



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:12 AM GMT

PDB ID : 2G3O
Title : The 2.1Å crystal structure of copGFP
Authors : Wilmann, P.G.
Deposited on : 2006-02-20
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

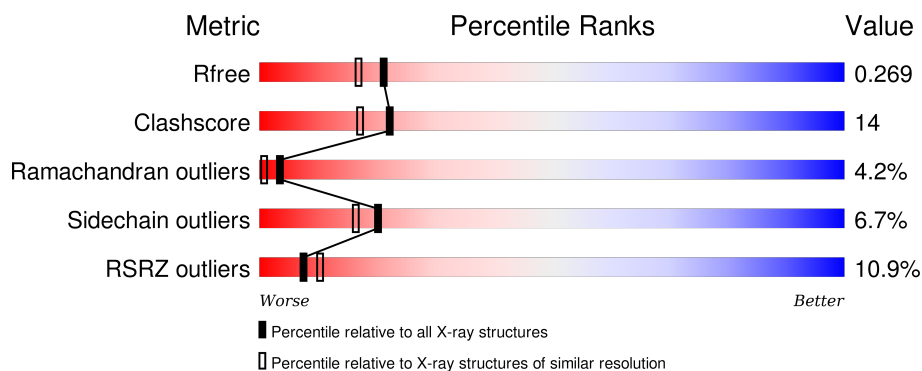
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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. 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	220	<div> <div>5%</div> <div>73% 17% 5% . .</div> </div>
1	B	220	<div> <div>7%</div> <div>75% 16% 5% . .</div> </div>
1	C	220	<div> <div>12%</div> <div>73% 20% . . .</div> </div>
1	D	220	<div> <div>13%</div> <div>76% 17% . . .</div> </div>
1	E	220	<div> <div>12%</div> <div>75% 17% 5% .</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	220	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: red (15%), green (77%), yellow (16%), and grey (5%). The percentages are labeled above or below the segments. The red segment is at the top left, followed by green, then yellow, and finally grey at the bottom right.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9837 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 green fluorescent protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	212	Total	C	N	O	S	0	0	0
			1621	1043	278	292	8			
1	B	213	Total	C	N	O	S	0	0	0
			1609	1034	278	289	8			
1	C	216	Total	C	N	O	S	0	0	0
			1605	1031	269	298	7			
1	D	216	Total	C	N	O	S	0	0	0
			1590	1023	265	295	7			
1	E	216	Total	C	N	O	S	0	0	0
			1603	1031	271	294	7			
1	F	216	Total	C	N	O	S	0	0	0
			1595	1026	267	295	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
A	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12
A	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
B	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
B	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12
B	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
C	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
C	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12
C	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
D	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
D	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12
D	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
E	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
E	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12
E	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
F	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12
F	57	CR2	TYR	CHROMOPHORE	UNP Q6WV12

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Chain	Residue	Modelled	Actual	Comment	Reference
F	57	CR2	GLY	CHROMOPHORE	UNP Q6WV12

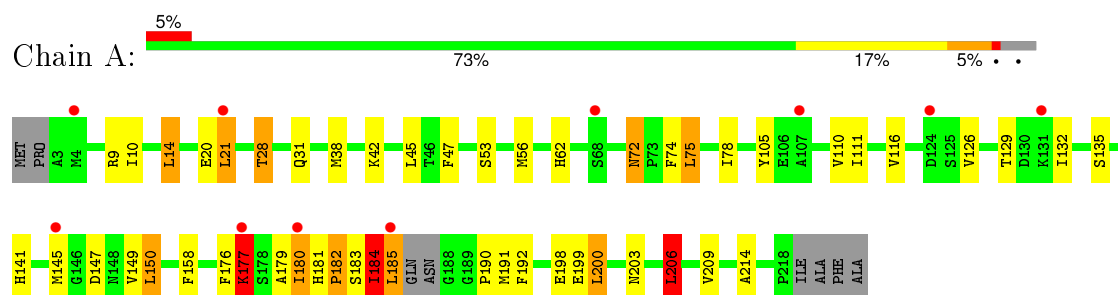
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	47	Total O 47 47	0	0
2	B	47	Total O 47 47	0	0
2	C	29	Total O 29 29	0	0
2	D	40	Total O 40 40	0	0
2	E	16	Total O 16 16	0	0
2	F	35	Total O 35 35	0	0

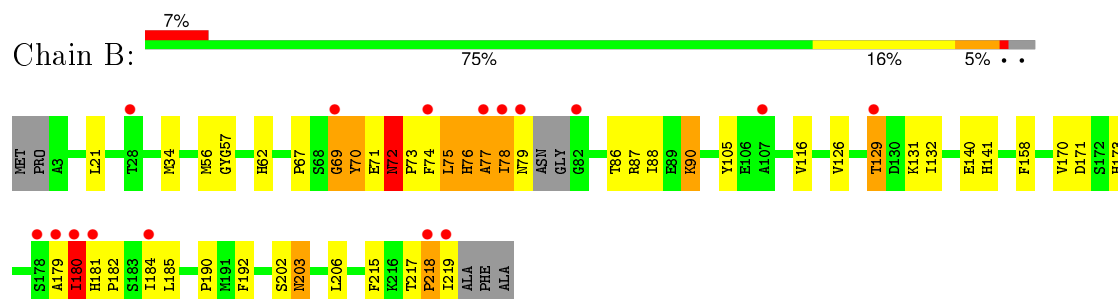
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

