



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:58 PM UTC

PDB ID : 8CN6 / pdb_00008cn6
Title : CD59 in complex with CP-06 peptide
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Bubeck, D.; Tate, E.
Deposited on : 2023-02-22
Resolution : 2.43 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

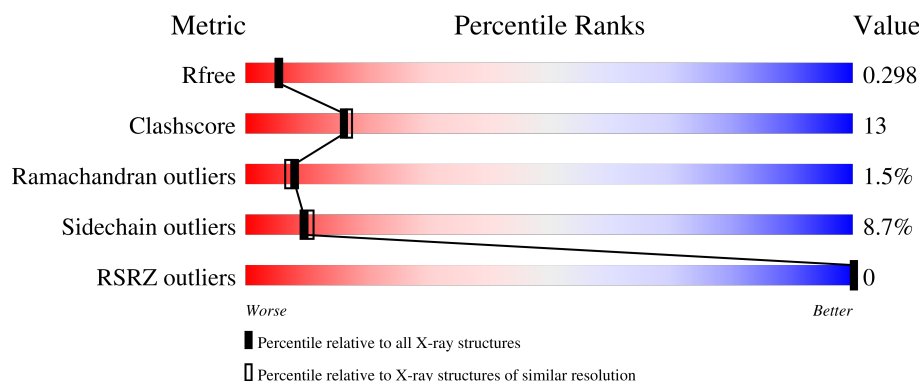
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	77	 66% 26% 6% .
1	B	77	 82% 14% . .
1	C	77	 73% 19% 6% .
1	D	77	 81% 18% .
1	E	77	 71% 19% 6% . .

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Mol	Chain	Length	Quality of chain
1	F	77	
2	G	16	
2	H	16	
2	J	16	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	DAR	J	13	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7804 atoms, of which 3741 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 CD59 glycoprotein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	77	Total	C	H	N	O	S	14	0	0
			1198	385	577	104	121	11			
1	B	76	Total	C	H	N	O	S	14	0	0
			1183	380	571	103	118	11			
1	C	76	Total	C	H	N	O	S	14	0	0
			1183	380	571	103	118	11			
1	D	77	Total	C	H	N	O	S	14	0	0
			1198	385	577	104	121	11			
1	E	76	Total	C	H	N	O	S	14	0	0
			1183	380	571	103	118	11			
1	F	77	Total	C	H	N	O	S	18	0	0
			1172	379	559	102	121	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P13987
B	0	MET	-	initiating methionine	UNP P13987
C	0	MET	-	initiating methionine	UNP P13987
D	0	MET	-	initiating methionine	UNP P13987
E	0	MET	-	initiating methionine	UNP P13987
F	0	MET	-	initiating methionine	UNP P13987

- Molecule 2 is a protein called Cyclic peptide CP-06.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	J	16	Total	C	H	N	O	S	5	0	1
			225	74	105	24	21	1			
2	G	16	Total	C	H	N	O	S	5	0	1
			225	74	105	24	21	1			
2	H	16	Total	C	H	N	O	S	5	0	1
			225	74	105	24	21	1			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Zn 1	0	0
3	F	1	Total 1	Zn 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	O 1	0	0
4	B	3	Total 3	O 3	0	0
4	C	3	Total 3	O 3	0	0
4	E	1	Total 1	O 1	0	0
4	F	1	Total 1	O 1	0	0
4	H	1	Total 1	O 1	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.

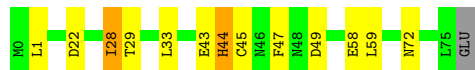
- Molecule 1: CD59 glycoprotein

Chain A: 



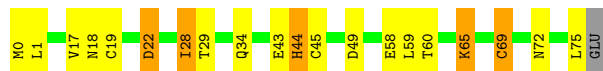
- Molecule 1: CD59 glycoprotein

Chain B: 



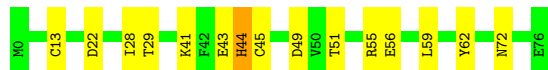
- Molecule 1: CD59 glycoprotein

Chain C: 



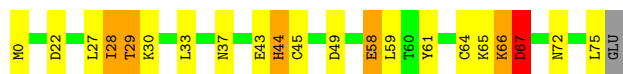
- Molecule 1: CD59 glycoprotein

Chain D: 



