



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:57 AM UTC

PDB ID : 4XA9 / pdb_00004xa9
Title : Crystal structure of the complex between the N-terminal domain of RavJ and LegL1 from Legionella pneumophila str. Philadelphia
Authors : Stogios, P.J.; Cuff, M.E.; Nocek, B.; Evdokimova, E.; Di Leo, R.; Yim, V.; Savchenko, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2014-12-13
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

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

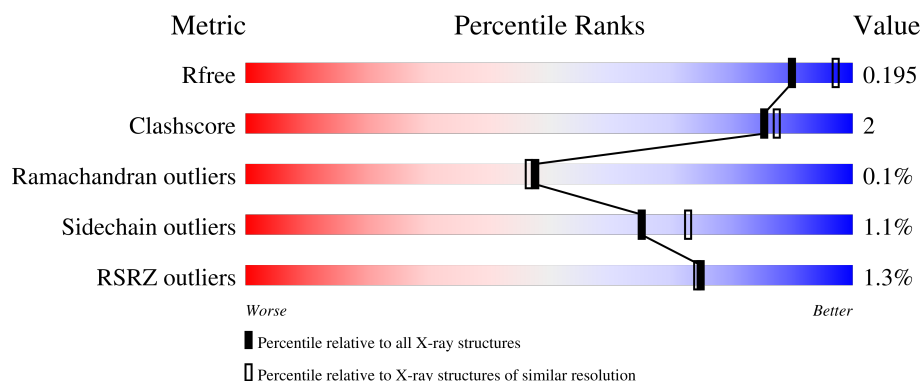
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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.



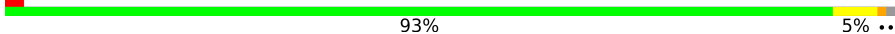
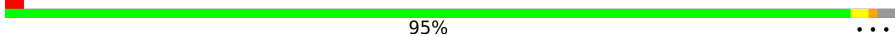
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 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	297	 79% . . 17%
1	B	297	 76% 7% 17%
1	C	297	 80% . 17%
1	D	297	 81% . 17%

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Mol	Chain	Length	Quality of chain
1	E	297	 79% 17%
1	F	297	 78% 5% 17%
1	G	297	 81% 16%
1	H	297	 80% 17%
2	a	231	 90% 8% ..
2	b	231	 90% 8% .
2	c	231	 89% 8% .
2	d	231	 93% 5% ..
2	e	231	 90% 7% .
2	f	231	 95% ...
2	g	231	 90% 7% ..
2	h	231	 88% 10% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34121 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 Gala protein type 1, 3 or 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	247	Total	C	N	O	S	0	10	0
			1916	1209	319	384	4			
1	B	247	Total	C	N	O	S	0	8	0
			1907	1200	317	386	4			
1	C	247	Total	C	N	O	S	0	3	0
			1889	1189	316	379	5			
1	D	247	Total	C	N	O	S	0	6	0
			1897	1195	316	382	4			
1	E	247	Total	C	N	O	S	0	6	0
			1898	1192	317	385	4			
1	F	247	Total	C	N	O	S	0	6	0
			1904	1198	319	383	4			
1	G	248	Total	C	N	O	S	0	4	0
			1900	1195	319	382	4			
1	H	247	Total	C	N	O	S	0	5	0
			1894	1188	318	384	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q5ZWY8
B	0	GLY	-	expression tag	UNP Q5ZWY8
C	0	GLY	-	expression tag	UNP Q5ZWY8
D	0	GLY	-	expression tag	UNP Q5ZWY8
E	0	GLY	-	expression tag	UNP Q5ZWY8
F	0	GLY	-	expression tag	UNP Q5ZWY8
G	0	GLY	-	expression tag	UNP Q5ZWY8
H	0	GLY	-	expression tag	UNP Q5ZWY8

