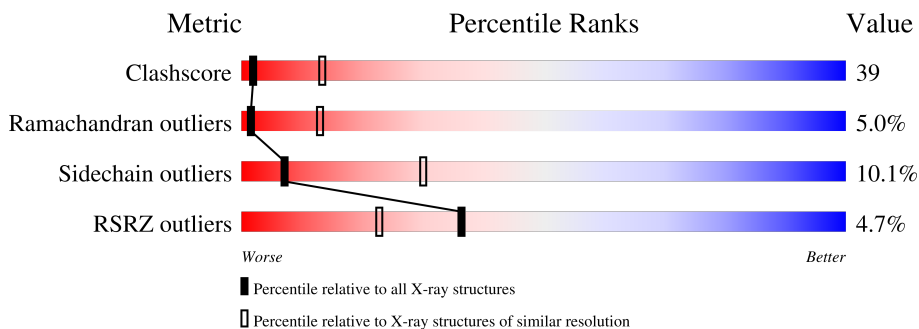
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.



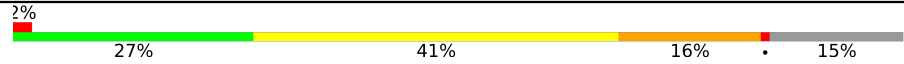
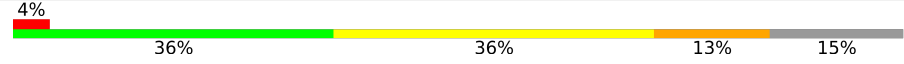
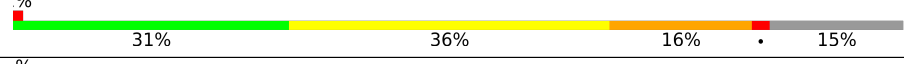
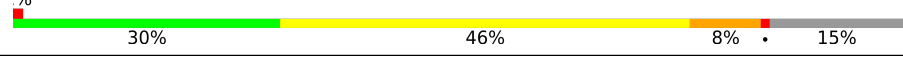
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	114	 28% 48% 20%
1	B	114	 37% 32% 10% 20%
1	C	114	 36% 38% 5% 20%
1	D	114	 31% 44% 5% 20%
1	E	114	 29% 38% 13% 20%
1	F	114	 32% 40% 7% 20%
1	G	114	 24% 47% 9% 20%

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Mol	Chain	Length	Quality of chain
2	H	118	
2	I	118	
2	J	118	
2	K	118	
2	L	118	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9117 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 Death domain-containing protein CRADD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	91	738	463	140	132	3	0	0	0
1	B	91	738	463	140	132	3	0	0	0
1	C	91	738	463	140	132	3	0	0	0
1	D	91	738	463	140	132	3	0	0	0
1	E	91	738	463	140	132	3	0	0	0
1	F	91	738	463	140	132	3	0	0	0
1	G	91	738	463	140	132	3	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	200	LEU	-	cloning artifact	UNP P78560
A	201	GLU	-	cloning artifact	UNP P78560
A	202	HIS	-	expression tag	UNP P78560
A	203	HIS	-	expression tag	UNP P78560
A	204	HIS	-	expression tag	UNP P78560
A	205	HIS	-	expression tag	UNP P78560
A	206	HIS	-	expression tag	UNP P78560
A	207	HIS	-	expression tag	UNP P78560
B	200	LEU	-	cloning artifact	UNP P78560
B	201	GLU	-	cloning artifact	UNP P78560
B	202	HIS	-	expression tag	UNP P78560
B	203	HIS	-	expression tag	UNP P78560
B	204	HIS	-	expression tag	UNP P78560
B	205	HIS	-	expression tag	UNP P78560
B	206	HIS	-	expression tag	UNP P78560

