



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2020 – 06:02 pm BST

PDB ID : 1PLF
Title : THE THREE-DIMENSIONAL STRUCTURE OF BOVINE PLATELET
FACTOR 4 AT 3.0 ANGSTROMS RESOLUTION
Authors : St Charles, R.; Edwards, B.F.P.
Deposited on : 1993-10-20
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

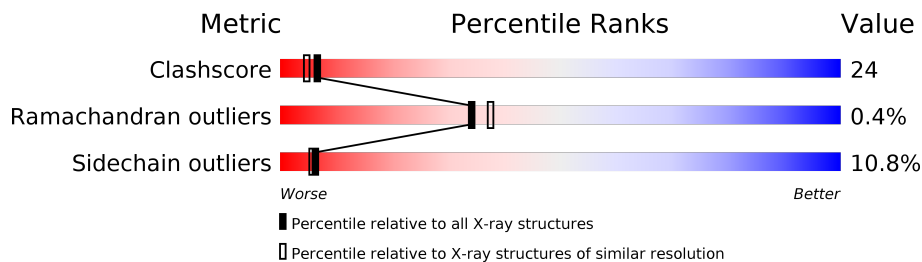
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 on 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	72	
1	B	72	
1	C	72	
1	D	72	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2058 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 PLATELET FACTOR 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	63	484	307	89	84	4	0	0	0
1	B	65	501	316	91	90	4	0	0	0
1	C	63	484	307	89	84	4	0	0	0
1	D	65	501	316	91	90	4	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

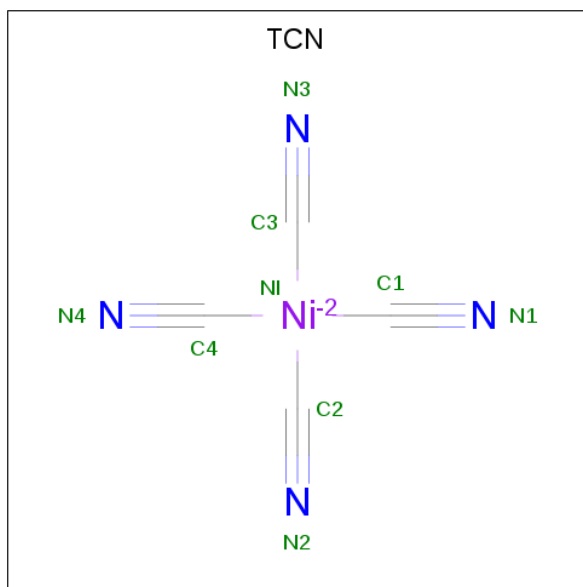
Chain	Residue	Modelled	Actual	Comment	Reference
A	49	LEU	THR	CONFLICT	UNP P02777
A	57	ILE	LEU	CONFLICT	UNP P02777
A	60	LEU	LYS	CONFLICT	UNP P02777
A	72	ASN	ARG	CONFLICT	UNP P02777
A	79	ILE	LEU	CONFLICT	UNP P02777
A	81	ARG	LYS	CONFLICT	UNP P02777
B	49	LEU	THR	CONFLICT	UNP P02777
B	57	ILE	LEU	CONFLICT	UNP P02777
B	60	LEU	LYS	CONFLICT	UNP P02777
B	72	ASN	ARG	CONFLICT	UNP P02777
B	79	ILE	LEU	CONFLICT	UNP P02777
B	81	ARG	LYS	CONFLICT	UNP P02777
C	49	LEU	THR	CONFLICT	UNP P02777
C	57	ILE	LEU	CONFLICT	UNP P02777
C	60	LEU	LYS	CONFLICT	UNP P02777
C	72	ASN	ARG	CONFLICT	UNP P02777
C	79	ILE	LEU	CONFLICT	UNP P02777
C	81	ARG	LYS	CONFLICT	UNP P02777
D	49	LEU	THR	CONFLICT	UNP P02777
D	57	ILE	LEU	CONFLICT	UNP P02777
D	60	LEU	LYS	CONFLICT	UNP P02777

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Chain	Residue	Modelled	Actual	Comment	Reference
D	72	ASN	ARG	CONFLICT	UNP P02777
D	79	ILE	LEU	CONFLICT	UNP P02777
D	81	ARG	LYS	CONFLICT	UNP P02777

- Molecule 2 is TETRACYANONICKELATE ION (three-letter code: TCN) (formula: C₄N₄Ni).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	Ni		
2	D	1	9	4	4	1	0	0

- Molecule 3 is water.