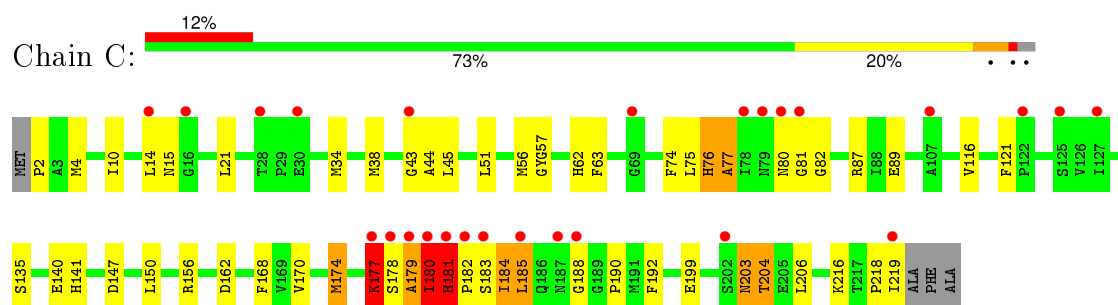
- Molecule 1: green fluorescent protein 2



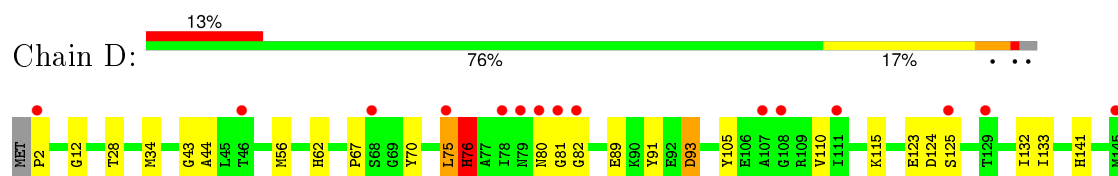
- Molecule 1: green fluorescent protein 2

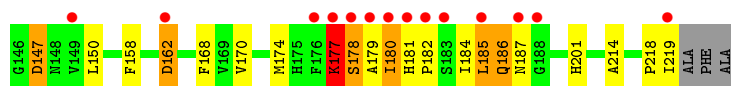


- Molecule 1: green fluorescent protein 2

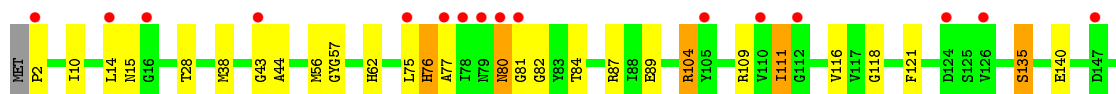
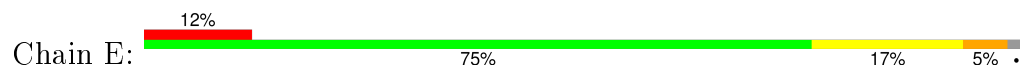


- Molecule 1: green fluorescent protein 2

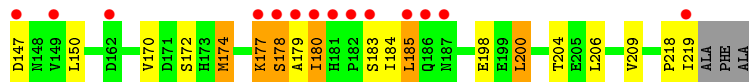
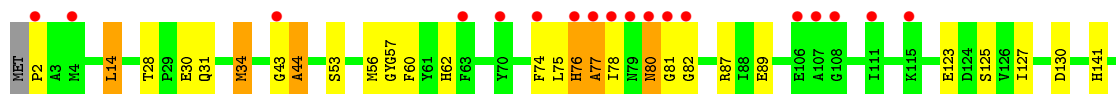
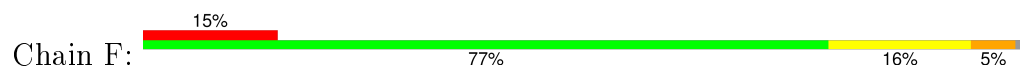




- Molecule 1: green fluorescent protein 2



- Molecule 1: green fluorescent protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	145.95Å 145.95Å 53.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.71 – 2.10 35.71 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (35.71-2.10) 99.5 (35.71-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.230 , 0.272 0.229 , 0.269	Depositor DCC
R_{free} test set	3752 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.136 for -h,-k,l 0.179 for h,-h-k,-l 0.096 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 74388 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9837	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CR2