- Molecule 1: CD59 glycoprotein

Chain E: 

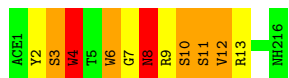
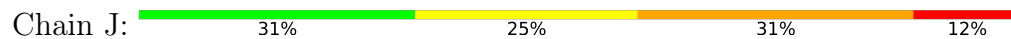


- Molecule 1: CD59 glycoprotein

Chain F: 



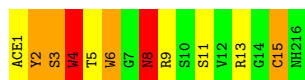
- Molecule 2: Cyclic peptide CP-06



- Molecule 2: Cyclic peptide CP-06



- Molecule 2: Cyclic peptide CP-06



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	30.94Å 85.88Å 96.57Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	48.33 – 2.43 48.33 – 2.43	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.33-2.43) 98.8 (48.33-2.43)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.235 , 0.298 0.234 , 0.298	Depositor DCC
R_{free} test set	969 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.408 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7804	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.75% 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: NH2, ACE, DCY, ZN, DAR, DSN

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	0.82	1/633 (0.2%)	1.53	9/856 (1.1%)
1	B	1.02	4/624 (0.6%)	1.62	12/844 (1.4%)
1	C	0.85	1/624 (0.2%)	1.57	10/844 (1.2%)
1	D	0.83	1/633 (0.2%)	1.48	7/856 (0.8%)
1	E	1.09	5/624 (0.8%)	1.68	15/844 (1.8%)
1	F	0.88	1/625 (0.2%)	1.75	18/848 (2.1%)
2	G	0.74	0/79	2.12	5/106 (4.7%)
2	H	0.72	0/79	3.01	7/106 (6.6%)
2	J	1.38	1/79 (1.3%)	2.06	3/106 (2.8%)
All	All	0.92	14/4000 (0.3%)	1.67	86/5410 (1.6%)

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
2	G	0	2
2	H	0	3
2	J	0	4
All	All	0	9

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	44	HIS	CB-CG	10.05	1.64	1.50
1	E	44	HIS	CD2-NE2	9.27	1.48	1.37
1	B	44	HIS	CB-CG	8.90	1.62	1.50
1	B	44	HIS	CD2-NE2	8.55	1.47	1.37
1	B	44	HIS	ND1-CE1	8.03	1.40	1.32
1	E	44	HIS	ND1-CE1	8.02	1.40	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	44	HIS	CB-CG	7.89	1.61	1.50
1	F	44	HIS	CB-CG	7.84	1.61	1.50
1	E	44	HIS	CG-CD2	7.26	1.43	1.35
1	B	44	HIS	CG-CD2	7.20	1.43	1.35
1	D	44	HIS	CB-CG	7.01	1.59	1.50
2	J	6	TRP	C-O	-6.60	1.15	1.23
1	A	44	HIS	CB-CG	6.57	1.59	1.50
1	E	44	HIS	CA-CB	5.27	1.60	1.53

