



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:24 am BST

PDB ID : 5GW9
Title : Crystal structure of C163, a backbone circularized G-CSF
Authors : Miyafusa, T.; Honda, S.
Deposited on : 2016-09-09
Resolution : 1.65 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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

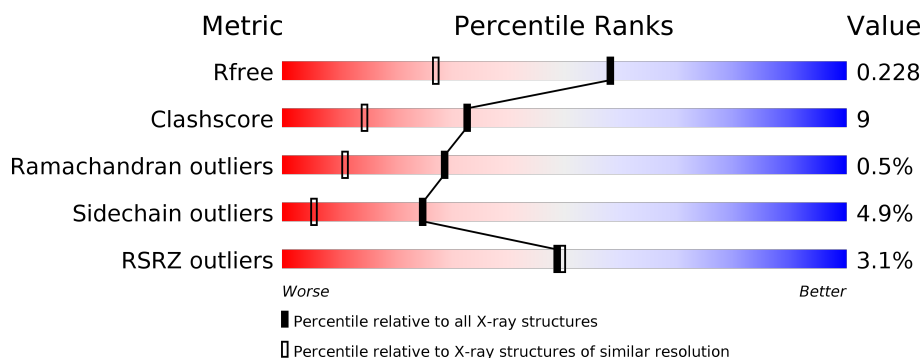
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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}	130704	1827 (1.66-1.66)
Clashscore	141614	1931 (1.66-1.66)
Ramachandran outliers	138981	1891 (1.66-1.66)
Sidechain outliers	138945	1891 (1.66-1.66)
RSRZ outliers	127900	1791 (1.66-1.66)

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 $\leq 5\%$. 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	163	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>17%</div> <div>••</div> </div> </div>
1	B	163	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>6%</div> <div>•</div> </div> </div>
1	C	163	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>24%</div> <div>7%</div> <div>•</div> </div> </div>
1	D	163	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>16%</div> <div>••</div> </div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5803 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 Granulocyte colony-stimulating factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	12	0
			1333	847	231	247	8			
1	B	163	Total	C	N	O	S	0	11	0
			1322	841	227	247	7			
1	C	163	Total	C	N	O	S	0	13	0
			1349	856	235	251	7			
1	D	163	Total	C	N	O	S	0	11	0
			1321	842	226	246	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	SER	PRO	engineered mutation	UNP P09919
A	18	SER	CYS	engineered mutation	UNP P09919
A	173	GLY	ALA	engineered mutation	UNP P09919
B	11	SER	PRO	engineered mutation	UNP P09919
B	18	SER	CYS	engineered mutation	UNP P09919
B	173	GLY	ALA	engineered mutation	UNP P09919
C	11	SER	PRO	engineered mutation	UNP P09919
C	18	SER	CYS	engineered mutation	UNP P09919
C	173	GLY	ALA	engineered mutation	UNP P09919
D	11	SER	PRO	engineered mutation	UNP P09919
D	18	SER	CYS	engineered mutation	UNP P09919
D	173	GLY	ALA	engineered mutation	UNP P09919

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	116	Total	O	0	0
			116	116		
2	B	126	Total	O	0	0
			126	126		

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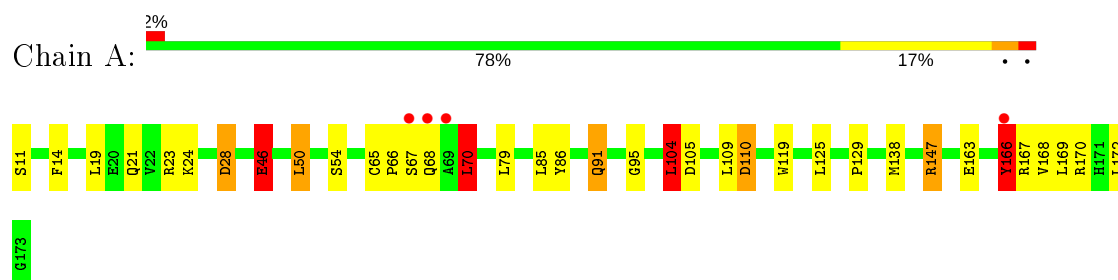
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	124	Total 124	O 124	0	0
2	D	112	Total 112	O 112	0	0