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	a	228	Total	C	N	O	S	Se	0	3	0
			1796	1139	312	340	2	3			
2	b	227	Total	C	N	O	S	Se	0	1	0
			1779	1128	310	337	2	2			
2	c	224	Total	C	N	O	S	Se	0	3	0
			1779	1132	309	334	2	2			
2	d	228	Total	C	N	O	S	Se	0	5	0
			1808	1149	313	341	2	3			
2	e	227	Total	C	N	O	S	Se	0	2	0
			1787	1134	311	337	2	3			
2	f	226	Total	C	N	O	S	Se	0	7	0
			1810	1151	314	340	2	3			
2	g	225	Total	C	N	O	S	Se	0	4	0
			1782	1132	310	335	2	3			
2	h	229	Total	C	N	O	S	Se	0	2	0
			1794	1137	312	340	2	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	0	GLY	-	expression tag	UNP Q5ZWHY9
b	0	GLY	-	expression tag	UNP Q5ZWHY9
c	0	GLY	-	expression tag	UNP Q5ZWHY9
d	0	GLY	-	expression tag	UNP Q5ZWHY9
e	0	GLY	-	expression tag	UNP Q5ZWHY9
f	0	GLY	-	expression tag	UNP Q5ZWHY9
g	0	GLY	-	expression tag	UNP Q5ZWHY9
h	0	GLY	-	expression tag	UNP Q5ZWHY9

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	284	Total	O	0	3
			287	287		
3	a	230	Total	O	0	4
			234	234		
3	B	288	Total	O	0	7
			295	295		
3	b	243	Total	O	0	5
			248	248		
3	C	326	Total	O	0	6
			332	332		
3	c	256	Total	O	0	5
			261	261		

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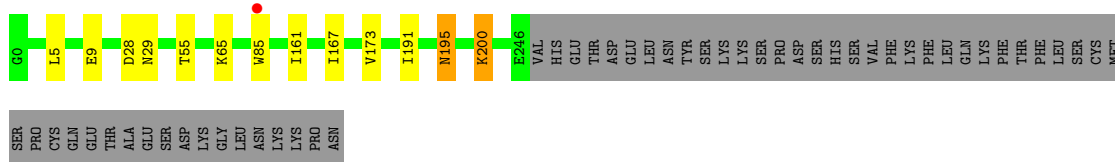
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	300	Total 306	O 306	0	6
3	d	249	Total 254	O 254	0	5
3	E	288	Total 294	O 294	0	6
3	e	306	Total 311	O 311	0	5
3	F	297	Total 301	O 301	0	4
3	f	338	Total 342	O 342	0	4
3	G	293	Total 295	O 295	0	2
3	g	273	Total 274	O 274	0	1
3	H	260	Total 262	O 262	0	2
3	h	281	Total 285	O 285	0	4

3 Residue-property plots [i](#)

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.

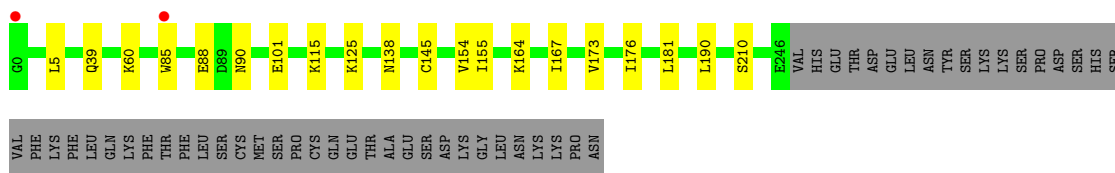
- Molecule 1: Gala protein type 1, 3 or 4

Chain A:  79% . . 17%



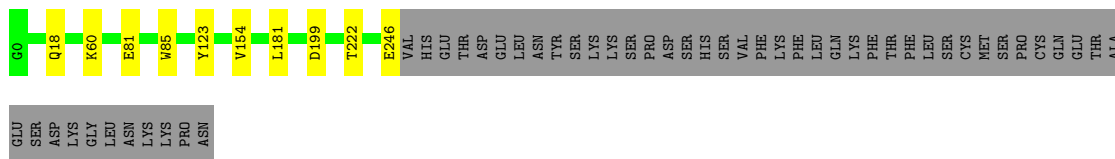
- Molecule 1: Gala protein type 1, 3 or 4

Chain B:  76% 7% 17%



- Molecule 1: Gala protein type 1, 3 or 4

Chain C:  80% . 17%



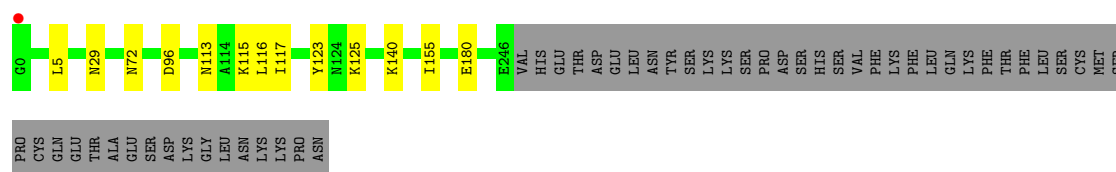
- Molecule 1: Gala protein type 1, 3 or 4