All (86) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	44	HIS	CA-CB-CG	16.48	130.28	113.80
1	B	44	HIS	CA-CB-CG	14.42	128.22	113.80
1	F	44	HIS	CA-CB-CG	14.24	128.04	113.80
1	C	44	HIS	CA-CB-CG	12.90	126.70	113.80
1	A	44	HIS	CA-CB-CG	12.61	126.41	113.80
1	D	44	HIS	CA-CB-CG	12.44	126.24	113.80
2	H	8	ASN	CA-CB-CG	-11.82	100.78	112.60
1	E	44	HIS	CB-CA-C	10.96	128.67	111.02
1	B	44	HIS	CB-CA-C	10.92	128.96	110.94
2	G	8	ASN	CB-CA-C	-10.87	89.45	110.10
2	H	4	TRP	CA-CB-CG	10.61	133.76	113.60
1	F	58	GLU	CB-CG-CD	10.31	130.12	112.60
1	F	44	HIS	CB-CA-C	10.30	127.94	110.94
1	C	44	HIS	CB-CA-C	10.14	127.35	111.02
1	D	44	HIS	CB-CA-C	9.74	126.71	111.02
1	A	44	HIS	CB-CA-C	9.56	126.42	111.02
1	B	22	ASP	CA-CB-CG	9.37	121.97	112.60
2	H	8	ASN	CB-CA-C	-9.28	92.46	110.10
1	C	45	CYS	CB-CA-C	-9.15	97.75	112.03
1	E	44	HIS	CB-CG-ND1	8.85	135.97	122.70
1	F	45	CYS	CB-CA-C	-8.64	97.17	111.68
2	H	2	TYR	CB-CA-C	8.59	126.43	110.10
1	D	45	CYS	CB-CA-C	-8.51	98.76	112.03
1	E	45	CYS	CB-CA-C	-8.49	97.41	111.68
2	H	4	TRP	N-CA-CB	-8.48	96.16	110.49
1	C	22	ASP	CA-CB-CG	8.40	121.00	112.60
2	H	6	TRP	N-CA-C	-8.40	96.22	109.23
1	A	45	CYS	CB-CA-C	-8.34	97.67	111.68
1	E	44	HIS	ND1-CG-CD2	-8.32	97.78	106.10
1	F	22	ASP	CA-CB-CG	7.74	120.33	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	67	ASP	CA-CB-CG	7.59	120.19	112.60
1	B	45	CYS	CB-CA-C	-7.47	100.38	112.03
2	H	4	TRP	N-CA-C	-7.18	95.52	110.80
1	F	76	GLU	CB-CG-CD	7.06	124.61	112.60
1	E	67	ASP	CA-CB-CG	7.01	119.61	112.60
1	B	44	HIS	ND1-CG-CD2	-6.98	99.12	106.10
1	E	58	GLU	CB-CG-CD	6.89	124.32	112.60
1	C	49	ASP	CA-CB-CG	6.88	119.48	112.60
1	F	57	ASN	CA-CB-CG	6.87	119.47	112.60
2	G	8	ASN	N-CA-C	6.83	130.11	111.00
1	E	44	HIS	CG-CD2-NE2	6.78	113.98	107.20
1	F	49	ASP	CA-CB-CG	6.71	119.31	112.60