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	0.54	2/1645 (0.1%)	0.69	3/2225 (0.1%)
1	B	0.48	0/1632	0.69	1/2210 (0.0%)
1	C	0.41	0/1630	0.68	3/2215 (0.1%)
1	D	0.55	3/1614 (0.2%)	0.71	4/2195 (0.2%)
1	E	0.41	0/1627	0.65	2/2210 (0.1%)
1	F	0.49	0/1619	0.65	1/2200 (0.0%)
All	All	0.48	5/9767 (0.1%)	0.68	14/13255 (0.1%)

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	E	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	177	LYS	CE-NZ	8.92	1.71	1.49
1	D	93	ASP	CG-OD2	7.02	1.41	1.25
1	A	185	LEU	C-O	6.09	1.34	1.23
1	D	93	ASP	CG-OD1	5.53	1.38	1.25
1	D	115	LYS	CE-NZ	5.03	1.61	1.49

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	LEU	CA-CB-CG	7.86	133.38	115.30
1	D	93	ASP	CB-CG-OD2	-6.75	112.22	118.30
1	D	2	PRO	N-CA-CB	6.02	110.52	103.30
1	A	200	LEU	CA-CB-CG	5.94	128.96	115.30
1	C	2	PRO	N-CA-CB	5.92	110.40	103.30
1	F	2	PRO	N-CA-CB	5.92	110.40	103.30
1	E	2	PRO	N-CA-CB	5.91	110.39	103.30
1	B	21	LEU	CA-CB-CG	5.68	128.35	115.30
1	D	186	GLN	N-CA-C	5.55	125.99	111.00
1	C	203	ASN	C-N-CA	5.53	135.53	121.70
1	A	206	LEU	CA-CB-CG	5.50	127.94	115.30
1	C	203	ASN	N-CA-C	5.43	125.66	111.00
1	D	75	LEU	CA-CB-CG	5.20	127.25	115.30
1	E	181	HIS	N-CA-C	5.00	124.50	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	180	ILE	Peptide
1	E	180	ILE	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	1621	0	1512	34	0
1	B	1609	0	1480	49	0
1	C	1605	0	1420	48	0
1	D	1590	0	1401	41	0
1	E	1603	0	1430	41	0
1	F	1595	0	1411	41	0
2	A	47	0	0	2	0
2	B	47	0	0	2	0
2	C	29	0	0	1	0
2	D	40	0	0	6	0
2	E	16	0	0	1	0
2	F	35	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9837	0	8654	253	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 14.