Chain D:  81% . 17%



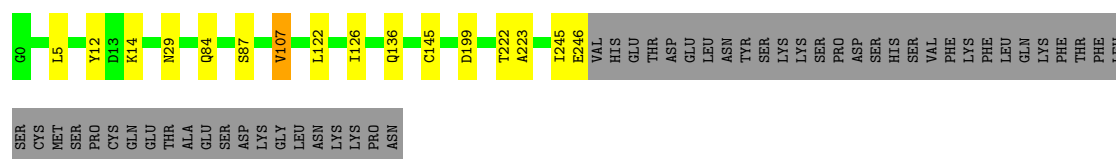
- Molecule 1: Gala protein type 1, 3 or 4

Chain E:  79% 17%



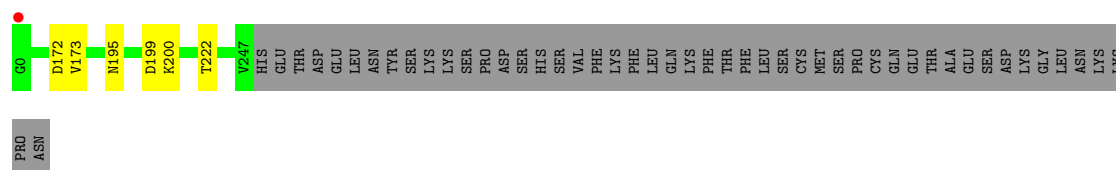
- Molecule 1: Gala protein type 1, 3 or 4

Chain F:  78% 5% 17%



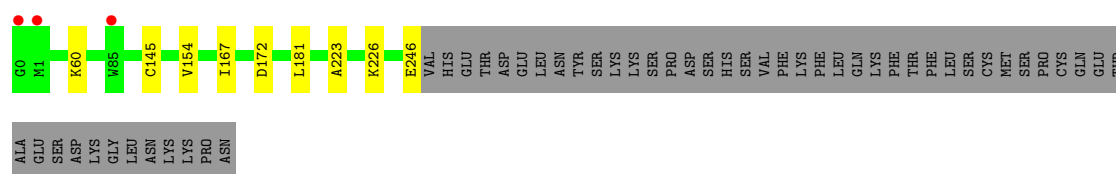
- Molecule 1: Gala protein type 1, 3 or 4

Chain G:  81% 16%



- Molecule 1: Gala protein type 1, 3 or 4

Chain H:  80% 17%



- Molecule 2: Uncharacterized protein

Chain a:  90% 8% 2%

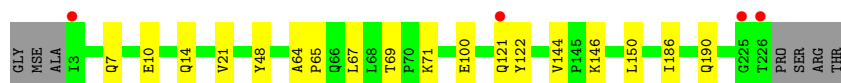
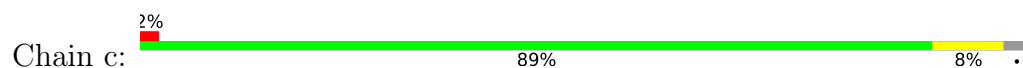