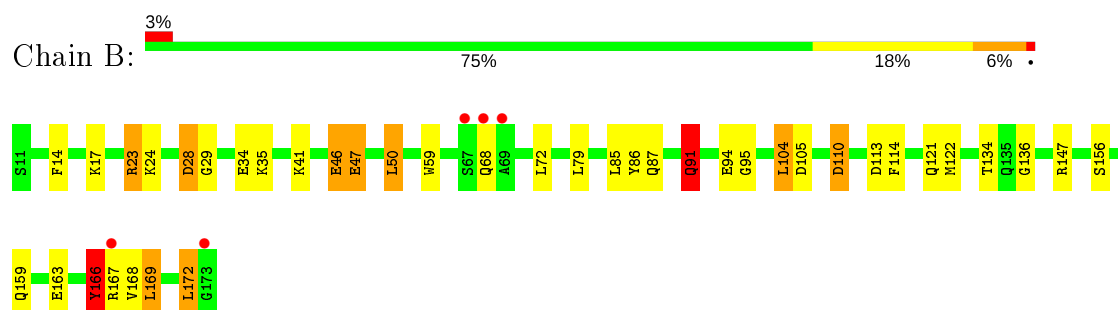
3 Residue-property plots [i](#)

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 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.

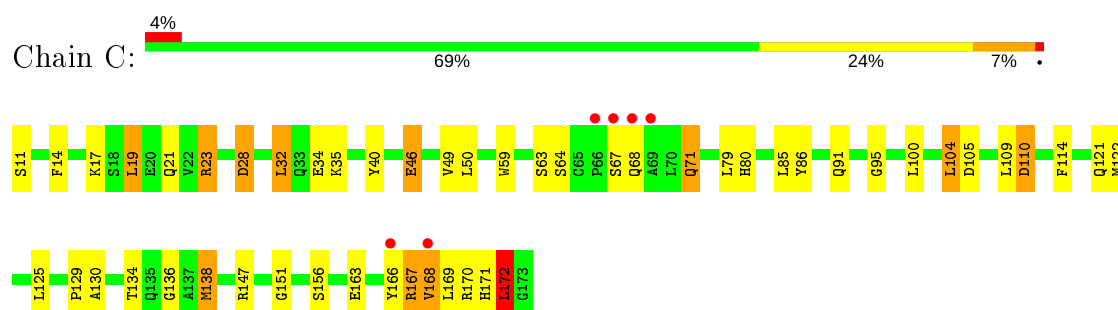
- Molecule 1: Granulocyte colony-stimulating factor



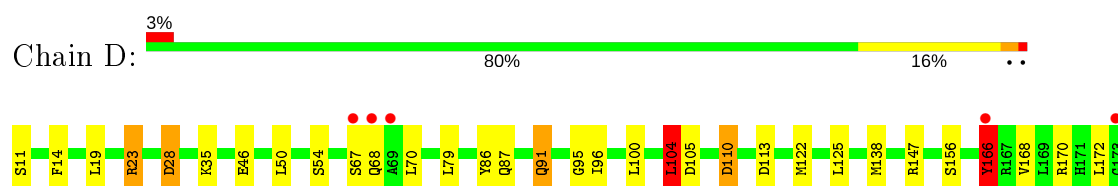
- Molecule 1: Granulocyte colony-stimulating factor