All (253) 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:A:177:LYS:CE	1:A:177:LYS:NZ	1.71	1.54
1:B:78:ILE:CB	1:B:79:ASN:HA	1.70	1.19
1:B:181:HIS:HB2	1:B:185:LEU:HG	1.28	1.16
1:F:80:ASN:HB3	1:F:81:GLY:HA2	1.21	1.12
1:D:185:LEU:HA	1:D:187:ASN:H	1.17	1.10
1:B:218:PRO:HB2	1:B:219:ILE:HA	1.13	1.08
1:E:75:LEU:HA	1:E:76:HIS:O	1.57	1.04
1:B:217:THR:HG22	1:B:218:PRO:HA	1.43	1.00
1:B:76:HIS:HA	1:B:78:ILE:HA	1.43	0.99
1:D:75:LEU:HA	1:D:76:HIS:O	1.62	0.97
1:D:185:LEU:HA	1:D:187:ASN:N	1.79	0.96
1:E:180:ILE:HG22	1:E:181:HIS:H	1.34	0.92
1:B:218:PRO:CB	1:B:219:ILE:HA	1.97	0.92
1:C:75:LEU:HA	1:C:76:HIS:O	1.71	0.91
1:E:80:ASN:HA	1:E:179:ALA:HB3	1.52	0.91
1:C:80:ASN:HA	1:C:179:ALA:HB3	1.51	0.89
1:C:180:ILE:HG22	1:C:181:HIS:H	1.37	0.88
1:B:218:PRO:HB2	1:B:219:ILE:CA	2.03	0.84
1:B:76:HIS:HA	1:B:77:ALA:HB3	1.58	0.84
1:C:10:ILE:HD12	1:C:38:MET:HE1	1.59	0.84
1:B:78:ILE:CB	1:B:79:ASN:CA	2.55	0.83
1:C:218:PRO:HA	1:C:219:ILE:CB	2.09	0.82
1:F:80:ASN:HB3	1:F:81:GLY:CA	2.09	0.82
1:F:80:ASN:CB	1:F:81:GLY:HA2	2.09	0.81
1:B:69:GLY:HA2	1:B:70:TYR:O	1.79	0.81
1:A:10:ILE:HD12	1:A:38:MET:HE1	1.62	0.80
1:E:77:ALA:HA	1:E:80:ASN:HB2	1.64	0.79
1:B:56:MET:HE1	1:B:206:LEU:HD23	1.65	0.79
1:E:75:LEU:HA	1:E:76:HIS:C	2.05	0.77
1:F:87:ARG:HD2	1:F:89:GLU:OE2	1.84	0.77
1:E:80:ASN:CB	1:E:81:GLY:HA2	2.16	0.76
1:D:180:ILE:HG22	1:D:181:HIS:H	1.50	0.76
1:D:218:PRO:HA	1:D:219:ILE:CB	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:LEU:HA	1:C:76:HIS:C	2.06	0.75
1:A:75:LEU:O	1:A:78:ILE:HG12	1.85	0.75
1:C:180:ILE:HG22	1:C:181:HIS:N	2.02	0.73
1:E:57:CR2:O2	1:E:87:ARG:NH2	2.22	0.73
1:B:73:PRO:HG3	1:B:184:ILE:HD11	1.71	0.71
1:B:76:HIS:CA	1:B:77:ALA:HB3	2.20	0.71
1:B:57:CR2:O2	1:B:87:ARG:NH2	2.24	0.70
1:D:80:ASN:HA	1:D:179:ALA:HB3	1.71	0.70
1:C:77:ALA:HA	1:C:80:ASN:HB2	1.72	0.70
1:B:217:THR:HG22	1:B:218:PRO:CA	2.21	0.70
1:A:181:HIS:O	1:A:183:SER:N	2.25	0.69
1:D:75:LEU:O	1:D:75:LEU:HD12	1.93	0.69
1:B:76:HIS:CA	1:B:78:ILE:HA	2.22	0.69
1:C:180:ILE:CG2	1:C:181:HIS:N	2.55	0.69
1:B:180:ILE:O	1:B:181:HIS:CD2	2.46	0.69
1:D:56:MET:HE3	1:D:201:HIS:HE1	1.58	0.68
1:C:56:MET:HE1	1:C:206:LEU:HD23	1.77	0.67
1:F:177:LYS:N	1:F:178:SER:O	2.28	0.67
1:A:182:PRO:C	1:A:184:ILE:O	2.34	0.66
1:D:185:LEU:CA	1:D:187:ASN:H	2.02	0.66
1:A:126:VAL:O	1:A:129:THR:HG22	1.95	0.66
1:E:56:MET:HE1	1:E:201:HIS:CE1	2.31	0.66
1:D:80:ASN:HB2	1:D:81:GLY:HA2	1.78	0.66
1:F:177:LYS:HB3	1:F:178:SER:CB	2.26	0.65
1:E:80:ASN:HB3	1:E:81:GLY:HA2	1.78	0.65
1:D:177:LYS:N	2:D:234:HOH:O	2.24	0.65
1:E:180:ILE:CG2	1:E:181:HIS:H	2.10	0.65
1:F:75:LEU:HA	1:F:76:HIS:C	2.17	0.65
1:E:10:ILE:HD12	1:E:38:MET:HE1	1.77	0.64
1:E:180:ILE:HG22	1:E:181:HIS:N	2.11	0.64
1:D:93:ASP:OD2	1:D:125:SER:HB2	1.96	0.64
1:E:87:ARG:HD3	1:E:170:VAL:HG11	1.79	0.63
1:A:180:ILE:HG13	1:A:184:ILE:HG13	1.80	0.63
1:B:218:PRO:HD2	1:B:219:ILE:CB	2.29	0.63
1:D:180:ILE:CG2	1:D:181:HIS:H	2.13	0.62
1:D:177:LYS:HB3	1:D:178:SER:CB	2.31	0.61
1:F:130:ASP:HA	2:F:253:HOH:O	2.00	0.61
1:D:80:ASN:HA	1:D:179:ALA:CB	2.31	0.61
1:B:56:MET:CE	1:B:206:LEU:HD23	2.30	0.60
1:C:147:ASP:HB2	1:C:180:ILE:HD11	1.82	0.60
1:B:87:ARG:HD3	1:B:170:VAL:HG11	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:75:LEU:HA	1:D:76:HIS:C	2.21	0.59
1:E:135:SER:OG	1:E:199:GLU:OE2	2.19	0.59
1:B:217:THR:CG2	1:B:218:PRO:HA	2.26	0.59
1:C:56:MET:HE1	1:C:206:LEU:HB3	1.84	0.59
1:B:202:SER:O	1:B:203:ASN:CB	2.51	0.59
1:A:56:MET:CE	1:A:206:LEU:HD12	2.33	0.59
1:B:76:HIS:CA	1:B:77:ALA:CB	2.80	0.59
1:A:62:HIS:H	1:A:62:HIS:CD2	2.21	0.59
1:E:109:ARG:NH1	1:E:111:ILE:HD12	2.18	0.59
1:D:147:ASP:N	1:D:147:ASP:OD1	2.32	0.58
1:F:74:PHE:O	1:F:77:ALA:HB2	2.04	0.58
1:E:56:MET:HE1	1:E:206:LEU:HB3	1.86	0.58
1:A:183:SER:HA	1:A:184:ILE:C	2.24	0.57
