



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 29, 2024 – 08:23 AM EDT

PDB ID : 3LMM
Title : Crystal Structure of the DIP2311 protein from Corynebacterium diphtheriae, Northeast Structural Genomics Consortium Target Cdr35
Authors : Forouhar, F.; Lew, S.; Seetharaman, J.; Mao, M.; Xiao, R.; Ciccocanti, C.; Buchwald, W.A.; Maglaqui, M.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2010-01-31
Resolution : 3.00 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

<https://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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

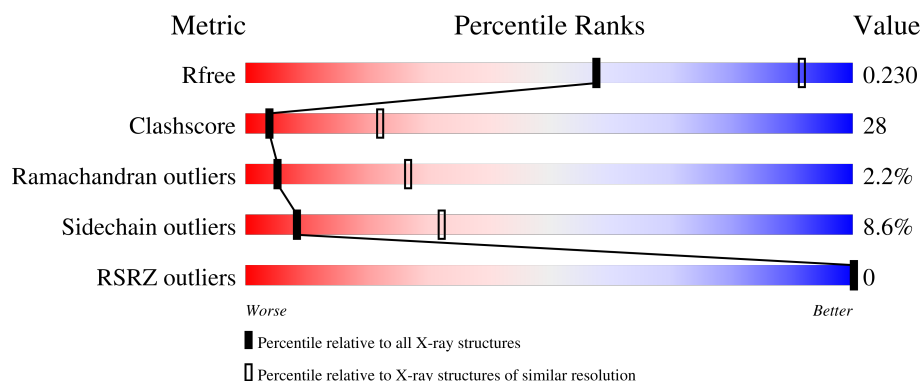
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	164625	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	583	
1	B	583	
1	C	583	
1	D	583	

Validation Pipeline (wwPDB-VP) : 2.39

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16408 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	492	Total	C	N	O	S	Se	0	0	0
			3798	2390	682	716	4	6			
1	B	555	Total	C	N	O	S	Se	0	0	0
			4262	2673	766	808	6	9			
1	C	477	Total	C	N	O	S	Se	0	0	0
			3676	2312	659	695	4	6			
1	D	556	Total	C	N	O	S	Se	0	0	0
			4271	2678	767	811	6	9			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	-	expression tag	UNP Q6NEG3
A	576	LEU	-	expression tag	UNP Q6NEG3
A	577	GLU	-	expression tag	UNP Q6NEG3
A	578	HIS	-	expression tag	UNP Q6NEG3
A	579	HIS	-	expression tag	UNP Q6NEG3
A	580	HIS	-	expression tag	UNP Q6NEG3
A	581	HIS	-	expression tag	UNP Q6NEG3
A	582	HIS	-	expression tag	UNP Q6NEG3
A	583	HIS	-	expression tag	UNP Q6NEG3
B	1	VAL	-	expression tag	UNP Q6NEG3
B	576	LEU	-	expression tag	UNP Q6NEG3
B	577	GLU	-	expression tag	UNP Q6NEG3
B	578	HIS	-	expression tag	UNP Q6NEG3
B	579	HIS	-	expression tag	UNP Q6NEG3
B	580	HIS	-	expression tag	UNP Q6NEG3
B	581	HIS	-	expression tag	UNP Q6NEG3
B	582	HIS	-	expression tag	UNP Q6NEG3
B	583	HIS	-	expression tag	UNP Q6NEG3
C	1	VAL	-	expression tag	UNP Q6NEG3
C	576	LEU	-	expression tag	UNP Q6NEG3
C	577	GLU	-	expression tag	UNP Q6NEG3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	578	HIS	-	expression tag	UNP Q6NEG3
C	579	HIS	-	expression tag	UNP Q6NEG3
C	580	HIS	-	expression tag	UNP Q6NEG3
C	581	HIS	-	expression tag	UNP Q6NEG3
C	582	HIS	-	expression tag	UNP Q6NEG3
C	583	HIS	-	expression tag	UNP Q6NEG3
D	1	VAL	-	expression tag	UNP Q6NEG3
D	576	LEU	-	expression tag	UNP Q6NEG3
D	577	GLU	-	expression tag	UNP Q6NEG3
D	578	HIS	-	expression tag	UNP Q6NEG3
D	579	HIS	-	expression tag	UNP Q6NEG3
D	580	HIS	-	expression tag	UNP Q6NEG3
D	581	HIS	-	expression tag	UNP Q6NEG3
D	582	HIS	-	expression tag	UNP Q6NEG3
D	583	HIS	-	expression tag	UNP Q6NEG3

