



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 09:53 PM UTC

PDB ID : 4Z42 / pdb_00004z42
Title : Crystal structure of urease from Yersinia enterocolitica
Authors : Studer, G.; Jakob, R.P.; Mahi, M.A.; Wiesand, U.; Schwede, T.; Maier, T.
Deposited on : 2015-04-01
Resolution : 3.01 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:

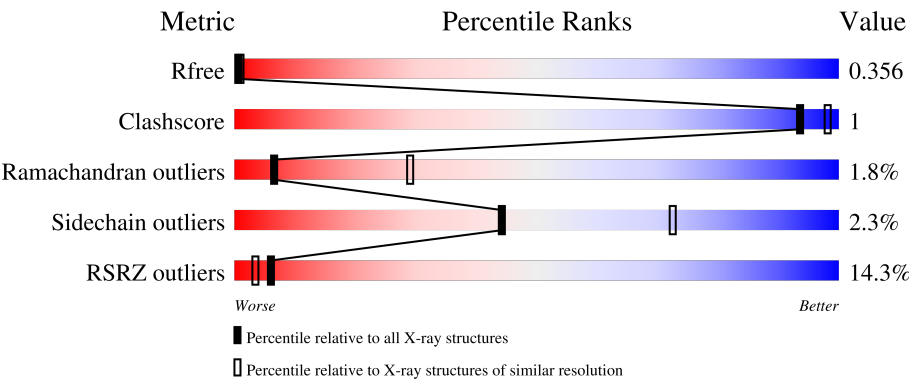
MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
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 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	100	9% 98% ..
1	D	100	4% 97% ..
1	G	100	11% 97% ..
1	J	100	7% 98% ..
2	B	164	12% 60% 7% .. 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	164	13%62%7%30%
2	H	164	23%61%5%30%
2	K	164	12%66%30%
3	C	572	19%94%6%
3	F	572	10%94%6%
3	I	572	15%94%6%
3	L	572	12%93%6%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 47288 atoms, of which 23471 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 Urease subunit gamma.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	99	Total	C	H	N	O	S	0	0	0
			1555	480	793	128	149	5			
1	D	99	Total	C	H	N	O	S	0	0	0
			1555	480	793	128	149	5			
1	G	99	Total	C	H	N	O	S	0	0	0
			1555	480	793	128	149	5			
1	J	99	Total	C	H	N	O	S	0	0	0
			1555	480	793	128	149	5			

- Molecule 2 is a protein called Urease subunit beta.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	114	Total	C	H	N	O	S	0	0	0
			1745	560	859	156	169	1			
2	E	114	Total	C	H	N	O	S	0	0	0
			1745	560	859	156	169	1			
2	H	114	Total	C	H	N	O	S	0	0	0
			1744	560	858	156	169	1			
2	K	114	Total	C	H	N	O	S	0	0	0
			1745	560	859	156	169	1			

- Molecule 3 is a protein called Urease subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	571	Total	C	H	N	O	S	0	0	0
			8493	2671	4216	759	822	25			
3	F	571	Total	C	H	N	O	S	0	0	0
			8493	2671	4216	759	822	25			
3	I	571	Total	C	H	N	O	S	0	0	0
			8493	2671	4216	759	822	25			
3	L	571	Total	C	H	N	O	S	0	0	0
			8493	2671	4216	759	822	25			

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	2	Total 2	Ni 2	0	0
4	F	2	Total 2	Ni 2	0	0
4	I	2	Total 2	Ni 2	0	0
4	L	2	Total 2	Ni 2	0	0

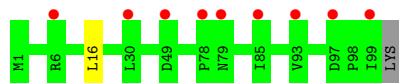
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	8	Total 8	O 8	0	0
5	C	15	Total 15	O 15	0	0
5	D	1	Total 1	O 1	0	0
5	E	8	Total 8	O 8	0	0
5	F	31	Total 31	O 31	0	0
5	I	17	Total 17	O 17	0	0
5	K	4	Total 4	O 4	0	0
5	L	25	Total 25	O 25	0	0