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Chain	Residue	Modelled	Actual	Comment	Reference
B	207	HIS	-	expression tag	UNP P78560
C	200	LEU	-	cloning artifact	UNP P78560
C	201	GLU	-	cloning artifact	UNP P78560
C	202	HIS	-	expression tag	UNP P78560
C	203	HIS	-	expression tag	UNP P78560
C	204	HIS	-	expression tag	UNP P78560
C	205	HIS	-	expression tag	UNP P78560
C	206	HIS	-	expression tag	UNP P78560
C	207	HIS	-	expression tag	UNP P78560
D	200	LEU	-	cloning artifact	UNP P78560
D	201	GLU	-	cloning artifact	UNP P78560
D	202	HIS	-	expression tag	UNP P78560
D	203	HIS	-	expression tag	UNP P78560
D	204	HIS	-	expression tag	UNP P78560
D	205	HIS	-	expression tag	UNP P78560
D	206	HIS	-	expression tag	UNP P78560
D	207	HIS	-	expression tag	UNP P78560
E	200	LEU	-	cloning artifact	UNP P78560
E	201	GLU	-	cloning artifact	UNP P78560
E	202	HIS	-	expression tag	UNP P78560
E	203	HIS	-	expression tag	UNP P78560
E	204	HIS	-	expression tag	UNP P78560
E	205	HIS	-	expression tag	UNP P78560
E	206	HIS	-	expression tag	UNP P78560
E	207	HIS	-	expression tag	UNP P78560
F	200	LEU	-	cloning artifact	UNP P78560
F	201	GLU	-	cloning artifact	UNP P78560
F	202	HIS	-	expression tag	UNP P78560
F	203	HIS	-	expression tag	UNP P78560
F	204	HIS	-	expression tag	UNP P78560
F	205	HIS	-	expression tag	UNP P78560
F	206	HIS	-	expression tag	UNP P78560
F	207	HIS	-	expression tag	UNP P78560
G	200	LEU	-	cloning artifact	UNP P78560
G	201	GLU	-	cloning artifact	UNP P78560
G	202	HIS	-	expression tag	UNP P78560
G	203	HIS	-	expression tag	UNP P78560
G	204	HIS	-	expression tag	UNP P78560
G	205	HIS	-	expression tag	UNP P78560
G	206	HIS	-	expression tag	UNP P78560
G	207	HIS	-	expression tag	UNP P78560

- Molecule 2 is a protein called Leucine-rich repeat and death domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	100	786	489	145	150	2	0	0	0
2	I	100	786	489	145	150	2	0	0	0
2	J	100	786	489	145	150	2	0	0	0
2	K	100	786	489	145	150	2	0	0	0
2	L	100	786	489	145	150	2	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	777	MET	-	cloning artifact	UNP Q9HB75
H	884	ALA	-	cloning artifact	UNP Q9HB75
H	885	ALA	-	cloning artifact	UNP Q9HB75
H	886	ALA	-	cloning artifact	UNP Q9HB75
H	887	LEU	-	cloning artifact	UNP Q9HB75
H	888	GLU	-	cloning artifact	UNP Q9HB75
H	889	HIS	-	expression tag	UNP Q9HB75
H	890	HIS	-	expression tag	UNP Q9HB75
H	891	HIS	-	expression tag	UNP Q9HB75
H	892	HIS	-	expression tag	UNP Q9HB75
H	893	HIS	-	expression tag	UNP Q9HB75
H	894	HIS	-	expression tag	UNP Q9HB75
I	777	MET	-	cloning artifact	UNP Q9HB75
I	884	ALA	-	cloning artifact	UNP Q9HB75
I	885	ALA	-	cloning artifact	UNP Q9HB75
I	886	ALA	-	cloning artifact	UNP Q9HB75
I	887	LEU	-	cloning artifact	UNP Q9HB75
I	888	GLU	-	cloning artifact	UNP Q9HB75
I	889	HIS	-	expression tag	UNP Q9HB75
I	890	HIS	-	expression tag	UNP Q9HB75
I	891	HIS	-	expression tag	UNP Q9HB75
I	892	HIS	-	expression tag	UNP Q9HB75
I	893	HIS	-	expression tag	UNP Q9HB75
I	894	HIS	-	expression tag	UNP Q9HB75
J	777	MET	-	cloning artifact	UNP Q9HB75
J	884	ALA	-	cloning artifact	UNP Q9HB75
J	885	ALA	-	cloning artifact	UNP Q9HB75
J	886	ALA	-	cloning artifact	UNP Q9HB75
J	887	LEU	-	cloning artifact	UNP Q9HB75
J	888	GLU	-	cloning artifact	UNP Q9HB75