1:D:56:MET:HE3	1:D:201:HIS:CE1	2.38	0.57
1:B:181:HIS:HB3	1:B:184:ILE:HG13	1.84	0.57
1:B:73:PRO:HG3	1:B:184:ILE:CD1	2.34	0.57
1:B:72:ASN:C	1:B:72:ASN:HD22	2.08	0.57
1:E:183:SER:O	1:E:185:LEU:N	2.38	0.57
1:A:72:ASN:C	1:A:72:ASN:HD22	2.07	0.57
1:A:56:MET:HE2	1:A:206:LEU:HD12	1.85	0.57
1:C:21:LEU:HD11	1:C:45:LEU:HD21	1.87	0.56
1:D:56:MET:CE	1:D:201:HIS:CE1	2.88	0.56
1:C:89:GLU:HG2	1:C:170:VAL:HG22	1.87	0.56
1:B:62:HIS:H	1:B:62:HIS:CD2	2.23	0.56
1:F:80:ASN:ND2	1:F:82:GLY:O	2.39	0.56
1:F:62:HIS:CD2	1:F:62:HIS:H	2.22	0.56
1:F:62:HIS:HB3	1:F:75:LEU:HD23	1.86	0.56
1:F:34:MET:HE1	1:F:60:PHE:HB2	1.86	0.56
1:C:80:ASN:CB	1:C:81:GLY:HA2	2.36	0.56
1:C:62:HIS:CD2	1:C:62:HIS:H	2.23	0.56
1:D:180:ILE:HG22	1:D:181:HIS:N	2.18	0.55
1:C:181:HIS:HB3	1:C:182:PRO:O	2.07	0.54
1:A:14:LEU:HD22	1:A:47:PHE:CD2	2.43	0.54
1:E:109:ARG:HH11	1:E:111:ILE:HD12	1.73	0.54
1:D:70:TYR:HA	2:D:251:HOH:O	2.07	0.54
1:A:145:MET:HG2	1:A:149:VAL:HB	1.91	0.53
1:C:183:SER:O	1:C:185:LEU:N	2.41	0.53
1:F:80:ASN:HB3	1:F:82:GLY:HA2	1.91	0.53
1:F:183:SER:C	1:F:185:LEU:H	2.11	0.53
1:E:56:MET:HE3	1:E:208:ILE:HG23	1.90	0.52
1:D:62:HIS:H	1:D:62:HIS:CD2	2.26	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:PHE:HA	2:B:254:HOH:O	2.10	0.52
1:C:141:HIS:CE1	1:C:190:PRO:HB3	2.44	0.52
1:B:180:ILE:O	1:B:181:HIS:CG	2.62	0.52
2:D:235:HOH:O	1:F:141:HIS:HE1	1.91	0.52
1:D:150:LEU:HD13	1:D:181:HIS:CD2	2.46	0.51
1:C:203:ASN:N	1:C:204:THR:OG1	2.42	0.51
1:F:44:ALA:H	1:F:204:THR:HG22	1.74	0.51
1:F:218:PRO:HA	1:F:219:ILE:CB	2.39	0.51
1:C:80:ASN:HD22	1:C:177:LYS:H	1.59	0.51
1:C:141:HIS:HD2	2:C:229:HOH:O	1.94	0.51
1:D:56:MET:CE	1:D:201:HIS:HE1	2.22	0.50
1:C:203:ASN:H	1:C:204:THR:HG1	1.58	0.50
1:F:150:LEU:HB3	1:F:174:MET:HG3	1.93	0.50
1:B:126:VAL:O	1:B:129:THR:HG22	2.11	0.50
1:F:76:HIS:O	1:F:78:ILE:N	2.45	0.50
1:E:62:HIS:H	1:E:62:HIS:CD2	2.30	0.50
1:E:80:ASN:HD21	1:E:176:PHE:HB3	1.76	0.50
1:E:14:LEU:HD12	1:E:118:GLY:HA3	1.93	0.50
1:A:147:ASP:O	1:A:180:ILE:HG12	2.12	0.49
1:A:150:LEU:HD13	1:A:180:ILE:HD12	1.93	0.49
1:F:147:ASP:HB2	1:F:180:ILE:HD12	1.94	0.49
1:E:56:MET:CE	1:E:201:HIS:CE1	2.95	0.49
1:C:177:LYS:HB3	1:C:178:SER:CB	2.43	0.49
1:C:21:LEU:HD21	1:C:206:LEU:HD13	1.94	0.49
1:D:162:ASP:N	1:D:162:ASP:OD2	2.44	0.49
1:D:80:ASN:CB	1:D:81:GLY:HA2	2.41	0.49
1:E:150:LEU:HB3	1:E:174:MET:HG3	1.94	0.49
1:A:181:HIS:C	1:A:183:SER:H	2.14	0.49
1:C:87:ARG:HD2	1:C:89:GLU:OE2	2.12	0.49
1:F:80:ASN:HA	1:F:179:ALA:HB3	1.94	0.48
1:D:132:ILE:HG23	1:D:158:PHE:HB3	1.96	0.48
1:A:141:HIS:CE1	1:A:190:PRO:HB3	2.48	0.47
1:B:69:GLY:HA2	1:B:70:TYR:C	2.34	0.47
1:E:184:ILE:O	1:E:185:LEU:CB	2.62	0.47
1:A:132:ILE:HG23	1:A:158:PHE:HB3	1.95	0.47
1:D:218:PRO:HB3	1:F:218:PRO:HB3	1.97	0.47
1:E:89:GLU:HG2	1:E:170:VAL:HG13	1.96	0.47
1:A:192:PHE:O	1:A:214:ALA:HA	2.14	0.47
1:B:76:HIS:N	1:B:77:ALA:CB	2.77	0.47
1:B:56:MET:HE1	1:B:206:LEU:HB3	1.96	0.47
1:C:180:ILE:HA	1:C:180:ILE:HD13	1.69	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:80:ASN:HB3	2:D:234:HOH:O	2.15	0.47
1:D:81:GLY:HA2	1:D:82:GLY:HA2	1.66	0.47
1:F:150:LEU:O	1:F:174:MET:HG2	2.15	0.47
1:A:135:SER:OG	1:A:199:GLU:OE2	2.32	0.47
1:F:81:GLY:HA2	1:F:82:GLY:HA2	1.63	0.47
1:C:190:PRO:O	1:C:216:LYS:HD3	2.15	0.47
1:E:104:ARG:HG3	1:E:111:ILE:HB	1.97	0.46
1:C:15:ASN:HD21	1:C:121:PHE:HB2	1.79	0.46
1:F:14:LEU:HD21	1:F:127:ILE:CD1	2.45	0.46
1:D:180:ILE:CG2	1:D:181:HIS:N	2.78	0.46
1:A:176:PHE:CD2	1:A:180:ILE:HG22	2.51	0.46
1:B:88:ILE:HG22	1:B:90:LYS:HE2	1.96	0.46
2:A:226:HOH:O	1:B:141:HIS:HE1	1.97	0.46
1:F:200:LEU:N	1:F:200:LEU:HD12	2.31	0.46
1:B:179:ALA:HA	1:B:180:ILE:CB	2.45	0.46
1:C:74:PHE:O	1:C:77:ALA:HB3	2.15	0.46
1:C:56:MET:CE	1:C:206:LEU:HD23	2.46	0.46
1:F:34:MET:CE	1:F:60:PHE:HB2	2.45	0.46