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: Urease subunit gamma



- Molecule 1: Urease subunit gamma



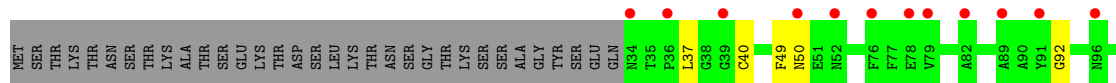
- Molecule 1: Urease subunit gamma

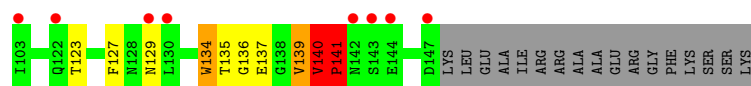


- Molecule 1: Urease subunit gamma

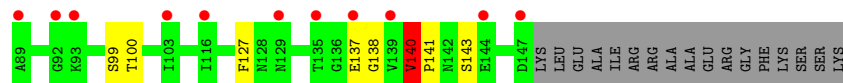
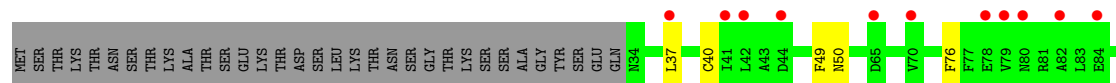


- Molecule 2: Urease subunit beta

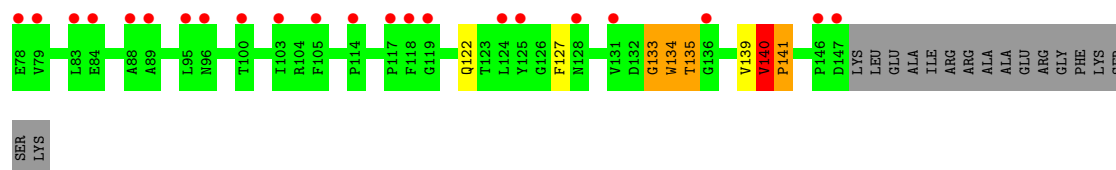
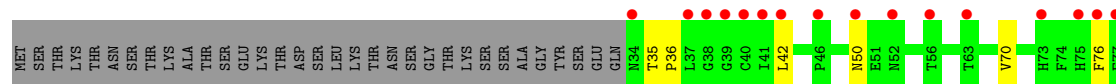




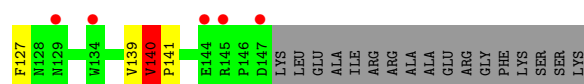
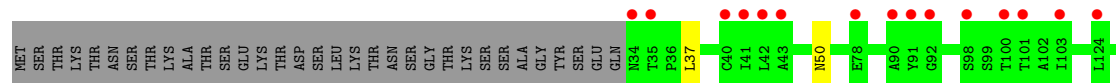
• Molecule 2: Urease subunit beta