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Chain	Residue	Modelled	Actual	Comment	Reference
J	889	HIS	-	expression tag	UNP Q9HB75
J	890	HIS	-	expression tag	UNP Q9HB75
J	891	HIS	-	expression tag	UNP Q9HB75
J	892	HIS	-	expression tag	UNP Q9HB75
J	893	HIS	-	expression tag	UNP Q9HB75
J	894	HIS	-	expression tag	UNP Q9HB75
K	777	MET	-	cloning artifact	UNP Q9HB75
K	884	ALA	-	cloning artifact	UNP Q9HB75
K	885	ALA	-	cloning artifact	UNP Q9HB75
K	886	ALA	-	cloning artifact	UNP Q9HB75
K	887	LEU	-	cloning artifact	UNP Q9HB75
K	888	GLU	-	cloning artifact	UNP Q9HB75
K	889	HIS	-	expression tag	UNP Q9HB75
K	890	HIS	-	expression tag	UNP Q9HB75
K	891	HIS	-	expression tag	UNP Q9HB75
K	892	HIS	-	expression tag	UNP Q9HB75
K	893	HIS	-	expression tag	UNP Q9HB75
K	894	HIS	-	expression tag	UNP Q9HB75
L	777	MET	-	cloning artifact	UNP Q9HB75
L	884	ALA	-	cloning artifact	UNP Q9HB75
L	885	ALA	-	cloning artifact	UNP Q9HB75
L	886	ALA	-	cloning artifact	UNP Q9HB75
L	887	LEU	-	cloning artifact	UNP Q9HB75
L	888	GLU	-	cloning artifact	UNP Q9HB75
L	889	HIS	-	expression tag	UNP Q9HB75
L	890	HIS	-	expression tag	UNP Q9HB75
L	891	HIS	-	expression tag	UNP Q9HB75
L	892	HIS	-	expression tag	UNP Q9HB75
L	893	HIS	-	expression tag	UNP Q9HB75
L	894	HIS	-	expression tag	UNP Q9HB75

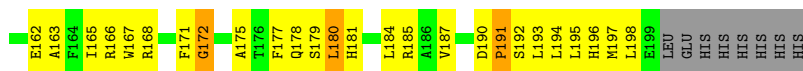
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total O 2 2	0	0
3	B	1	Total O 1 1	0	0
3	C	3	Total O 3 3	0	0
3	D	2	Total O 2 2	0	0

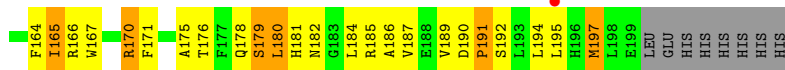
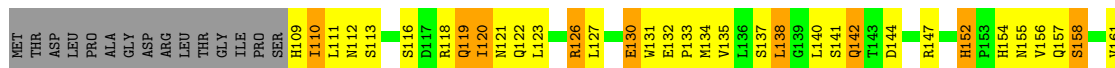
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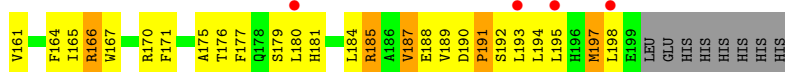
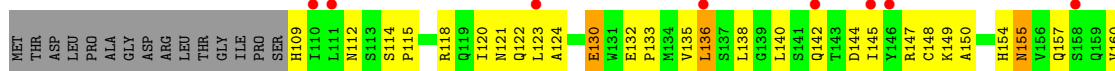
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	2	Total O 2 2	0	0
3	H	5	Total O 5 5	0	0
3	J	3	Total O 3 3	0	0
3	K	3	Total O 3 3	0	0