- Molecule 1: Granulocyte colony-stimulating factor



- Molecule 1: Granulocyte colony-stimulating factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	60.94Å 60.94Å 178.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.08 – 1.65 34.08 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.08-1.65) 99.9 (34.08-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.177 , 0.218 0.190 , 0.228	Depositor DCC
R_{free} test set	4463 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	22.5	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.486 for -h,-k,l 0.487 for h,-h-k,-l 0.487 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5803	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	1.71	17/1360 (1.2%)	1.58	26/1845 (1.4%)
1	B	1.70	19/1348 (1.4%)	1.43	15/1827 (0.8%)
1	C	1.66	19/1376 (1.4%)	1.51	24/1865 (1.3%)
1	D	1.64	13/1347 (1.0%)	1.42	13/1826 (0.7%)
All	All	1.68	68/5431 (1.3%)	1.49	78/7363 (1.1%)

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	B	0	1
1	C	0	1
1	D	0	1
All	All	0	3

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	166	TYR	CB-CG	12.01	1.69	1.51
1	D	166	TYR	CB-CG	11.08	1.68	1.51
1	B	166	TYR	CB-CG	10.57	1.67	1.51
1	C	166	TYR	CB-CG	10.43	1.67	1.51
1	C	23[A]	ARG	CZ-NH1	10.29	1.46	1.33
1	C	23[B]	ARG	CZ-NH1	10.29	1.46	1.33
1	B	46[A]	GLU	CD-OE2	10.06	1.36	1.25
1	B	46[B]	GLU	CD-OE2	10.06	1.36	1.25
1	A	166	TYR	CZ-OH	8.95	1.53	1.37
1	D	156[A]	SER	CA-CB	8.88	1.66	1.52
1	D	156[B]	SER	CA-CB	8.88	1.66	1.52
1	D	166	TYR	CZ-OH	8.79	1.52	1.37
1	D	23[A]	ARG	CZ-NH1	8.39	1.44	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	23[B]	ARG	CZ-NH1	8.39	1.44	1.33
1	A	23[A]	ARG	CZ-NH1	8.20	1.43	1.33
1	A	23[B]	ARG	CZ-NH1	8.20	1.43	1.33
1	B	166	TYR	CZ-OH	7.58	1.50	1.37
1	A	46[A]	GLU	CG-CD	7.23	1.62	1.51
1	A	46[B]	GLU	CG-CD	7.23	1.62	1.51
1	C	166	TYR	N-CA	7.12	1.60	1.46
1	B	166	TYR	N-CA	6.80	1.59	1.46
1	A	166	TYR	N-CA	6.76	1.59	1.46
1	B	172	LEU	N-CA	-6.32	1.33	1.46
1	C	28	ASP	CG-OD2	6.25	1.39	1.25
1	D	166	TYR	N-CA	6.17	1.58	1.46
1	C	59	TRP	CG-CD1	6.14	1.45	1.36
1	D	28	ASP	CG-OD2	6.08	1.39	1.25
1	B	163	GLU	CD-OE1	5.97	1.32	1.25
1	B	167	ARG	N-CA	-5.93	1.34	1.46
1	C	163	GLU	CD-OE1	5.86	1.32	1.25
1	B	59	TRP	CG-CD1	5.85	1.45	1.36
1	B	110	ASP	CG-OD2	-5.79	1.12	1.25
1	B	24	LYS	N-CA	-5.70	1.34	1.46
1	D	170	ARG	C-O	-5.65	1.12	1.23
1	A	28	ASP	CG-OD2	5.64	1.38	1.25
1	C	14	PHE	CG-CD2	5.61	1.47	1.38
1	D	86	TYR	CE1-CZ	-5.60	1.31	1.38
1	C	156[A]	SER	CA-CB	5.57	1.61	1.52
1	C	156[B]	SER	CA-CB	5.57	1.61	1.52
1	C	156[C]	SER	CA-CB	5.57	1.61	1.52
1	A	167	ARG	N-CA	-5.56	1.35	1.46
1	B	147	ARG	CZ-NH2	-5.55	1.25	1.33
1	B	28	ASP	CG-OD2	5.51	1.38	1.25
1	A	91[A]	GLN	CD-NE2	5.48	1.46	1.32
1	A	91[B]	GLN	CD-NE2	5.48	1.46	1.32
1	A	163	GLU	CD-OE1	5.48	1.31	1.25
1	B	91[A]	GLN	CG-CD	5.48	1.63	1.51
1	B	91[B]	GLN	CG-CD	5.48	1.63	1.51
1	C	163	GLU	CD-OE2	5.39	1.31	1.25
1	C	110	ASP	CG-OD2	-5.39	1.12	1.25
1	C	21	GLN	CD-NE2	-5.38	1.19	1.32
1	B	86	TYR	CE2-CZ	5.31	1.45	1.38
1	A	54	SER	CB-OG	-5.29	1.35	1.42
1	C	130	ALA	C-O	5.27	1.33	1.23
1	A	21	GLN	CD-NE2	-5.23	1.19	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46[A]	GLU	CD-OE2	5.21	1.31	1.25
1	A	46[B]	GLU	CD-OE2	5.21	1.31	1.25
1	C	63	SER	CB-OG	-5.21	1.35	1.42
1	D	110	ASP	CG-OD2	-5.17	1.13	1.25
1	D	54	SER	CB-OG	-5.17	1.35	1.42
1	A	24	LYS	N-CA	-5.16	1.36	1.46
1	C	151	GLY	N-CA	5.09	1.53	1.46
1	B	156[A]	SER	CA-CB	5.06	1.60	1.52
1	B	156[B]	SER	CA-CB	5.06	1.60	1.52
1	D	110	ASP	CG-OD1	5.03	1.36	1.25
1	B	29	GLY	N-CA	-5.02	1.38	1.46
1	C	46[A]	GLU	CG-CD	5.02	1.59	1.51
1	C	46[B]	GLU	CG-CD	5.02	1.59	1.51