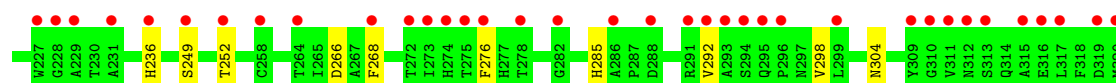
• Molecule 2: Urease subunit beta



• Molecule 2: Urease subunit beta

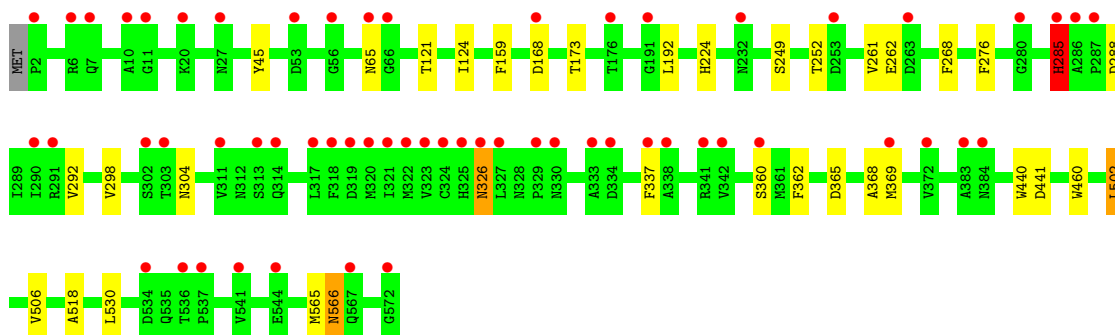
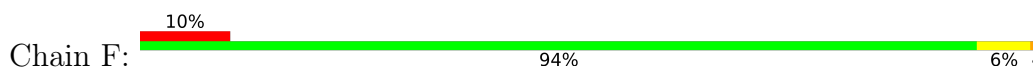


• Molecule 3: Urease subunit alpha

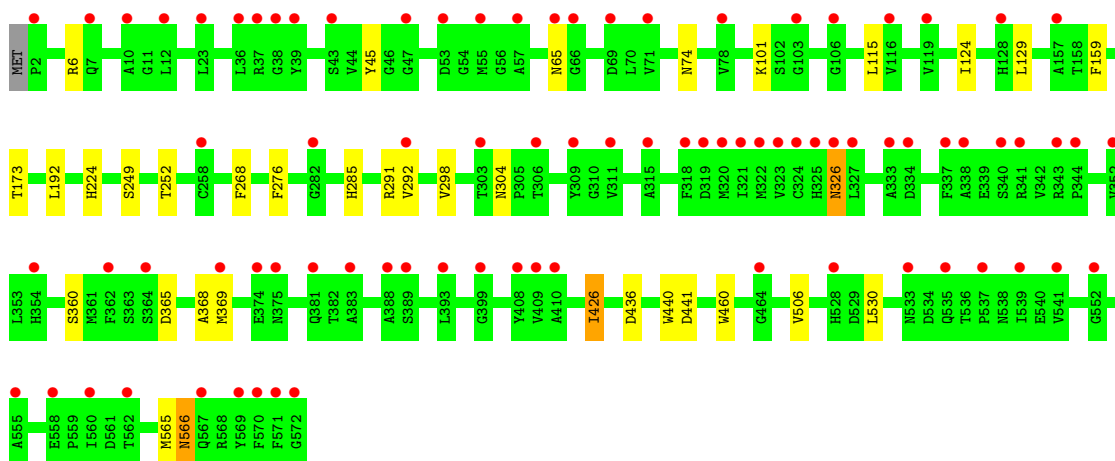
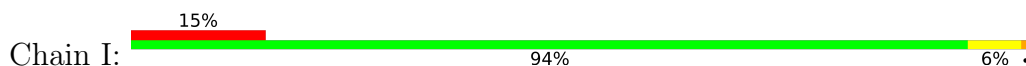