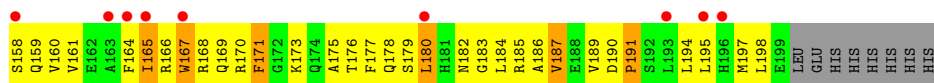
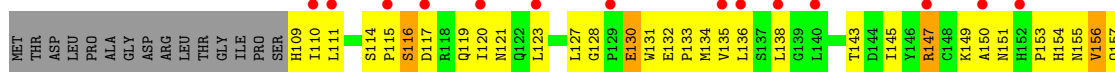
- Molecule 1: Death domain-containing protein CRADD



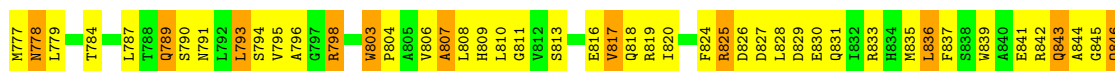
- Molecule 1: Death domain-containing protein CRADD



- Molecule 1: Death domain-containing protein CRADD

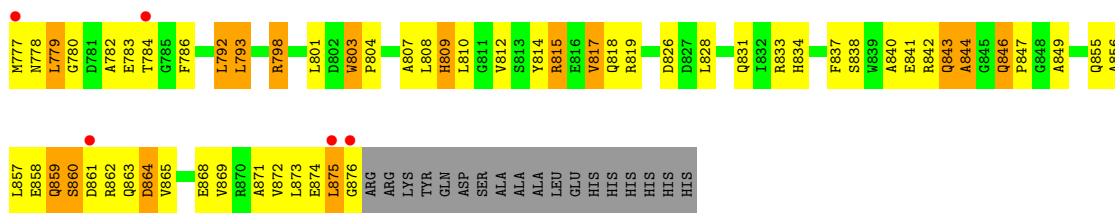


- Molecule 2: Leucine-rich repeat and death domain-containing protein

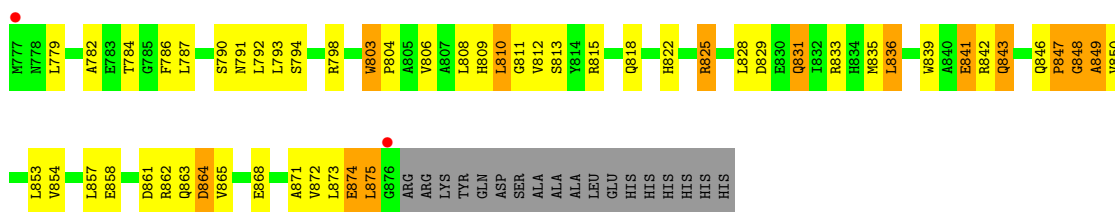


- Molecule 2: Leucine-rich repeat and death domain-containing protein

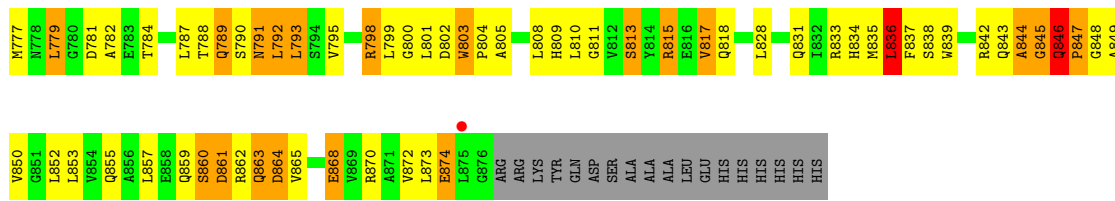




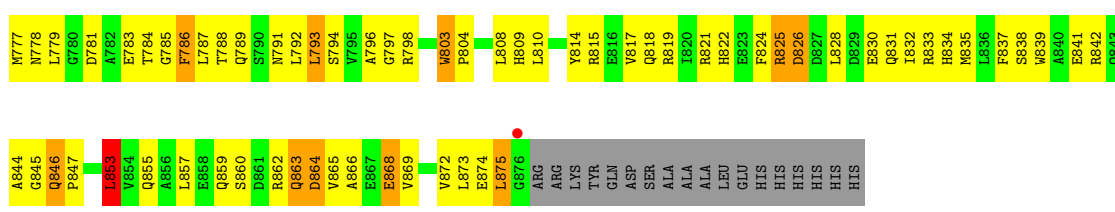
• Molecule 2: Leucine-rich repeat and death domain-containing protein



• Molecule 2: Leucine-rich repeat and death domain-containing protein



• Molecule 2: Leucine-rich repeat and death domain-containing protein



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	138.40Å 138.40Å 207.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.20 30.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.20) 93.2 (30.00-3.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 3.19Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.275 (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	92.0	Xtrriage
Anisotropy	0.463	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.044 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9117	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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	0.53	0/755	0.95	5/1023 (0.5%)
1	B	0.54	0/755	1.09	6/1023 (0.6%)
1	C	0.59	0/755	1.07	8/1023 (0.8%)
1	D	0.54	0/755	1.02	4/1023 (0.4%)