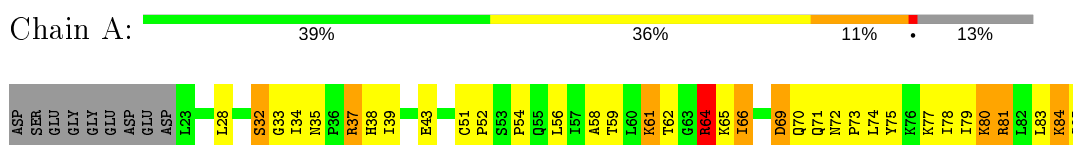
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	25	Total	O	0	0
			25	25		
3	C	19	Total	O	0	0
			19	19		
3	D	20	Total	O	0	0
			20	20		

3 Residue-property plots [i](#)

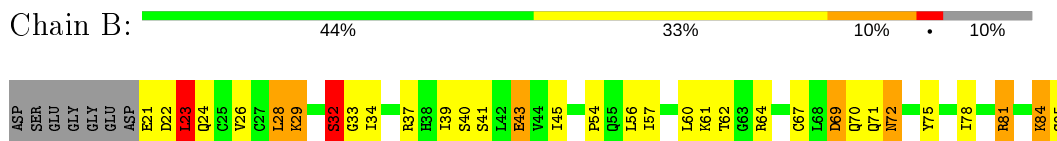
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

Note EDS was not executed.

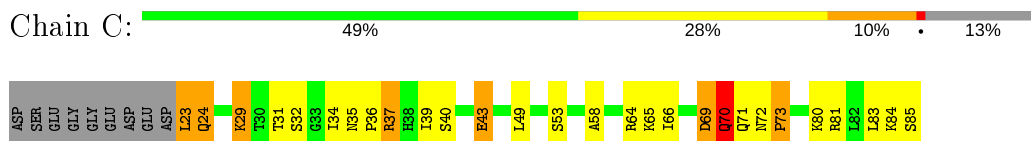
- Molecule 1: PLATELET FACTOR 4



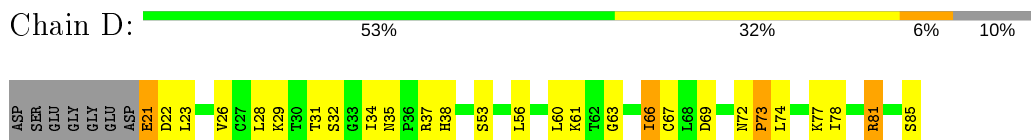
- Molecule 1: PLATELET FACTOR 4



- Molecule 1: PLATELET FACTOR 4



- Molecule 1: PLATELET FACTOR 4



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.70Å 68.00Å 80.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROFFT, X-PLOR	Depositor
R, R_{free}	0.209 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2058	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