1	B	49	ASP	CA-CB-CG	6.62	119.22	112.60
1	E	44	HIS	N-CA-C	-6.58	104.56	112.59
1	E	22	ASP	CA-CB-CG	6.50	119.10	112.60
1	F	44	HIS	N-CA-C	-6.49	105.33	112.72
2	G	7	GLY	N-CA-C	6.47	120.27	110.18
1	B	1	LEU	N-CA-CB	-6.34	100.30	110.63
1	C	58	GLU	CB-CG-CD	6.31	123.32	112.60
1	E	49	ASP	CA-CB-CG	6.25	118.85	112.60
1	B	44	HIS	N-CA-C	-6.22	105.62	112.72
1	B	44	HIS	CG-CD2-NE2	6.18	113.38	107.20
1	F	56	GLU	CA-C-N	6.16	131.00	120.71
1	F	56	GLU	C-N-CA	6.16	131.00	120.71
2	J	4	TRP	CA-CB-CG	6.16	125.30	113.60
1	A	67	ASP	CB-CA-C	6.15	119.49	109.90
1	A	49	ASP	CB-CA-C	6.03	120.80	110.79
1	C	44	HIS	N-CA-C	-5.84	105.46	112.59
1	D	49	ASP	CB-CA-C	5.76	120.36	110.79
1	A	12	ASP	CA-CB-CG	5.75	118.35	112.60
1	E	49	ASP	CB-CA-C	5.72	120.58	110.85
1	C	49	ASP	CB-CA-C	5.64	120.45	110.85
1	F	44	HIS	ND1-CG-CD2	-5.63	100.47	106.10
1	A	58	GLU	CB-CG-CD	5.59	122.10	112.60
1	B	49	ASP	CB-CA-C	5.58	120.05	110.79
1	E	29	THR	OG1-CB-CG2	-5.55	98.20	109.30
1	A	44	HIS	N-CA-C	-5.49	105.89	112.59
1	D	49	ASP	CA-CB-CG	5.48	118.08	112.60
2	J	2	TYR	CA-C-O	5.44	130.05	120.80
1	B	44	HIS	CE1-NE2-CD2	-5.42	103.58	109.00
1	D	44	HIS	CB-CG-ND1	5.35	130.73	122.70
2	G	3	SER	N-CA-C	5.35	122.20	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	64	CYS	CA-CB-SG	-5.33	102.14	114.40
1	F	18	ASN	CA-CB-CG	5.32	117.92	112.60
1	A	44	HIS	CB-CG-ND1	5.27	130.61	122.70
1	D	44	HIS	N-CA-C	-5.26	106.18	112.59
2	J	4	TRP	N-CA-CB	-5.23	101.66	110.49
1	B	58	GLU	CB-CG-CD	5.22	121.48	112.60
1	F	57	ASN	CB-CA-C	5.22	119.56	110.79
1	C	44	HIS	CB-CG-ND1	5.18	130.48	122.70
1	E	65	LYS	N-CA-CB	-5.17	102.67	111.20
2	G	8	ASN	CA-CB-CG	-5.13	107.47	112.60
1	F	44	HIS	CB-CG-ND1	5.05	130.28	122.70
1	E	44	HIS	CE1-NE2-CD2	-5.03	103.97	109.00
1	C	44	HIS	ND1-CG-CD2	-5.02	101.08	106.10
1	F	49	ASP	CB-CA-C	5.02	119.38	110.85