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23[A]	ARG	NE-CZ-NH1	-13.10	113.75	120.30
1	A	23[B]	ARG	NE-CZ-NH1	-13.10	113.75	120.30
1	D	147	ARG	NE-CZ-NH2	-12.18	114.21	120.30
1	C	147[A]	ARG	NE-CZ-NH2	-10.86	114.87	120.30
1	C	147[B]	ARG	NE-CZ-NH2	-10.86	114.87	120.30
1	A	105	ASP	CB-CG-OD1	9.57	126.92	118.30
1	D	138	MET	CG-SD-CE	-9.47	85.05	100.20
1	D	147	ARG	CG-CD-NE	-9.07	92.75	111.80
1	C	105	ASP	CB-CG-OD1	8.82	126.24	118.30
1	A	110	ASP	CB-CG-OD1	8.81	126.23	118.30
1	A	23[A]	ARG	NH1-CZ-NH2	8.78	129.06	119.40
1	A	23[B]	ARG	NH1-CZ-NH2	8.78	129.06	119.40
1	A	147	ARG	NE-CZ-NH2	-8.73	115.94	120.30
1	C	172	LEU	CA-CB-CG	-8.56	95.60	115.30
1	C	19	LEU	CB-CG-CD2	8.55	125.54	111.00
1	A	138[A]	MET	CG-SD-CE	-8.38	86.80	100.20
1	A	138[B]	MET	CG-SD-CE	-8.38	86.80	100.20
1	A	50	LEU	CB-CG-CD1	8.38	125.24	111.00
1	B	105	ASP	CB-CG-OD1	7.83	125.35	118.30
1	C	147[A]	ARG	CG-CD-NE	-7.61	95.82	111.80
1	C	147[B]	ARG	CG-CD-NE	-7.61	95.82	111.80
1	B	50	LEU	CB-CG-CD1	7.47	123.70	111.00
1	A	147	ARG	CG-CD-NE	-7.46	96.13	111.80
1	B	110	ASP	CB-CG-OD1	7.34	124.91	118.30
1	B	86	TYR	CZ-CE2-CD2	-7.16	113.36	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	86	TYR	CB-CG-CD1	-7.10	116.74	121.00
1	A	86	TYR	CB-CG-CD1	-7.04	116.78	121.00
1	C	122	MET	CG-SD-CE	-6.73	89.44	100.20
1	A	170[A]	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	170[B]	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	C	147[A]	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	C	147[B]	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	D	105	ASP	CB-CG-OD1	6.56	124.21	118.30
1	C	86	TYR	CB-CG-CD1	-6.53	117.08	121.00
1	C	167	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	A	23[A]	ARG	NE-CZ-NH2	-6.47	117.07	120.30
1	A	23[B]	ARG	NE-CZ-NH2	-6.47	117.07	120.30
1	B	122	MET	CG-SD-CE	-6.33	90.07	100.20
1	C	168	VAL	CB-CA-C	-6.33	99.38	111.40
1	A	110	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	A	19	LEU	CB-CG-CD2	6.17	121.49	111.00
1	D	110	ASP	CB-CG-OD1	6.08	123.77	118.30
1	C	110	ASP	CB-CG-OD1	6.05	123.75	118.30