- Molecule 2: Uncharacterized protein

Chain b:  90% 8% 3%



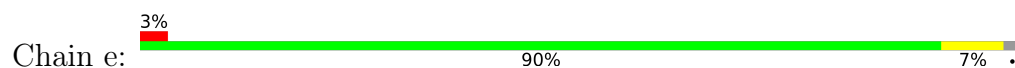
- Molecule 2: Uncharacterized protein



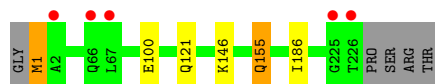
- Molecule 2: Uncharacterized protein



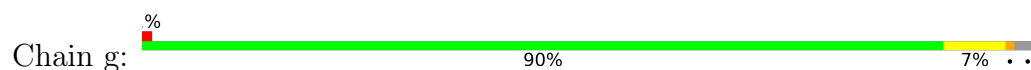
- Molecule 2: Uncharacterized protein



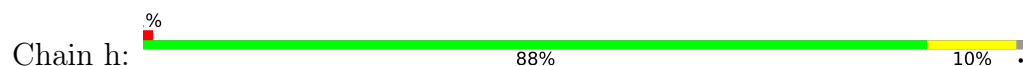
- Molecule 2: Uncharacterized protein



- Molecule 2: Uncharacterized protein



- Molecule 2: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	219.61Å 120.89Å 149.29Å 90.00° 92.05° 90.00°	Depositor
Resolution (Å)	29.94 – 2.00 29.94 – 2.00	Depositor EDS
% Data completeness (in resolution range)	86.6 (29.94-2.00) 95.8 (29.94-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.22 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.158 , 0.195 0.159 , 0.195	Depositor DCC
R_{free} test set	12932 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	23.0	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 61.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.001 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.004 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.010 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.003 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	34121	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.81 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6723e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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	0.48	2/1964 (0.1%)	0.71	1/2663 (0.0%)
1	B	0.41	0/1952	0.67	0/2650
1	C	0.37	0/1919	0.69	0/2603
1	D	0.35	0/1936	0.68	0/2627
1	E	0.37	0/1934	0.68	0/2625
1	F	0.40	1/1941 (0.1%)	0.69	0/2635
1	G	0.38	0/1934	0.70	0/2626
1	H	0.35	0/1930	0.70	0/2620
2	a	0.44	0/1850	0.75	2/2516 (0.1%)
2	b	0.43	0/1827	0.73	2/2486 (0.1%)
2	c	0.40	0/1833	0.73	0/2492
2	d	0.48	0/1868	0.72	0/2541
2	e	0.49	0/1838	0.73	0/2500
2	f	0.47	0/1876	0.72	0/2551
2	g	0.47	1/1838 (0.1%)	0.75	1/2497 (0.0%)
2	h	0.50	2/1844 (0.1%)	0.74	2/2506 (0.1%)
All	All	0.43	6/30284 (0.0%)	0.71	8/41138 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	h	94	GLU	C-O	-6.54	1.16	1.24
1	A	195	ASN	C-O	-6.34	1.16	1.24
1	F	107	VAL	C-O	-6.12	1.16	1.24
2	g	104	PHE	C-O	-5.83	1.17	1.24
1	A	29	ASN	C-O	-5.10	1.17	1.24

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	b	115	ASP	CA-C-N	5.79	124.99	118.97
2	b	115	ASP	C-N-CA	5.79	124.99	118.97
2	g	100	GLU	N-CA-C	5.48	116.59	108.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	a	100	GLU	N-CA-C	5.47	116.29	108.74
1	A	85	TRP	CA-CB-CG	-5.44	103.27	113.60

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	1916	0	1982	6	0
1	B	1907	0	1951	13	0
1	C	1889	0	1931	4	0
1	D	1897	0	1946	3	0
1	E	1898	0	1934	8	0
1	F	1904	0	1942	10	0
1	G	1900	0	1936	4	0
1	H	1894	0	1926	6	0
2	a	1796	0	1778	14	0
2	b	1779	0	1753	10	0
2	c	1779	0	1761	10	0
2	d	1808	0	1799	10	0
2	e	1787	0	1768	14	0
2	f	1810	0	1803	5	0
2	g	1782	0	1772	13	0
2	h	1794	0	1773	14	0
3	A	287	0	0	0	0
3	B	295	0	0	3	0
3	C	332	0	0	0	0
3	D	306	0	0	0	0
3	E	294	0	0	1	0
3	F	301	0	0	1	0
3	G	295	0	0	1	0
3	H	262	0	0	2	0
3	a	234	0	0	2	0
3	b	248	0	0	1	0
3	c	261	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	d	254	0	0	4	0
3	e	311	0	0	7	0
3	f	342	0	0	2	0
3	g	274	0	0	7	0
3	h	285	0	0	3	0
All	All	34121	0	29755	129	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 2.

The worst 5 of 129 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)
2:a:119:ARG:HB2	3:a:449:HOH:O	1.83	0.76
1:F:107:VAL:HG11	1:F:126:ILE:HD13	1.71	0.70
2:f:146:LYS:NZ	3:f:595:HOH:O	2.24	0.69
1:E:29[A]:ASN:OD1	2:g:149:ARG:NH2	2.26	0.67
2:d:61:GLN:OE1	3:d:546:HOH:O	2.12	0.66