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	2	TYR	Peptide
2	G	8	ASN	Peptide
2	H	2	TYR	Peptide
2	H	8	ASN	Peptide
2	H	9	DAR	Peptide
2	J	10	DSN	Peptide
2	J	11	DSN	Peptide
2	J	4	TRP	Peptide
2	J	8	ASN	Peptide

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	621	577	576	22	0
1	B	612	571	570	5	0
1	C	612	571	570	11	0
1	D	621	577	576	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	612	571	570	13	0
1	F	613	559	554	18	0
2	G	120	105	101	9	0
2	H	120	105	102	10	0
2	J	120	105	101	17	0
3	C	1	0	0	0	0
3	F	1	0	0	0	0
4	A	1	0	0	0	0
4	B	3	0	0	1	0
4	C	3	0	0	1	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
All	All	4063	3741	3720	102	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 13.

All (102) 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:E:66:LYS:O	1:E:67:ASP:HB2	1.62	0.98
1:F:66:LYS:O	1:F:67:ASP:HB2	1.67	0.94
2:J:9:DAR:C	2:J:10:DSN:OG	2.14	0.92
1:F:0:MET:O	1:F:0:MET:SD	2.36	0.83
1:A:27:LEU:HD11	1:A:29:THR:CG2	2.09	0.83
2:J:6:TRP:O	2:J:12:VAL:HG12	1.78	0.82
1:E:27:LEU:HD11	1:E:29:THR:CG2	2.11	0.81
2:J:4:TRP:HB3	2:J:13:DAR:HH12	1.54	0.71
1:F:60:THR:HG22	2:H:8:ASN:OD1	1.92	0.70
2:J:4:TRP:CD1	2:J:13:DAR:HH12	2.10	0.69
1:C:0:MET:HE2	1:C:18:ASN:HB3	1.73	0.69
1:D:62:TYR:HD1	2:H:13:DAR:HB2	1.60	0.66
1:A:22:ASP:OD2	1:A:23:PHE:CD2	2.49	0.66
2:J:6:TRP:O	2:J:12:VAL:CG1	2.44	0.64
1:A:61:TYR:CZ	2:G:14:GLY:HA3	2.34	0.62
2:G:8:ASN:HB3	2:G:9:DAR:HA	1.81	0.62
1:D:55:ARG:HG3	1:D:55:ARG:HH11	1.65	0.62
1:A:22:ASP:OD2	1:A:23:PHE:CE2	2.52	0.62
1:A:55:ARG:HH11	1:A:55:ARG:HG3	1.64	0.61
2:G:8:ASN:O	2:G:9:DAR:HB2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LYS:HG2	1:A:35:VAL:HG22	1.83	0.60
1:A:1:LEU:HD11	1:A:26:CYS:SG	2.41	0.60
2:H:3:SER:HA	2:H:15:DCY:SG	2.41	0.60
2:G:8:ASN:O	2:G:9:DAR:CB	2.49	0.59
2:J:4:TRP:HB3	2:J:13:DAR:NH1	2.15	0.59
1:A:1:LEU:CD1	1:A:3:CYS:SG	2.91	0.58
1:F:64:CYS:SG	1:F:65:LYS:N	2.70	0.57
1:C:43:GLU:OE1	1:C:44:HIS:NE2	2.38	0.56
1:C:60:THR:HG22	2:G:8:ASN:OD1	2.04	0.56
2:G:8:ASN:HB2	2:G:10:DSN:HA	1.86	0.56
1:D:43:GLU:OE2	1:D:44:HIS:NE2	2.39	0.56
1:B:43:GLU:OE2	1:B:44:HIS:NE2	2.39	0.55
1:A:0:MET:N	1:F:34:GLN:OE1	2.28	0.55
2:H:4:TRP:CH2	2:H:13:DAR:NH1	2.74	0.55
1:A:1:LEU:HD13	1:A:3:CYS:SG	2.47	0.55
1:A:43:GLU:OE2	1:A:44:HIS:NE2	2.40	0.55
1:A:22:ASP:OD1	1:A:41:LYS:HE3	2.07	0.55
1:F:43:GLU:OE2	1:F:44:HIS:NE2	2.40	0.55
1:C:75:LEU:C	4:C:203:HOH:O	2.51	0.54
1:E:28:ILE:CD1	1:E:72:ASN:HA	2.38	0.54
1:E:43:GLU:OE2	1:E:44:HIS:NE2	2.41	0.53
1:E:66:LYS:O	1:E:67:ASP:CB	2.44	0.53
1:F:75:LEU:O	1:F:76:GLU:C	2.51	0.53
1:A:59:LEU:C	1:A:59:LEU:HD12	2.34	0.53
1:C:59:LEU:HD12	1:C:59:LEU:C	2.33	0.53
1:F:59:LEU:C	1:F:59:LEU:HD12	2.34	0.53
1:E:58:GLU:HG2	2:J:9:DAR:NH2	2.24	0.53