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

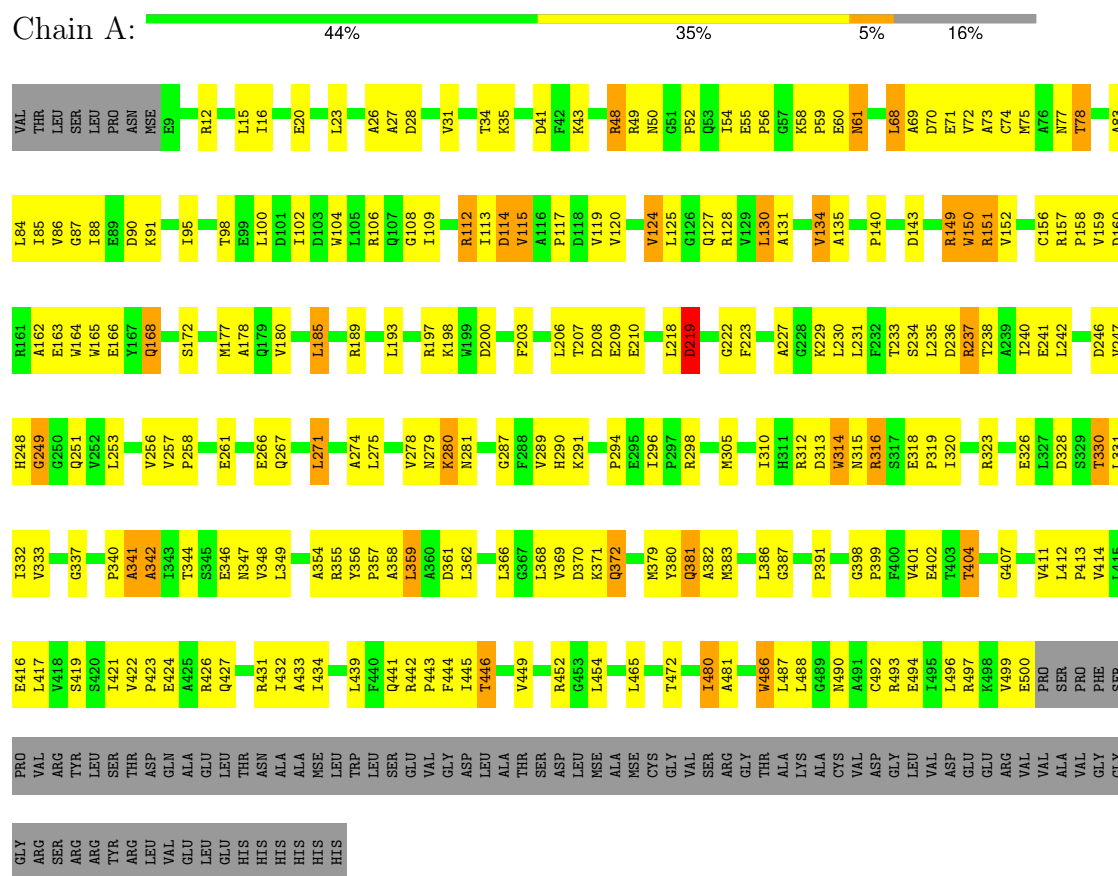
- Molecule 4 is water.