1:D:123:GLU:OE2	1:D:123:GLU:HA	2.16	0.45
1:B:202:SER:O	1:B:203:ASN:HB3	2.15	0.45
1:A:203:ASN:HB2	2:A:247:HOH:O	2.15	0.45
1:B:181:HIS:CB	1:B:185:LEU:HG	2.20	0.45
1:C:218:PRO:CA	1:C:219:ILE:CB	2.90	0.45
1:B:62:HIS:HE1	1:B:105:TYR:OH	1.99	0.45
1:B:76:HIS:N	1:B:77:ALA:HB3	2.32	0.44
1:E:80:ASN:ND2	1:E:178:SER:O	2.50	0.44
1:E:76:HIS:HB3	1:E:77:ALA:H	1.49	0.44
1:A:198:GLU:HB2	1:A:209:VAL:HB	1.99	0.44
1:F:56:MET:HE1	1:F:206:LEU:HD23	1.98	0.44
1:C:38:MET:HE1	1:C:56:MET:HB3	2.00	0.44
1:B:141:HIS:CE1	1:B:190:PRO:HB3	2.53	0.44
1:A:20:GLU:HB3	1:A:42:LYS:HD2	1.99	0.44
1:D:67:PRO:HD3	1:D:214:ALA:O	2.17	0.44
1:F:80:ASN:ND2	1:F:177:LYS:H	2.15	0.44
1:C:184:ILE:O	1:C:185:LEU:CB	2.65	0.44
1:F:75:LEU:HD12	1:F:75:LEU:O	2.18	0.44
1:C:80:ASN:CB	1:C:82:GLY:HA2	2.48	0.44
1:B:71:GLU:O	1:B:72:ASN:CB	2.65	0.44
1:E:84:THR:O	1:E:174:MET:HA	2.17	0.43
1:C:177:LYS:HB3	1:C:178:SER:CA	2.48	0.43
1:B:132:ILE:HG23	1:B:158:PHE:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:TYR:CD2	1:D:110:VAL:HG12	2.52	0.43
1:E:75:LEU:HD12	1:E:75:LEU:O	2.18	0.43
1:C:81:GLY:HA2	1:C:82:GLY:HA2	1.64	0.43
1:B:67:PRO:O	1:B:70:TYR:HB2	2.17	0.43
1:C:135:SER:OG	1:C:199:GLU:OE2	2.28	0.43
1:B:87:ARG:HD3	1:B:170:VAL:CG1	2.47	0.43
1:F:198:GLU:HB2	1:F:209:VAL:HB	2.00	0.43
1:B:215:PHE:HB2	1:B:217:THR:O	2.19	0.43
1:D:105:TYR:HD2	1:D:110:VAL:HG12	1.84	0.43
1:A:78:ILE:HG22	1:A:105:TYR:CE2	2.54	0.43
1:A:141:HIS:HE1	2:B:223:HOH:O	2.01	0.43
1:C:147:ASP:HB2	1:C:180:ILE:CD1	2.48	0.43
1:A:72:ASN:ND2	1:A:75:LEU:H	2.17	0.43
1:E:140:GLU:O	1:E:192:PHE:HA	2.19	0.43
1:E:81:GLY:HA2	1:E:82:GLY:HA2	1.66	0.42
1:A:10:ILE:CD1	1:A:38:MET:HE1	2.40	0.42
1:A:28:THR:HG23	1:A:31:GLN:HG2	2.01	0.42
1:F:80:ASN:O	1:F:179:ALA:HB2	2.19	0.42
1:D:141:HIS:HE1	2:F:227:HOH:O	2.03	0.42
1:E:76:HIS:CD2	1:E:182:PRO:HG3	2.54	0.42
1:C:150:LEU:HB3	1:C:174:MET:CG	2.49	0.42
1:E:15:ASN:HD21	1:E:121:PHE:HB2	1.84	0.42
1:F:80:ASN:ND2	1:F:178:SER:O	2.53	0.42
1:C:76:HIS:HB3	1:C:77:ALA:H	1.54	0.41
1:E:109:ARG:HH11	1:E:111:ILE:CD1	2.33	0.41
1:F:125:SER:OG	1:F:127:ILE:HG12	2.20	0.41
1:D:141:HIS:HD2	2:D:228:HOH:O	2.03	0.41
1:A:53:SER:HA	1:A:56:MET:HE3	2.01	0.41
1:C:57:CR2:O2	1:C:87:ARG:NH2	2.50	0.41
1:C:140:GLU:O	1:C:192:PHE:HA	2.20	0.41
1:B:140:GLU:O	1:B:192:PHE:HA	2.20	0.41
1:E:176:PHE:HB3	2:E:228:HOH:O	2.20	0.41
1:A:72:ASN:HD22	1:A:74:PHE:H	1.67	0.41
1:E:177:LYS:HB3	1:E:178:SER:CB	2.51	0.41
1:D:177:LYS:HA	1:D:177:LYS:HE2	2.03	0.41
1:F:76:HIS:HB3	1:F:77:ALA:H	1.62	0.41
1:C:156:ARG:HD3	1:C:168:PHE:CZ	2.56	0.41
1:E:180:ILE:CG2	1:E:181:HIS:N	2.76	0.41
1:A:105:TYR:CD2	1:A:110:VAL:HG12	2.55	0.41
1:D:91:TYR:CD2	1:D:168:PHE:HB3	2.56	0.41
1:E:177:LYS:CG	1:E:178:SER:CB	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:LEU:HD12	1:C:75:LEU:O	2.20	0.41
1:C:80:ASN:CA	1:C:179:ALA:HB3	2.36	0.41
1:B:129:THR:HG23	1:B:131:LYS:HG2	2.03	0.41
1:F:141:HIS:HD2	2:F:249:HOH:O	2.03	0.41
1:F:80:ASN:HD21	1:F:177:LYS:H	1.69	0.40
1:F:89:GLU:HG2	1:F:170:VAL:HG22	2.04	0.40
1:C:80:ASN:HB2	1:C:82:GLY:HA2	2.04	0.40
1:A:184:ILE:HA	1:A:185:LEU:CB	2.50	0.40
1:E:198:GLU:HB2	1:E:209:VAL:HB	2.03	0.40
1:B:90:LYS:NZ	1:B:171:ASP:OD2	2.55	0.40
1:D:89:GLU:HG2	1:D:170:VAL:HG22	2.03	0.40
1:C:4:MET:HB3	1:C:63:PHE:HE2	1.87	0.40
1:F:57:CR2:O2	1:F:87:ARG:NH2	2.55	0.40
1:F:53:SER:HA	1:F:56:MET:CE	2.51	0.40
1:D:12:GLY:HA2	2:D:241:HOH:O	2.20	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	205/220 (93%)	193 (94%)	9 (4%)	3 (2%)	13	7
1	B	206/220 (94%)	186 (90%)	9 (4%)	11 (5%)	2	0
1	C	211/220 (96%)	189 (90%)	10 (5%)	12 (6%)	2	0
1	D	211/220 (96%)	192 (91%)	9 (4%)	10 (5%)	3	1
1	E	211/220 (96%)	191 (90%)	12 (6%)	8 (4%)	4	1
1	F	211/220 (96%)	192 (91%)	10 (5%)	9 (4%)	3	1
All	All	1255/1320 (95%)	1143 (91%)	59 (5%)	53 (4%)	3	1