1:E:59:LEU:C	1:E:59:LEU:HD12	2.34	0.52
2:H:1:ACE:H3	2:H:15:DCY:C	2.39	0.52
1:B:28:ILE:CD1	1:B:72:ASN:HA	2.40	0.52
1:E:27:LEU:HD11	1:E:29:THR:HG22	1.91	0.52
1:E:64:CYS:CB	2:J:3:SER:HB3	2.40	0.52
2:J:4:TRP:CB	2:J:13:DAR:HH12	2.21	0.52
1:F:31:ALA:O	1:F:34:GLN:NE2	2.44	0.51
1:D:59:LEU:C	1:D:59:LEU:HD12	2.35	0.51
2:H:8:ASN:HB2	2:H:11:DSN:HA	1.92	0.51
2:J:4:TRP:CD1	2:J:13:DAR:NH1	2.77	0.51
2:J:4:TRP:HD1	2:J:13:DAR:NH1	2.09	0.51
1:B:59:LEU:C	1:B:59:LEU:HD12	2.36	0.51
1:E:30:LYS:HE3	1:E:75:LEU:HD12	1.93	0.50
1:F:28:ILE:CD1	1:F:72:ASN:HA	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:HD11	1:A:29:THR:HG22	1.90	0.49
2:G:8:ASN:HB2	2:G:11:DSN:HA	1.95	0.48
1:C:69:CYS:O	1:C:69:CYS:SG	2.68	0.48
2:J:4:TRP:HD1	2:J:13:DAR:HH12	1.58	0.48
1:C:28:ILE:CD1	1:C:72:ASN:HA	2.44	0.47
2:J:4:TRP:CG	2:J:13:DAR:HH12	2.32	0.47
1:F:61:TYR:O	2:H:6:TRP:HA	2.14	0.47
1:A:28:ILE:CD1	1:A:72:ASN:HA	2.45	0.47
1:B:47:PHE:HB2	4:B:103:HOH:O	2.14	0.47
1:D:28:ILE:CD1	1:D:72:ASN:HA	2.45	0.47
1:E:29:THR:HG22	1:E:61:TYR:CB	2.46	0.47
1:A:12:ASP:O	1:A:14:LYS:HD2	2.15	0.46
1:E:28:ILE:HD11	1:E:72:ASN:HA	1.98	0.46
1:C:65:LYS:HE3	1:C:65:LYS:HB2	1.71	0.45
1:A:67:ASP:OD2	1:F:32:GLY:HA3	2.16	0.45
1:F:66:LYS:O	1:F:67:ASP:CB	2.48	0.45
1:C:59:LEU:HD12	1:C:59:LEU:O	2.17	0.44
1:D:62:TYR:CD1	2:H:13:DAR:HB2	2.47	0.44
2:J:6:TRP:O	2:J:12:VAL:HA	2.17	0.44
1:C:1:LEU:CD1	1:C:65:LYS:O	2.66	0.44
1:E:28:ILE:C	1:E:29:THR:CG2	2.91	0.44
1:A:29:THR:HG22	1:A:61:TYR:CB	2.48	0.43
1:A:61:TYR:O	2:G:13:DAR:HB3	2.18	0.43
1:F:63:CYS:O	2:H:4:TRP:HA	2.17	0.43
2:G:8:ASN:CB	2:G:10:DSN:HA	2.49	0.43
2:H:4:TRP:CZ2	2:H:13:DAR:NH1	2.86	0.43
1:F:69:CYS:SG	1:F:70:ASN:N	2.87	0.43
2:J:7:GLY:HA2	2:J:11:DSN:OG	2.19	0.43
1:D:51:THR:HB	1:D:56:GLU:O	2.19	0.42
1:A:51:THR:HB	1:A:56:GLU:O	2.20	0.42
1:F:59:LEU:HD12	1:F:59:LEU:O	2.19	0.41
2:J:7:GLY:CA	2:J:11:DSN:OG	2.68	0.41
1:C:0:MET:HE3	1:C:19:CYS:O	2.21	0.41
1:D:59:LEU:HD12	1:D:59:LEU:O	2.20	0.41
1:A:59:LEU:HD12	1:A:59:LEU:O	2.21	0.41
1:A:28:ILE:C	1:A:29:THR:CG2	2.92	0.41
1:F:28:ILE:HD11	1:F:72:ASN:HA	2.03	0.41
2:J:8:ASN:O	2:J:11:DSN:HB2	2.21	0.41
1:B:28:ILE:HD11	1:B:72:ASN:HA	2.03	0.41
1:D:43:GLU:OE2	1:D:44:HIS:CD2	2.73	0.40
1:F:51:THR:HB	1:F:56:GLU:O	2.21	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	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
1	B	74/77 (96%)	74 (100%)	0	0	100	100
1	C	74/77 (96%)	74 (100%)	0	0	100	100
1	D	75/77 (97%)	73 (97%)	1 (1%)	1 (1%)	9	9
1	E	74/77 (96%)	73 (99%)	0	1 (1%)	9	8
1	F	75/77 (97%)	74 (99%)	0	1 (1%)	9	9
2	G	9/16 (56%)	8 (89%)	0	1 (11%)	0	0
2	H	9/16 (56%)	7 (78%)	1 (11%)	1 (11%)	0	0
2	J	9/16 (56%)	6 (67%)	1 (11%)	2 (22%)	0	0
All	All	474/510 (93%)	462 (98%)	5 (1%)	7 (2%)	8	7