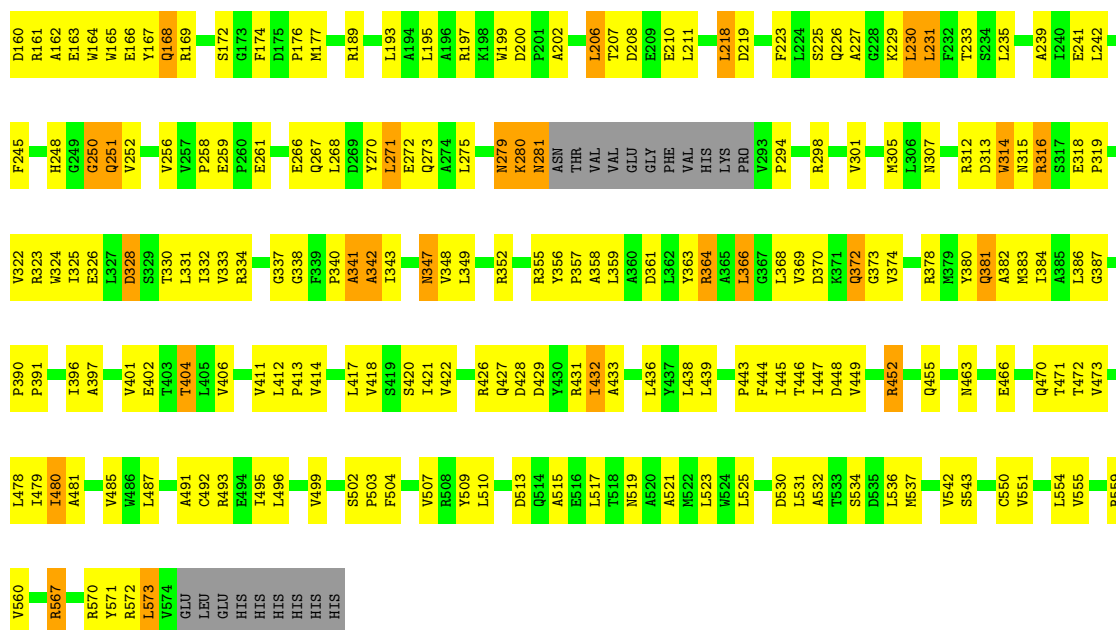
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total 128	O 128	0	0
4	B	64	Total 64	O 64	0	0
4	C	109	Total 109	O 109	0	0
4	D	90	Total 90	O 90	0	0

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.

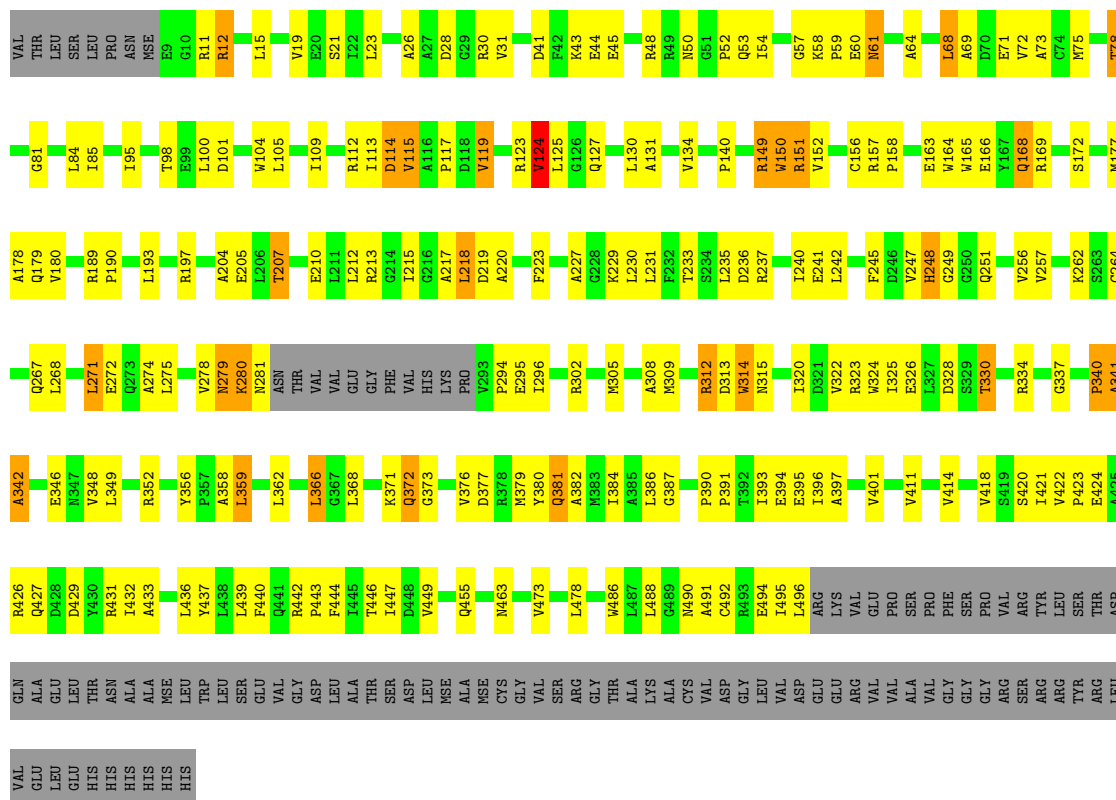
• Molecule 1: Uncharacterized protein





• Molecule 1: Uncharacterized protein

Chain C: 46% 31% 5% 18%



• Molecule 1: Uncharacterized protein

Chain D: 53% 37% 6% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	147.31Å 102.03Å 164.51Å 90.00° 116.00° 90.00°	Depositor
Resolution (Å)	19.99 – 3.00 19.99 – 3.00	Depositor EDS
% Data completeness (in resolution range)	81.4 (19.99-3.00) 93.0 (19.99-3.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 3.00Å)	Xtriage
Refinement program	CNS 1.2 & XtalView, REFMAC	Depositor
R, R_{free}	0.183 , 0.231 0.203 , 0.230	Depositor DCC
R_{free} test set	4078 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 14.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.056 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16408	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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](#)