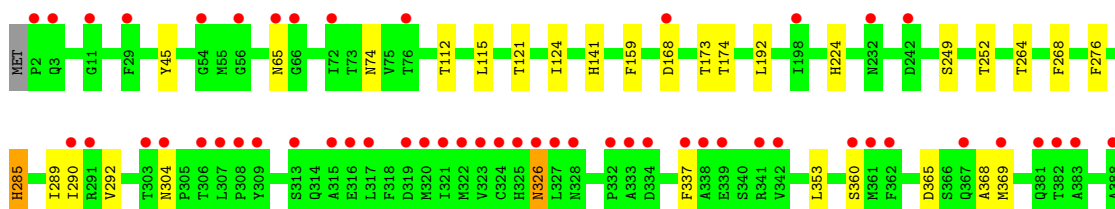
• Molecule 3: Urease subunit alpha

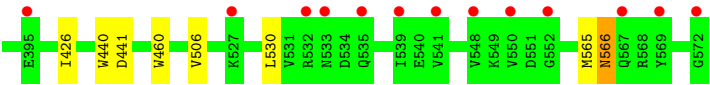


• Molecule 3: Urease subunit alpha



• Molecule 3: Urease subunit alpha





4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	157.20Å 157.20Å 774.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.71 – 3.01 29.71 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.71-3.01) 99.3 (29.71-3.01)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.00Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.277 , 0.298 0.331 , 0.356	Depositor DCC
R_{free} test set	3666 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 70.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	47288	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.98% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.78	0/770	0.96	0/1040
1	D	0.80	0/770	0.99	1/1040 (0.1%)
1	G	0.78	0/770	0.95	0/1040
1	J	0.78	0/770	0.98	0/1040
2	B	0.80	0/908	1.06	3/1235 (0.2%)
2	E	0.83	1/908 (0.1%)	1.05	1/1235 (0.1%)
2	H	0.82	1/908 (0.1%)	1.07	4/1235 (0.3%)
2	K	0.81	1/908 (0.1%)	1.04	0/1235
3	C	0.74	0/4362	1.04	5/5924 (0.1%)
3	F	0.74	0/4362	1.04	5/5924 (0.1%)
3	I	0.75	0/4362	1.04	3/5924 (0.1%)
3	L	0.75	0/4362	1.04	5/5924 (0.1%)
All	All	0.76	3/24160 (0.0%)	1.03	27/32796 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	140	VAL	CA-C	6.08	1.59	1.52
2	H	140	VAL	CA-C	5.10	1.58	1.52
2	K	140	VAL	CA-C	5.09	1.58	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	133	GLY	N-CA-C	7.50	120.68	112.29
3	C	268	PHE	CA-CB-CG	7.24	121.04	113.80
1	D	21	PHE	CA-CB-CG	7.16	120.96	113.80
3	I	268	PHE	CA-CB-CG	7.15	120.95	113.80
3	F	268	PHE	CA-CB-CG	7.04	120.84	113.80

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	762	793	793	0	0
1	D	762	793	793	0	0
1	G	762	793	793	0	0
1	J	762	793	793	0	0
2	B	886	859	859	14	7
2	E	886	859	859	4	0
2	H	886	858	858	11	2
2	K	886	859	859	2	0
3	C	4277	4216	4216	8	2
3	F	4277	4216	4216	10	0
3	I	4277	4216	4216	8	7
3	L	4277	4216	4216	11	0
4	C	2	0	0	0	0
4	F	2	0	0	0	0
4	I	2	0	0	0	0
4	L	2	0	0	0	0
5	B	8	0	0	0	0
5	C	15	0	0	0	0
5	D	1	0	0	0	0
5	E	8	0	0	0	0
5	F	31	0	0	0	0
5	I	17	0	0	0	0
5	K	4	0	0	0	0
5	L	25	0	0	0	0
All	All	23817	23471	23471	66	9

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 1.

The worst 5 of 66 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:H:122:GLN:HB3	2:H:135:THR:CG2	1.98	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:122:GLN:HB3	2:H:135:THR:HG21	1.61	0.81
2:B:139:VAL:C	2:B:140:VAL:HG13	2.13	0.73
2:B:134:TRP:CZ2	2:B:136:GLY:HA2	2.23	0.72
2:H:134:TRP:CD1	2:H:135:THR:H	2.12	0.67

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:139:VAL:HG12	3:I:291:ARG:NH2[3_545]	0.59	1.01
2:B:139:VAL:HG12	3:I:291:ARG:HH22[3_545]	0.67	0.93
2:B:139:VAL:CG1	3:I:291:ARG:NH2[3_545]	1.31	0.89
2:B:139:VAL:HG12	3:I:291:ARG:HH21[3_545]	0.94	0.66
2:B:139:VAL:CG1	3:I:291:ARG:HH22[3_545]	1.30	0.30

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
1	D	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
1	G	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
1	J	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
2	B	112/164 (68%)	95 (85%)	12 (11%)	5 (4%)	2	11
2	E	112/164 (68%)	96 (86%)	13 (12%)	3 (3%)	4	20
2	H	112/164 (68%)	96 (86%)	11 (10%)	5 (4%)	2	11
2	K	112/164 (68%)	99 (88%)	10 (9%)	3 (3%)	4	20
3	C	569/572 (100%)	512 (90%)	47 (8%)	10 (2%)	6	29
3	F	569/572 (100%)	510 (90%)	50 (9%)	9 (2%)	7	32