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: TCN

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	1.03	0/490	1.84	9/658 (1.4%)
1	B	1.03	0/507	2.11	21/681 (3.1%)
1	C	1.03	0/490	1.85	11/658 (1.7%)
1	D	0.97	0/507	1.71	4/681 (0.6%)
All	All	1.01	0/1994	1.88	45/2678 (1.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	81	ARG	NE-CZ-NH2	-12.37	114.12	120.30
1	B	69	ASP	CB-CG-OD2	-11.82	107.66	118.30
1	B	69	ASP	CB-CG-OD1	11.79	128.91	118.30
1	B	23	LEU	CA-CB-CG	10.39	139.21	115.30
1	D	69	ASP	CB-CG-OD2	-10.24	109.09	118.30
1	A	37	ARG	NE-CZ-NH1	9.74	125.17	120.30
1	B	43	GLU	OE1-CD-OE2	9.03	134.14	123.30
1	C	81	ARG	NE-CZ-NH2	-8.20	116.20	120.30
1	B	22	ASP	CB-CG-OD1	7.93	125.44	118.30
1	B	75	TYR	CB-CG-CD1	-7.86	116.28	121.00
1	B	21	GLU	OE1-CD-OE2	7.85	132.72	123.30
1	C	43	GLU	CG-CD-OE2	-7.72	102.85	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	64	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	B	32	SER	C-N-CA	-6.57	108.51	122.30
1	C	40	SER	CB-CA-C	6.48	122.41	110.10
1	D	31	THR	CA-CB-CG2	6.37	121.32	112.40
1	C	70	GLN	CA-CB-CG	6.35	127.37	113.40
1	C	40	SER	O-C-N	-6.28	112.64	122.70
1	A	69	ASP	CB-CG-OD1	6.12	123.81	118.30
1	C	37	ARG	CG-CD-NE	-6.09	99.00	111.80
1	A	69	ASP	CA-CB-CG	6.03	126.67	113.40
1	B	81	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	B	33	GLY	CA-C-O	-5.92	109.94	120.60
1	C	64	ARG	CD-NE-CZ	5.92	131.89	123.60
1	B	43	GLU	CG-CD-OE2	-5.88	106.55	118.30
1	D	60	LEU	O-C-N	5.82	132.01	122.70
1	C	43	GLU	OE1-CD-OE2	5.78	130.24	123.30
1	B	21	GLU	CG-CD-OE1	-5.69	106.92	118.30
1	A	33	GLY	CA-C-O	-5.56	110.59	120.60
1	A	69	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	B	60	LEU	CB-CA-C	5.47	120.60	110.20
1	D	85	SER	CB-CA-C	-5.45	99.75	110.10
1	A	81	ARG	NE-CZ-NH1	5.33	122.97	120.30
1	B	37	ARG	CA-C-O	-5.33	108.90	120.10
1	A	84	LYS	O-C-N	5.31	131.19	122.70
1	C	80	LYS	CA-CB-CG	5.25	124.96	113.40
1	B	72	ASN	CB-CA-C	5.25	120.91	110.40
1	B	64	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	B	37	ARG	NE-CZ-NH1	5.19	122.90	120.30
1	B	62	THR	N-CA-CB	5.18	120.14	110.30
1	B	75	TYR	CB-CG-CD2	5.13	124.08	121.00
1	A	66	ILE	O-C-N	5.10	130.86	122.70
1	B	81	ARG	CD-NE-CZ	-5.06	116.51	123.60
1	A	59	THR	CA-CB-OG1	-5.03	98.43	109.00
1	C	69	ASP	CB-CG-OD1	5.03	122.83	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	ARG	Sidechain

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	484	0	530	30	0
1	B	501	0	540	26	0
1	C	484	0	530	22	0
1	D	501	0	540	34	0
2	D	9	0	0	0	0
3	A	15	0	0	0	0
3	B	25	0	0	4	0
3	C	19	0	0	1	0
3	D	20	0	0	0	0
All	All	2058	0	2140	97	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 24.