1	E	0.51	0/755	1.06	6/1023 (0.6%)
1	F	0.38	0/755	0.94	3/1023 (0.3%)
1	G	1.05	6/755 (0.8%)	3.02	10/1023 (1.0%)
2	H	0.56	0/798	1.08	5/1079 (0.5%)
2	I	0.50	0/798	1.10	7/1079 (0.6%)
2	J	0.60	0/798	1.07	2/1079 (0.2%)
2	K	0.59	0/798	1.14	8/1079 (0.7%)
2	L	0.50	0/798	0.98	4/1079 (0.4%)
All	All	0.59	6/9275 (0.1%)	1.32	68/12556 (0.5%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	171	PHE	CD2-CE2	13.44	1.78	1.38
1	G	171	PHE	CD1-CE1	13.35	1.78	1.38
1	G	171	PHE	CE1-CZ	-10.96	1.05	1.38
1	G	171	PHE	CE2-CZ	-10.93	1.05	1.38
1	G	171	PHE	CG-CD1	7.25	1.54	1.38

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	171	PHE	CE1-CZ-CE2	-53.36	23.95	120.00
1	G	171	PHE	CD1-CE1-CZ	-46.43	36.43	120.00
1	G	171	PHE	CZ-CE2-CD2	-46.21	36.83	120.00
1	G	171	PHE	CG-CD1-CE1	-21.25	84.57	120.70
1	G	171	PHE	CG-CD2-CE2	-21.22	84.63	120.70

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	738	0	730	66	0
1	B	738	0	730	48	0
1	C	738	0	730	52	0
1	D	738	0	730	56	0
1	E	738	0	730	65	0
1	F	738	0	730	70	0
1	G	738	0	730	69	0
2	H	786	0	767	82	0
2	I	786	0	767	50	0
2	J	786	0	767	55	0
2	K	786	0	767	77	0
2	L	786	0	767	67	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	H	5	0	0	2	0
3	J	3	0	0	0	0
3	K	3	0	0	2	0
All	All	9117	0	8945	703	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 39.

The worst 5 of 703 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:D:133:PRO:HG3	1:F:157:GLN:HG2	1.43	1.00
1:E:155:ASN:ND2	1:E:158:SER:HB2	1.77	1.00
2:H:807:ALA:HB2	2:H:835:MET:HE2	1.46	0.97
1:E:135:VAL:HB	1:E:140:LEU:HD12	1.47	0.96
2:H:803:TRP:HZ3	2:H:831:GLN:HE21	1.15	0.95