1	D	110	ASP	CB-CG-OD2	-6.05	112.86	118.30
1	C	40	TYR	CG-CD2-CE2	5.96	126.07	121.30
1	C	23[A]	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	C	23[B]	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	D	122	MET	CG-SD-CE	-5.89	90.78	100.20
1	D	113	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	A	163	GLU	OE1-CD-OE2	5.77	130.23	123.30
1	B	105	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	C	170	ARG	NE-CZ-NH2	5.63	123.11	120.30
1	A	105	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	D	104[A]	LEU	CB-CG-CD2	5.48	120.31	111.00
1	D	104[B]	LEU	CB-CG-CD2	5.48	120.31	111.00
1	A	85	LEU	CB-CG-CD1	5.47	120.30	111.00
1	A	169	LEU	CB-CG-CD2	5.35	120.10	111.00
1	B	85	LEU	CB-CG-CD1	5.34	120.08	111.00
1	D	166	TYR	CG-CD1-CE1	5.26	125.51	121.30
1	C	105	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	D	100	LEU	CA-CB-CG	5.26	127.39	115.30
1	B	113	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	C	138	MET	CA-CB-CG	5.22	122.17	113.30
1	A	86	TYR	CB-CG-CD2	5.18	124.11	121.00
1	B	114	PHE	CB-CG-CD1	5.18	124.42	120.80
1	B	172	LEU	CB-CA-C	5.18	120.03	110.20
1	D	86	TYR	CD1-CE1-CZ	5.17	124.45	119.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	85	LEU	CB-CG-CD1	5.13	119.72	111.00
1	B	85	LEU	CB-CG-CD2	-5.13	102.28	111.00
1	C	49	VAL	CG1-CB-CG2	5.12	119.09	110.90
1	B	163	GLU	OE1-CD-OE2	5.12	129.44	123.30
1	C	32	LEU	CD1-CG-CD2	5.08	125.75	110.50
1	A	104	LEU	CB-CG-CD2	5.08	119.64	111.00
1	A	86	TYR	CD1-CE1-CZ	5.08	124.37	119.80
1	B	47	GLU	CA-CB-CG	5.06	124.53	113.40
1	A	70	LEU	CA-CB-CG	5.04	126.89	115.30
1	B	169	LEU	CB-CG-CD2	5.00	119.51	111.00
1	C	114	PHE	CB-CG-CD1	5.00	124.30	120.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	169	LEU	Mainchain
1	C	169	LEU	Mainchain
1	D	166	TYR	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	1333	0	1331	23	0
1	B	1322	0	1323	27	0
1	C	1349	0	1346	34	0
1	D	1321	0	1325	18	0
2	A	116	0	0	2	0
2	B	126	0	0	11	0
2	C	124	0	0	15	0
2	D	112	0	0	5	0
All	All	5803	0	5325	93	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 9.