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	67	ASP
1	F	67	ASP
2	J	3	SER
2	J	4	TRP
1	D	13	CYS
2	G	3	SER
2	H	4	TRP

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	72/72 (100%)	68 (94%)	4 (6%)	19	25
1	B	71/72 (99%)	68 (96%)	3 (4%)	26	37
1	C	71/72 (99%)	64 (90%)	7 (10%)	7	7
1	D	72/72 (100%)	69 (96%)	3 (4%)	26	37
1	E	71/72 (99%)	66 (93%)	5 (7%)	14	17
1	F	70/72 (97%)	62 (89%)	8 (11%)	5	5
2	G	7/7 (100%)	3 (43%)	4 (57%)	0	0
2	H	7/7 (100%)	4 (57%)	3 (43%)	0	0
2	J	7/7 (100%)	5 (71%)	2 (29%)	0	0
All	All	448/453 (99%)	409 (91%)	39 (9%)	9	11

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LEU
1	A	12	ASP
1	A	14	LYS
1	A	22	ASP
1	B	28	ILE
1	B	29	THR
1	B	33	LEU
1	C	17	VAL
1	C	22	ASP
1	C	28	ILE
1	C	29	THR
1	C	34	GLN
1	C	65	LYS
1	C	69	CYS
1	D	22	ASP
1	D	29	THR
1	D	41	LYS
1	E	0	MET
1	E	28	ILE
1	E	33	LEU
1	E	37	ASN
1	E	66	LYS
1	F	14	LYS

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Mol	Chain	Res	Type
1	F	22	ASP
1	F	28	ILE
1	F	29	THR
1	F	34	GLN
1	F	57	ASN
1	F	64	CYS
1	F	76	GLU
2	J	8	ASN
2	J	12	VAL
2	G	2	TYR
2	G	3	SER
2	G	5	THR
2	G	12	VAL
2	H	3	SER
2	H	4	TRP
2	H	5	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	37	ASN
1	C	34	GLN
1	C	37	ASN
1	D	37	ASN
1	F	37	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

15 non-standard protein/DNA/RNA residues are 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	DCY	H	15	2	4,5,6	0.98	0	1,5,7	2.36	1 (100%)
2	DCY	J	15	2	4,5,6	0.62	0	1,5,7	1.52	0
2	DCY	G	15	2	4,5,6	0.69	0	1,5,7	1.22	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DCY	H	15	2	-	1/1/4/6	-
2	DCY	J	15	2	-	0/1/4/6	-
2	DCY	G	15	2	-	1/1/4/6	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	15	DCY	CA-CB-SG	-2.36	109.35	114.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	15	DCY	N-CA-CB-SG
2	H	15	DCY	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	15	DCY	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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

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 [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(Å²)	Q<0.9		
1	A	77/77 (100%)	-0.65	0	100	100	56, 74, 104, 121	0
1	B	76/77 (98%)	-0.63	0	100	100	46, 71, 98, 114	0
1	C	76/77 (98%)	-0.49	0	100	100	47, 84, 123, 130	0
1	D	77/77 (100%)	-0.58	0	100	100	51, 72, 102, 105	0
1	E	76/77 (98%)	-0.58	0	100	100	48, 72, 99, 121	0
1	F	77/77 (100%)	-0.51	0	100	100	47, 83, 121, 135	0
2	G	9/16 (56%)	-0.95	0	100	100	53, 64, 86, 109	0
2	H	9/16 (56%)	-0.81	0	100	100	54, 63, 93, 127	0
2	J	9/16 (56%)	-0.51	0	100	100	51, 65, 111, 125	0
All	All	486/510 (95%)	-0.58	0	100	100	46, 75, 112, 135	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	DSN	J	11	6/7	0.96	0.08	30,67,81,132	1
2	DSN	H	10	6/7	0.97	0.06	30,74,82,85	1
2	DAR	H	9	11/12	0.97	0.07	76,85,92,95	0
2	DAR	H	13	11/12	0.97	0.08	51,82,113,116	0
2	DCY	G	15	6/7	0.97	0.05	83,94,104,111	0
2	DCY	H	15	6/7	0.97	0.07	77,91,100,105	0
2	DAR	J	9	11/12	0.98	0.07	87,98,114,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DSN	G	11	6/7	0.98	0.05	30,62,69,69	1
2	DSN	H	11	6/7	0.98	0.05	30,56,62,64	1
2	DAR	J	13	11/12	0.98	0.06	56,69,79,82	0
2	DAR	G	13	11/12	0.98	0.09	61,88,144,147	0
2	DSN	J	10	6/7	0.98	0.06	30,86,102,104	1
2	DSN	G	10	6/7	0.98	0.05	30,67,76,77	1
2	DAR	G	9	11/12	0.98	0.06	59,66,96,101	0
2	DCY	J	15	6/7	0.99	0.04	70,75,85,89	0

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
3	ZN	C	101	1/1	0.99	0.03	93,93,93,93	0
3	ZN	F	101	1/1	1.00	0.02	90,90,90,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.