All (97) 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:84:LYS:O	1:B:85:SER:HB3	1.51	1.10
1:B:34:ILE:HD13	1:B:39:ILE:HD11	1.44	0.96
1:C:34:ILE:HD12	1:C:39:ILE:HD11	1.52	0.88
1:D:35:ASN:CB	1:D:38:HIS:CE1	2.57	0.87
1:B:26:VAL:HG22	1:D:23:LEU:HD23	1.59	0.85
1:A:83:LEU:O	1:B:70:GLN:NE2	2.08	0.85
1:D:35:ASN:HB2	1:D:38:HIS:CE1	2.13	0.83
1:C:34:ILE:HD13	1:C:66:ILE:HD11	1.58	0.82
1:D:35:ASN:HB3	1:D:38:HIS:CE1	2.16	0.80
1:C:72:ASN:OD1	1:C:73:PRO:HD2	1.84	0.78
1:A:28:LEU:HD11	1:C:29:LYS:HB2	1.66	0.77
1:A:39:ILE:HG13	1:A:78:ILE:HD13	1.67	0.76
1:B:84:LYS:O	1:B:85:SER:CB	2.29	0.76
1:C:85:SER:HB3	3:C:424:HOH:O	1.85	0.76
1:A:74:LEU:O	1:A:77:LYS:HB2	1.86	0.75
1:A:80:LYS:O	1:A:84:LYS:HD2	1.87	0.75
1:B:71:GLN:O	1:B:71:GLN:HG2	1.92	0.69
1:C:34:ILE:HG21	1:C:66:ILE:HD13	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:GLN:O	1:B:71:GLN:CG	2.40	0.68
1:B:34:ILE:HD11	1:B:78:ILE:HD11	1.76	0.67
1:A:85:SER:HB3	3:B:455:HOH:O	1.97	0.65
1:D:34:ILE:CD1	1:D:74:LEU:HD21	2.27	0.64
1:B:40:SER:HB3	1:B:61:LYS:HG3	1.81	0.63
1:D:34:ILE:HD12	1:D:74:LEU:HD21	1.81	0.63
1:B:28:LEU:HD13	1:D:21:GLU:O	1.98	0.63
1:A:28:LEU:CD1	1:C:29:LYS:HB2	2.29	0.62
3:B:501:HOH:O	1:D:22:ASP:HB3	1.97	0.62
1:A:61:LYS:O	1:D:63:GLY:HA2	2.00	0.62
1:D:72:ASN:OD1	1:D:73:PRO:HD2	2.00	0.61
1:A:62:THR:HB	1:A:64:ARG:HD3	1.82	0.61
1:C:70:GLN:H	1:C:70:GLN:HE21	1.46	0.61
1:A:65:LYS:NZ	1:C:43:GLU:OE1	2.33	0.61
1:A:37:ARG:O	1:A:61:LYS:HE3	1.99	0.61
1:C:34:ILE:CD1	1:C:39:ILE:HD11	2.26	0.61
1:C:70:GLN:H	1:C:70:GLN:NE2	2.00	0.60
1:A:34:ILE:HG12	1:A:66:ILE:CD1	2.32	0.60
1:D:34:ILE:O	1:D:34:ILE:HD12	2.02	0.60
1:C:84:LYS:O	1:C:85:SER:OXT	2.20	0.60
1:D:74:LEU:O	1:D:78:ILE:HD12	2.02	0.59
1:B:32:SER:OG	1:B:72:ASN:ND2	2.37	0.58
1:B:24:GLN:HB3	1:D:28:LEU:HD11	1.86	0.57
1:A:69:ASP:OD1	1:A:71:GLN:HB2	2.03	0.57
1:D:22:ASP:HB2	1:D:23:LEU:HD12	1.87	0.57
1:B:69:ASP:OD1	1:B:71:GLN:HB3	2.05	0.57
1:A:81:ARG:O	1:A:85:SER:HB2	2.05	0.57
1:C:69:ASP:OD1	1:C:71:GLN:HB2	2.05	0.56
1:A:54:PRO:HG2	1:A:70:GLN:HE22	1.71	0.54
1:B:45:ILE:O	1:B:54:PRO:HA	2.07	0.54
1:B:23:LEU:HA	1:D:26:VAL:O	2.07	0.54
1:C:39:ILE:HD12	1:C:58:ALA:HB1	1.89	0.54
1:D:38:HIS:O	1:D:61:LYS:HG3	2.07	0.53
1:B:26:VAL:O	1:D:23:LEU:HA	2.09	0.53
1:A:80:LYS:HG3	1:A:84:LYS:NZ	2.24	0.52
1:D:38:HIS:O	1:D:61:LYS:N	2.39	0.52
1:A:35:ASN:HB3	1:A:38:HIS:ND1	2.24	0.51
1:C:34:ILE:HG21	1:C:66:ILE:CD1	2.42	0.50
1:D:72:ASN:OD1	1:D:73:PRO:CD	2.60	0.49
1:D:35:ASN:CB	1:D:38:HIS:ND1	2.75	0.49
1:B:45:ILE:HD11	1:B:57:ILE:CD1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:ALA:O	1:A:65:LYS:HA	2.13	0.49
1:B:45:ILE:HD11	1:B:57:ILE:HD12	1.94	0.49
1:A:39:ILE:HG13	1:A:78:ILE:CD1	2.40	0.48
1:C:34:ILE:HD13	1:C:66:ILE:CD1	2.39	0.47
1:D:35:ASN:HB3	1:D:38:HIS:ND1	2.30	0.46
1:B:45:ILE:CD1	1:B:57:ILE:CD1	2.93	0.46
1:D:34:ILE:HG21	1:D:66:ILE:CD1	2.46	0.46
1:D:34:ILE:HD11	1:D:74:LEU:CD2	2.46	0.45
1:D:37:ARG:HG2	1:D:81:ARG:NH2	2.30	0.45
1:A:54:PRO:CG	1:A:70:GLN:HE22	2.30	0.45
1:C:23:LEU:HB2	1:C:24:GLN:H	1.51	0.45
1:B:23:LEU:HD22	1:D:67:CYS:SG	2.57	0.45
1:B:45:ILE:CD1	1:B:57:ILE:HD12	2.47	0.45
1:A:72:ASN:OD1	1:A:72:ASN:C	2.55	0.44
1:A:72:ASN:OD1	1:A:73:PRO:HD2	2.16	0.44
1:D:37:ARG:O	1:D:61:LYS:HE3	2.18	0.44
1:C:83:LEU:CD2	1:D:56:LEU:HD21	2.49	0.43
1:A:35:ASN:HB3	1:A:38:HIS:CE1	2.54	0.43
1:A:75:TYR:O	1:A:79:ILE:HG13	2.18	0.43
1:C:31:THR:OG1	1:C:32:SER:N	2.51	0.43
1:A:34:ILE:HG12	1:A:66:ILE:HD11	1.99	0.42
1:D:35:ASN:HB2	1:D:38:HIS:HE1	1.78	0.42
3:B:463:HOH:O	1:D:29:LYS:CE	2.66	0.42
1:B:71:GLN:HG3	1:B:71:GLN:O	2.19	0.42
1:B:81:ARG:HG3	1:B:81:ARG:O	2.19	0.42
1:B:56:LEU:O	1:B:67:CYS:HA	2.19	0.42
1:A:32:SER:OG	1:A:72:ASN:ND2	2.52	0.42
1:C:35:ASN:OD1	1:C:37:ARG:HB3	2.20	0.42
1:D:72:ASN:OD1	1:D:73:PRO:N	2.52	0.42
1:D:56:LEU:O	1:D:67:CYS:HA	2.20	0.41
1:A:51:CYS:HA	1:A:52:PRO:HD3	1.61	0.41
1:B:29:LYS:HD2	1:D:21:GLU:O	2.21	0.41
3:B:463:HOH:O	1:D:29:LYS:HE2	2.20	0.41
1:D:34:ILE:HD11	1:D:74:LEU:HG	2.04	0.40
1:A:43:GLU:OE1	1:C:65:LYS:HE2	2.21	0.40
1:A:80:LYS:HG3	1:A:84:LYS:HZ3	1.87	0.40
1:A:43:GLU:HB2	1:B:43:GLU:HG3	2.02	0.40
1:C:34:ILE:CG2	1:C:66:ILE:HD13	2.45	0.40