All (93) 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:91[B]:GLN:OE1	2:B:201:HOH:O	1.68	1.11
1:C:91[B]:GLN:NE2	2:C:201:HOH:O	1.87	1.08
1:B:87:GLN:O	1:B:91[A]:GLN:HG2	1.70	0.91
1:D:91[B]:GLN:OE1	2:D:201:HOH:O	1.89	0.89
1:B:14:PHE:CE2	1:B:172:LEU:HD12	2.08	0.89
1:D:35[A]:LYS:HG3	2:D:234:HOH:O	1.73	0.86
1:B:35[A]:LYS:HG3	2:B:238:HOH:O	1.78	0.83
1:C:35[A]:LYS:HG3	2:C:225:HOH:O	1.80	0.82
1:C:79[B]:LEU:HD11	1:C:168:VAL:HG21	1.62	0.80
1:B:14:PHE:CZ	1:B:172:LEU:HD12	2.16	0.80
1:D:23[B]:ARG:NH2	2:D:202:HOH:O	2.05	0.80
1:D:79[B]:LEU:HD11	1:D:168:VAL:HG11	1.63	0.79
1:D:87:GLN:O	1:D:91[A]:GLN:HG3	1.84	0.77
1:B:23[A]:ARG:NH1	2:B:204:HOH:O	2.16	0.76
1:A:91[A]:GLN:OE1	2:A:201:HOH:O	2.04	0.75
1:C:134:THR:HG22	1:C:136:GLY:H	1.50	0.75
1:A:109[B]:LEU:HG	1:C:109[B]:LEU:HD21	1.68	0.75
1:C:19:LEU:O	1:C:23[B]:ARG:HG3	1.92	0.69
1:C:35[B]:LYS:HG2	1:C:100:LEU:CD1	2.23	0.69
1:C:35[B]:LYS:HG2	1:C:100:LEU:HD13	1.75	0.68
1:B:79[B]:LEU:HD11	1:B:168:VAL:HG11	1.76	0.68
1:B:35[A]:LYS:HE2	2:B:238:HOH:O	1.93	0.67
1:A:109[B]:LEU:HD21	1:C:109[B]:LEU:HG	1.76	0.65
1:C:28:ASP:OD1	2:C:203:HOH:O	2.15	0.64
1:C:167:ARG:HB2	2:C:208:HOH:O	1.97	0.64
1:A:79[B]:LEU:HD11	1:A:168:VAL:HG11	1.80	0.63
1:D:125:LEU:HD11	1:D:172:LEU:HD12	1.81	0.63
1:A:65:CYS:O	1:A:70:LEU:HD22	1.99	0.62
1:B:134:THR:HG22	1:B:136:GLY:H	1.64	0.62
1:C:28:ASP:OD2	1:C:110:ASP:OD2	2.19	0.60
1:A:46[B]:GLU:HA	1:A:46[B]:GLU:OE1	2.01	0.60
1:B:17:LYS:NZ	2:B:208:HOH:O	2.34	0.60
1:A:95:GLY:HA2	1:A:104:LEU:HD12	1.84	0.59
1:B:121:GLN:NE2	2:B:202:HOH:O	2.08	0.59
1:C:17:LYS:NZ	2:C:205:HOH:O	2.30	0.59
1:C:95:GLY:HA2	1:C:104:LEU:HD12	1.84	0.59
1:B:28:ASP:OD2	1:B:110:ASP:OD2	2.21	0.58
1:A:125:LEU:HD11	1:A:172:LEU:HD12	1.85	0.58
1:D:35[A]:LYS:HE2	2:D:234:HOH:O	2.01	0.58
1:C:171:HIS:CE1	2:C:265:HOH:O	2.58	0.57
1:A:28:ASP:OD2	1:A:110:ASP:OD2	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79[B]:LEU:CD1	1:D:168:VAL:HG11	2.32	0.57
1:D:28:ASP:OD2	1:D:110:ASP:OD2	2.23	0.56
1:C:121:GLN:NE2	2:C:202:HOH:O	2.14	0.56
1:D:87:GLN:O	1:D:91[A]:GLN:CG	2.52	0.56
1:B:79[B]:LEU:CD1	1:B:168:VAL:HG11	2.38	0.54
1:B:87:GLN:HG2	2:B:203:HOH:O	2.06	0.54
1:A:109[B]:LEU:CD2	1:C:109[B]:LEU:HG	2.37	0.54
1:C:23[B]:ARG:NH2	2:C:206:HOH:O	2.31	0.54
1:C:168:VAL:N	2:C:208:HOH:O	2.40	0.53
1:C:125:LEU:HD11	1:C:172:LEU:HD23	1.91	0.53
1:B:46[B]:GLU:OE1	1:B:46[B]:GLU:HA	2.09	0.53
1:A:166:TYR:CE2	1:B:166:TYR:CE2	2.97	0.53