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

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	0.41	0/3860	0.62	1/5239 (0.0%)
1	B	0.37	0/4325	0.58	0/5862
1	C	0.40	0/3734	0.60	0/5067
1	D	0.36	0/4334	0.57	0/5874
All	All	0.39	0/16253	0.59	1/22042 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	290	HIS	CB-CA-C	-6.45	97.49	110.40

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	3798	0	3826	221	0
1	B	4262	0	4290	257	0
1	C	3676	0	3699	196	0
1	D	4271	0	4296	227	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	0	2	0
3	B	1	0	0	1	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	128	0	0	11	0
4	B	64	0	0	3	0
4	C	109	0	0	9	0
4	D	90	0	0	5	0
All	All	16408	0	16111	885	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 28.

The worst 5 of 885 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:B:446:THR:HG22	1:B:449:VAL:HG23	1.19	1.19
1:C:271:LEU:HD12	1:C:305:MSE:HE1	1.32	1.10
1:D:446:THR:HG22	1:D:449:VAL:HG23	1.32	1.07
1:C:78:THR:HG23	1:C:150:TRP:HB2	1.42	1.01
1:B:177:MSE:HG2	1:B:359:LEU:HB2	1.51	0.93

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	490/583 (84%)	432 (88%)	46 (9%)	12 (2%)	5	25
1	B	551/583 (94%)	488 (89%)	51 (9%)	12 (2%)	5	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	473/583 (81%)	431 (91%)	30 (6%)	12 (2%)	4	24
1	D	552/583 (95%)	492 (89%)	51 (9%)	9 (2%)	8	34
All	All	2066/2332 (89%)	1843 (89%)	178 (9%)	45 (2%)	5	27

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	341	ALA
1	A	342	ALA
1	B	280	LYS
1	B	341	ALA
1	B	342	ALA

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	396/462 (86%)	363 (92%)	33 (8%)	9	34
1	B	445/462 (96%)	405 (91%)	40 (9%)	8	30
1	C	382/462 (83%)	352 (92%)	30 (8%)	10	35
1	D	446/462 (96%)	406 (91%)	40 (9%)	8	30
All	All	1669/1848 (90%)	1526 (91%)	143 (9%)	8	32

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	157	ARG
1	D	261	GLU
1	D	403	THR
1	B	168	GLN
1	B	167	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	490	ASN
1	D	107	GLN
1	D	14	GLN
1	D	50	ASN
1	D	279	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](#)

Of 10 ligands modelled in this entry, 10 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	486/583 (83%)	-1.95	0 100 100	9, 29, 65, 98	0
1	B	546/583 (93%)	-1.86	0 100 100	14, 45, 85, 119	0
1	C	471/583 (80%)	-1.93	0 100 100	9, 34, 74, 103	0
1	D	547/583 (93%)	-1.84	0 100 100	14, 47, 88, 126	0
All	All	2050/2332 (87%)	-1.89	0 100 100	9, 39, 82, 126	0

There are no RSRZ outliers to report.

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 monosaccharides 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(Å ²)	Q<0.9
3	CL	A	585	1/1	0.99	0.08	71,71,71,71	0
3	CL	A	586	1/1	0.99	0.03	58,58,58,58	0
2	CO	C	601	1/1	1.00	0.03	106,106,106,106	0
2	CO	D	601	1/1	1.00	0.02	93,93,93,93	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CL	A	584	1/1	1.00	0.02	28,28,28,28	0
2	CO	A	601	1/1	1.00	0.03	93,93,93,93	0
2	CO	B	601	1/1	1.00	0.02	88,88,88,88	0
3	CL	B	584	1/1	1.00	0.02	40,40,40,40	0
3	CL	C	584	1/1	1.00	0.03	37,37,37,37	0
3	CL	D	584	1/1	1.00	0.02	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.