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	61/72 (85%)	59 (97%)	2 (3%)	0	100	100
1	B	63/72 (88%)	60 (95%)	2 (3%)	1 (2%)	9	7
1	C	61/72 (85%)	59 (97%)	2 (3%)	0	100	100
1	D	63/72 (88%)	59 (94%)	4 (6%)	0	100	100
All	All	248/288 (86%)	237 (96%)	10 (4%)	1 (0%)	34	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	84	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	57/64 (89%)	52 (91%)	5 (9%)	10	10
1	B	59/64 (92%)	54 (92%)	5 (8%)	10	10
1	C	57/64 (89%)	49 (86%)	8 (14%)	3	3
1	D	59/64 (92%)	52 (88%)	7 (12%)	5	4
All	All	232/256 (91%)	207 (89%)	25 (11%)	6	6

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	56	LEU
1	A	61	LYS
1	A	64	ARG
1	A	80	LYS
1	B	23	LEU
1	B	28	LEU
1	B	29	LYS
1	B	32	SER
1	B	41	SER
1	C	23	LEU
1	C	24	GLN
1	C	29	LYS
1	C	36	PRO
1	C	49	LEU
1	C	53	SER
1	C	70	GLN
1	C	73	PRO
1	D	21	GLU
1	D	32	SER
1	D	53	SER
1	D	66	ILE
1	D	73	PRO
1	D	77	LYS
1	D	81	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	HIS
1	A	70	GLN
1	B	72	ASN
1	C	70	GLN
1	C	71	GLN
1	D	38	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TCN	D	1	-	8,8,8	0.22	0	-		

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.