1:B:46[B]:GLU:OE1	1:B:46[B]:GLU:CA	2.57	0.52
1:A:79[B]:LEU:CD1	1:A:168:VAL:HG11	2.40	0.52
1:A:109[B]:LEU:HG	1:C:109[B]:LEU:CD2	2.38	0.51
1:D:96:ILE:HG13	1:D:104[B]:LEU:HD11	1.92	0.51
1:C:64:SER:HB3	1:C:71:GLN:HG3	1.91	0.51
1:B:94:GLU:HG3	2:B:307:HOH:O	2.11	0.51
1:C:35[A]:LYS:HE2	2:C:225:HOH:O	2.11	0.50
1:A:129:PRO:HG2	1:C:129:PRO:HG2	1.94	0.50
1:B:87:GLN:NE2	2:B:203:HOH:O	2.13	0.50
1:A:65:CYS:N	1:A:66:PRO:CD	2.75	0.49
1:A:119:TRP:CZ3	1:C:80:HIS:HE1	2.30	0.49
1:A:91[A]:GLN:HB2	1:A:91[A]:GLN:HE21	1.48	0.48
1:C:35[B]:LYS:HG2	1:C:100:LEU:HD11	1.96	0.48
1:A:166:TYR:HE2	1:B:166:TYR:CE2	2.33	0.47
1:A:147:ARG:NH1	2:A:204:HOH:O	2.42	0.47
1:D:11:SER:HB3	1:D:14:PHE:HB3	1.97	0.46
1:B:91[A]:GLN:NE2	2:B:201:HOH:O	2.48	0.46
1:C:171:HIS:HE1	2:C:265:HOH:O	1.97	0.46
1:C:23[A]:ARG:HG3	2:C:270:HOH:O	2.16	0.46
1:C:11:SER:HB2	2:C:202:HOH:O	2.16	0.46
1:D:96:ILE:CG1	1:D:104[B]:LEU:HD11	2.45	0.46
1:B:159[B]:GLN:HG2	2:B:237:HOH:O	2.16	0.46
1:C:23[B]:ARG:HG2	2:C:270:HOH:O	2.14	0.46
1:B:72:LEU:HD11	1:B:172:LEU:CD2	2.46	0.45
1:B:95:GLY:HA2	1:B:104:LEU:HD12	1.97	0.45
1:C:168:VAL:HG22	2:C:208:HOH:O	2.17	0.44
1:D:95:GLY:HA2	1:D:104[A]:LEU:HD12	1.98	0.44
1:B:72:LEU:HD11	1:B:172:LEU:HD21	1.99	0.44
1:C:138:MET:HB2	1:C:138:MET:HE3	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:46:GLU:HG2	2:D:227:HOH:O	2.18	0.42
1:A:125:LEU:HD11	1:A:172:LEU:CD1	2.49	0.42
1:D:50:LEU:HD23	1:D:50:LEU:HA	1.88	0.42
1:C:32:LEU:CD1	1:C:100:LEU:HD12	2.50	0.42
1:B:14:PHE:CZ	1:B:172:LEU:CD1	2.98	0.41
1:D:172:LEU:HD13	1:D:172:LEU:HA	1.75	0.41
1:C:50:LEU:HA	1:C:50:LEU:HD23	1.86	0.41
1:A:166:TYR:CE2	1:B:166:TYR:HE2	2.38	0.41
1:A:46[B]:GLU:CA	1:A:46[B]:GLU:OE1	2.69	0.41
1:D:19:LEU:O	1:D:23[B]:ARG:HG3	2.21	0.41
1:A:11:SER:HB3	1:A:14:PHE:HB3	2.02	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	173/163 (106%)	167 (96%)	5 (3%)	1 (1%)	25	8
1	B	172/163 (106%)	168 (98%)	3 (2%)	1 (1%)	25	8
1	C	175/163 (107%)	170 (97%)	5 (3%)	0	100	100
1	D	172/163 (106%)	167 (97%)	4 (2%)	1 (1%)	25	8
All	All	692/652 (106%)	672 (97%)	17 (2%)	3 (0%)	29	16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	TYR
1	D	166	TYR
1	B	166	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	144/132 (109%)	137 (95%)	7 (5%)	25	5
1	B	143/132 (108%)	133 (93%)	10 (7%)	15	2
1	C	146/132 (111%)	138 (94%)	8 (6%)	21	4
1	D	143/132 (108%)	136 (95%)	7 (5%)	25	5
All	All	576/528 (109%)	544 (94%)	32 (6%)	25	4