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ILE
1	B	70	TYR
1	B	76	HIS
1	B	77	ALA
1	B	182	PRO
1	B	218	PRO
1	C	76	HIS
1	C	177	LYS
1	C	180	ILE
1	C	184	ILE
1	C	185	LEU
1	C	204	THR
1	D	76	HIS
1	D	177	LYS
1	D	180	ILE
1	D	186	GLN
1	E	76	HIS
1	E	177	LYS
1	E	179	ALA
1	E	184	ILE
1	E	185	LEU
1	F	77	ALA
1	F	80	ASN
1	A	179	ALA
1	A	182	PRO
1	B	75	LEU
1	B	180	ILE
1	C	44	ALA
1	C	77	ALA
1	C	179	ALA
1	D	43	GLY
1	E	43	GLY
1	F	43	GLY
1	F	180	ILE
1	F	184	ILE
1	B	72	ASN
1	C	43	GLY
1	C	188	GLY
1	D	44	ALA
1	D	184	ILE
1	D	185	LEU
1	F	185	LEU
1	B	78	ILE

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Mol	Chain	Res	Type
1	C	181	HIS
1	F	44	ALA
1	E	44	ALA
1	F	178	SER
1	B	69	GLY
1	B	203	ASN
1	D	178	SER
1	F	177	LYS
1	E	188	GLY
1	D	182	PRO