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	I	569/572 (100%)	510 (90%)	49 (9%)	10 (2%)	6	29
3	L	569/572 (100%)	511 (90%)	48 (8%)	10 (2%)	6	29
All	All	3112/3344 (93%)	2805 (90%)	252 (8%)	55 (2%)	6	29

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	50	ASN
2	B	140	VAL
2	E	50	ASN
2	E	140	VAL
2	H	140	VAL

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	86/87 (99%)	85 (99%)	1 (1%)	63	81
1	D	86/87 (99%)	85 (99%)	1 (1%)	63	81
1	G	86/87 (99%)	84 (98%)	2 (2%)	44	72
1	J	86/87 (99%)	85 (99%)	1 (1%)	63	81
2	B	96/138 (70%)	90 (94%)	6 (6%)	16	46
2	E	96/138 (70%)	93 (97%)	3 (3%)	35	67
2	H	96/138 (70%)	95 (99%)	1 (1%)	68	83
2	K	96/138 (70%)	94 (98%)	2 (2%)	47	74
3	C	457/458 (100%)	449 (98%)	8 (2%)	51	76
3	F	457/458 (100%)	444 (97%)	13 (3%)	38	69
3	I	457/458 (100%)	446 (98%)	11 (2%)	43	72
3	L	457/458 (100%)	446 (98%)	11 (2%)	43	72
All	All	2556/2732 (94%)	2496 (98%)	60 (2%)	44	72

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	460	TRP
3	L	440	TRP
3	I	45	TYR
3	L	426	ILE
3	L	566	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	528	HIS
3	L	247	GLN
2	K	52	ASN
3	L	147	GLN
3	L	295	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	99/100 (99%)	0.98	9 (9%) 15 8	79, 103, 127, 142	0
1	D	99/100 (99%)	1.16	4 (4%) 42 23	83, 111, 137, 152	0
1	G	99/100 (99%)	1.09	11 (11%) 10 6	90, 115, 137, 145	0
1	J	99/100 (99%)	1.04	7 (7%) 22 11	77, 101, 128, 137	0
2	B	114/164 (69%)	1.32	20 (17%) 4 2	24, 106, 143, 153	0
2	E	114/164 (69%)	1.48	22 (19%) 3 2	60, 105, 146, 165	0
2	H	114/164 (69%)	1.75	38 (33%) 1 1	24, 163, 195, 203	0
2	K	114/164 (69%)	1.26	20 (17%) 4 2	63, 102, 161, 164	0
3	C	571/572 (99%)	1.17	108 (18%) 3 2	27, 98, 201, 231	0
3	F	571/572 (99%)	0.85	59 (10%) 12 6	15, 80, 165, 225	0
3	I	571/572 (99%)	1.07	84 (14%) 6 3	16, 91, 176, 222	0
3	L	571/572 (99%)	0.83	66 (11%) 9 5	15, 82, 169, 201	0
All	All	3136/3344 (93%)	1.06	448 (14%) 6 3	15, 96, 176, 231	0

The worst 5 of 448 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	325	HIS	8.7
3	I	324	CYS	8.2
3	L	66	GLY	6.6
3	I	326	ASN	6.4
3	I	323	VAL	5.9

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NI	F	601	1/1	0.88	0.10	53,53,53,53	0
4	NI	F	602	1/1	0.93	0.15	45,45,45,45	0
4	NI	L	601	1/1	0.94	0.09	52,52,52,52	0
4	NI	I	601	1/1	0.96	0.09	41,41,41,41	0
4	NI	C	601	1/1	0.96	0.09	81,81,81,81	0
4	NI	C	602	1/1	0.97	0.06	82,82,82,82	0
4	NI	L	602	1/1	0.97	0.07	43,43,43,43	0
4	NI	I	602	1/1	0.99	0.13	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.