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46[A]	GLU
1	A	46[B]	GLU
1	A	50	LEU
1	A	67	SER
1	A	68	GLN
1	A	70	LEU
1	A	104	LEU
1	B	23[A]	ARG
1	B	23[B]	ARG
1	B	34	GLU
1	B	41	LYS
1	B	47	GLU
1	B	50	LEU
1	B	68	GLN
1	B	91[A]	GLN
1	B	91[B]	GLN
1	B	104	LEU
1	C	34	GLU
1	C	46[A]	GLU
1	C	46[B]	GLU
1	C	67	SER
1	C	68	GLN
1	C	71	GLN
1	C	104	LEU

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Mol	Chain	Res	Type
1	C	172	LEU
1	D	67	SER
1	D	68	GLN
1	D	70	LEU
1	D	91[A]	GLN
1	D	91[B]	GLN
1	D	104[A]	LEU
1	D	104[B]	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	26	GLN
1	A	171	HIS
1	B	21	GLN
1	B	26	GLN
1	C	21	GLN
1	C	26	GLN
1	D	21	GLN
1	D	26	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	163/163 (100%)	-0.27	4 (2%) 57 58	17, 30, 49, 89	0
1	B	163/163 (100%)	-0.32	5 (3%) 49 49	17, 30, 50, 80	0
1	C	163/163 (100%)	-0.24	6 (3%) 41 41	17, 30, 48, 82	0
1	D	163/163 (100%)	-0.33	5 (3%) 49 49	17, 29, 50, 86	0
All	All	652/652 (100%)	-0.29	20 (3%) 49 49	17, 30, 50, 89	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	69	ALA	7.5
1	B	69	ALA	5.4
1	C	69	ALA	4.6
1	D	69	ALA	4.2
1	C	67	SER	4.2
1	A	68	GLN	3.2
1	D	68	GLN	3.0
1	C	66	PRO	2.9
1	C	166	TYR	2.9
1	D	67	SER	2.8
1	B	167	ARG	2.4
1	B	68	GLN	2.4
1	C	168	VAL	2.3
1	D	173	GLY	2.3
1	D	166	TYR	2.2
1	A	67	SER	2.2
1	B	67	SER	2.2
1	B	173	GLY	2.1
1	A	166	TYR	2.1
1	C	68	GLN	2.1

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 carbohydrates 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.