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	255/297 (86%)	244 (96%)	11 (4%)	0	100	100
1	B	253/297 (85%)	243 (96%)	10 (4%)	0	100	100
1	C	248/297 (84%)	239 (96%)	8 (3%)	1 (0%)	30	27
1	D	251/297 (84%)	240 (96%)	11 (4%)	0	100	100
1	E	251/297 (84%)	243 (97%)	7 (3%)	1 (0%)	30	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	251/297 (84%)	241 (96%)	10 (4%)	0	100	100
1	G	250/297 (84%)	239 (96%)	11 (4%)	0	100	100
1	H	250/297 (84%)	240 (96%)	10 (4%)	0	100	100
2	a	229/231 (99%)	226 (99%)	3 (1%)	0	100	100
2	b	226/231 (98%)	224 (99%)	2 (1%)	0	100	100
2	c	225/231 (97%)	224 (100%)	1 (0%)	0	100	100
2	d	231/231 (100%)	227 (98%)	4 (2%)	0	100	100
2	e	227/231 (98%)	224 (99%)	3 (1%)	0	100	100
2	f	231/231 (100%)	229 (99%)	2 (1%)	0	100	100
2	g	227/231 (98%)	222 (98%)	5 (2%)	0	100	100
2	h	229/231 (99%)	227 (99%)	2 (1%)	0	100	100
All	All	3834/4224 (91%)	3732 (97%)	100 (3%)	2 (0%)	48	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	123	TYR
1	C	123	TYR

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	222/260 (85%)	219 (99%)	3 (1%)	59	66
1	B	220/260 (85%)	220 (100%)	0	100	100
1	C	215/260 (83%)	213 (99%)	2 (1%)	70	78
1	D	218/260 (84%)	218 (100%)	0	100	100
1	E	218/260 (84%)	218 (100%)	0	100	100
1	F	218/260 (84%)	217 (100%)	1 (0%)	81	87
1	G	217/260 (84%)	217 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	217/260 (84%)	217 (100%)	0	100	100
2	a	198/194 (102%)	195 (98%)	3 (2%)	57	64
2	b	195/194 (100%)	193 (99%)	2 (1%)	68	75
2	c	195/194 (100%)	191 (98%)	4 (2%)	47	52
2	d	200/194 (103%)	195 (98%)	5 (2%)	42	45
2	e	196/194 (101%)	191 (97%)	5 (3%)	40	44
2	f	200/194 (103%)	196 (98%)	4 (2%)	48	54
2	g	196/194 (101%)	191 (97%)	5 (3%)	40	44
2	h	197/194 (102%)	194 (98%)	3 (2%)	57	64
All	All	3322/3632 (92%)	3285 (99%)	37 (1%)	65	73

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	f	186	ILE
2	h	190	GLN
2	g	1	MSE
2	g	100	GLU
2	c	100	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	g	34	GLN
2	g	138	HIS
2	h	7	GLN
2	c	152	GLN
2	c	9	GLN

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 [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

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	247/297 (83%)	-0.47	1 (0%) 88 88	12, 23, 38, 64	10 (4%)
1	B	247/297 (83%)	-0.52	2 (0%) 82 82	14, 22, 37, 62	8 (3%)
1	C	247/297 (83%)	-0.56	0 100 100	11, 21, 36, 74	3 (1%)
1	D	247/297 (83%)	-0.49	2 (0%) 82 82	13, 23, 36, 61	6 (2%)
1	E	247/297 (83%)	-0.45	1 (0%) 88 88	11, 23, 41, 77	6 (2%)
1	F	247/297 (83%)	-0.44	0 100 100	11, 23, 42, 72	6 (2%)
1	G	248/297 (83%)	-0.42	1 (0%) 88 88	12, 22, 42, 89	4 (1%)
1	H	247/297 (83%)	-0.33	3 (1%) 76 76	15, 25, 40, 67	5 (2%)
2	a	225/231 (97%)	0.02	5 (2%) 62 61	17, 31, 60, 91	3 (1%)
2	b	225/231 (97%)	-0.00	8 (3%) 46 45	15, 31, 62, 133	2 (0%)
2	c	222/231 (96%)	-0.07	4 (1%) 67 67	10, 29, 55, 110	3 (1%)
2	d	225/231 (97%)	-0.13	5 (2%) 62 61	11, 27, 55, 75	5 (2%)
2	e	224/231 (96%)	-0.28	6 (2%) 56 55	10, 24, 48, 79	2 (0%)
2	f	223/231 (96%)	-0.36	5 (2%) 62 61	10, 23, 41, 83	7 (3%)
2	g	222/231 (96%)	-0.21	3 (1%) 73 73	11, 27, 49, 80	4 (1%)
2	h	226/231 (97%)	-0.24	3 (1%) 75 74	11, 26, 47, 62	3 (1%)
All	All	3769/4224 (89%)	-0.32	49 (1%) 75 74	10, 25, 47, 133	77 (2%)

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	c	226	THR	4.9
2	c	225	GLY	4.5
1	B	85	TRP	4.2
2	e	67	LEU	4.2
2	f	226	THR	4.0

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.