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	89/114 (78%)	74 (83%)	12 (14%)	3 (3%)	3	20
1	B	89/114 (78%)	78 (88%)	8 (9%)	3 (3%)	3	20
1	C	89/114 (78%)	77 (86%)	10 (11%)	2 (2%)	5	29
1	D	89/114 (78%)	66 (74%)	21 (24%)	2 (2%)	5	29
1	E	89/114 (78%)	79 (89%)	8 (9%)	2 (2%)	5	29
1	F	89/114 (78%)	76 (85%)	10 (11%)	3 (3%)	3	20
1	G	89/114 (78%)	64 (72%)	21 (24%)	4 (4%)	2	15
2	H	98/118 (83%)	77 (79%)	10 (10%)	11 (11%)	0	2
2	I	98/118 (83%)	73 (74%)	18 (18%)	7 (7%)	1	6
2	J	98/118 (83%)	76 (78%)	15 (15%)	7 (7%)	1	6
2	K	98/118 (83%)	82 (84%)	11 (11%)	5 (5%)	1	13
2	L	98/118 (83%)	80 (82%)	11 (11%)	7 (7%)	1	6
All	All	1113/1388 (80%)	902 (81%)	155 (14%)	56 (5%)	1	13

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	ASN
1	F	155	ASN
2	H	778	ASN
2	H	844	ALA
2	H	847	PRO

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	82/102 (80%)	79 (96%)	3 (4%)	30	63
1	B	82/102 (80%)	74 (90%)	8 (10%)	7	31
1	C	82/102 (80%)	77 (94%)	5 (6%)	17	49
1	D	82/102 (80%)	78 (95%)	4 (5%)	22	55
1	E	82/102 (80%)	69 (84%)	13 (16%)	2	13
1	F	82/102 (80%)	77 (94%)	5 (6%)	17	49
1	G	82/102 (80%)	75 (92%)	7 (8%)	10	37
2	H	81/96 (84%)	71 (88%)	10 (12%)	4	22
2	I	81/96 (84%)	70 (86%)	11 (14%)	3	18
2	J	81/96 (84%)	71 (88%)	10 (12%)	4	22
2	K	81/96 (84%)	67 (83%)	14 (17%)	2	10
2	L	81/96 (84%)	72 (89%)	9 (11%)	6	25
All	All	979/1194 (82%)	880 (90%)	99 (10%)	7	30

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	793	LEU
2	J	841	GLU
2	I	803	TRP
2	I	873	LEU
2	J	868	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	859	GLN
2	L	855	GLN
2	K	778	ASN
2	K	859	GLN

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Mol	Chain	Res	Type
1	E	122	GLN

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 [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	91/114 (79%)	-0.00	1 (1%) 78 61	79, 113, 155, 168	0
1	B	91/114 (79%)	-0.13	1 (1%) 78 61	77, 104, 141, 163	0
1	C	91/114 (79%)	-0.28	2 (2%) 62 42	73, 92, 120, 148	0
1	D	91/114 (79%)	-0.13	2 (2%) 62 42	73, 97, 132, 154	0
1	E	91/114 (79%)	0.04	1 (1%) 78 61	82, 104, 148, 174	0
1	F	91/114 (79%)	0.77	12 (13%) 7 6	148, 175, 199, 200	0
1	G	91/114 (79%)	1.49	23 (25%) 1 2	186, 199, 200, 200	0
2	H	100/118 (84%)	-0.06	2 (2%) 65 45	78, 98, 129, 137	0
2	I	100/118 (84%)	0.03	5 (5%) 34 22	82, 114, 170, 182	0
2	J	100/118 (84%)	-0.20	2 (2%) 65 45	71, 92, 120, 130	0
2	K	100/118 (84%)	-0.30	1 (1%) 79 63	75, 90, 111, 147	0
2	L	100/118 (84%)	-0.15	1 (1%) 79 63	89, 111, 161, 167	0
All	All	1137/1388 (81%)	0.08	53 (4%) 36 23	71, 105, 198, 200	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	193	LEU	6.6
1	G	117	ASP	5.8
1	G	140	LEU	5.2
1	G	123	LEU	4.7
1	G	164	PHE	4.6

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.