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	161/183 (88%)	145 (90%)	16 (10%)	10	6
1	B	156/183 (85%)	148 (95%)	8 (5%)	29	26
1	C	150/183 (82%)	141 (94%)	9 (6%)	24	20
1	D	147/183 (80%)	138 (94%)	9 (6%)	23	19
1	E	150/183 (82%)	141 (94%)	9 (6%)	24	20
1	F	148/183 (81%)	138 (93%)	10 (7%)	20	16
All	All	912/1098 (83%)	851 (93%)	61 (7%)	20	16

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	14	LEU
1	A	21	LEU
1	A	28	THR
1	A	45	LEU
1	A	72	ASN
1	A	75	LEU
1	A	111	ILE

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Mol	Chain	Res	Type
1	A	116	VAL
1	A	150	LEU
1	A	177	LYS
1	A	180	ILE
1	A	184	ILE
1	A	191	MET
1	A	200	LEU
1	A	206	LEU
1	B	34	MET
1	B	72	ASN
1	B	75	LEU
1	B	86	THR
1	B	90	LYS
1	B	116	VAL
1	B	129	THR
1	B	173	HIS
1	C	14	LEU
1	C	34	MET
1	C	51	LEU
1	C	116	VAL
1	C	162	ASP
1	C	174	MET
1	C	177	LYS
1	C	180	ILE
1	C	181	HIS
1	D	28	THR
1	D	34	MET
1	D	76	HIS
1	D	124	ASP
1	D	133	ILE
1	D	147	ASP
1	D	162	ASP
1	D	174	MET
1	D	177	LYS
1	E	28	THR
1	E	80	ASN
1	E	104	ARG
1	E	111	ILE
1	E	116	VAL
1	E	135	SER
1	E	174	MET
1	E	177	LYS

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Mol	Chain	Res	Type
1	E	217	THR
1	F	14	LEU
1	F	28	THR
1	F	30	GLU
1	F	31	GLN
1	F	34	MET
1	F	76	HIS
1	F	123	GLU
1	F	172	SER
1	F	174	MET
1	F	200	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	HIS
1	A	72	ASN
1	A	141	HIS
1	A	148	ASN
1	B	62	HIS
1	B	72	ASN
1	B	141	HIS
1	C	15	ASN
1	C	62	HIS
1	C	80	ASN
1	C	141	HIS
1	D	62	HIS
1	D	141	HIS
1	E	62	HIS
1	E	76	HIS
1	E	80	ASN
1	E	141	HIS
1	F	62	HIS
1	F	141	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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$
1	CR2	A	57	1	20,20,21	2.45	4 (20%)	25,27,29	5.48	9 (36%)
1	CR2	B	57	1	20,20,21	2.46	4 (20%)	25,27,29	5.40	10 (40%)
1	CR2	C	57	1	20,20,21	2.55	5 (25%)	25,27,29	6.15	9 (36%)
1	CR2	D	57	1	20,20,21	2.51	4 (20%)	25,27,29	5.58	10 (40%)
1	CR2	E	57	1	20,20,21	2.43	5 (25%)	25,27,29	5.93	10 (40%)
1	CR2	F	57	1	20,20,21	2.52	5 (25%)	25,27,29	5.57	10 (40%)

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
1	CR2	A	57	1	-	0/6/25/26	0/2/2/2
1	CR2	B	57	1	-	0/6/25/26	0/2/2/2
1	CR2	C	57	1	-	0/6/25/26	0/2/2/2
1	CR2	D	57	1	-	0/6/25/26	0/2/2/2
1	CR2	E	57	1	-	0/6/25/26	0/2/2/2
1	CR2	F	57	1	-	0/6/25/26	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	57	CR2	CG2-CB2	-8.71	1.29	1.46
1	D	57	CR2	CG2-CB2	-8.69	1.29	1.46
1	F	57	CR2	CG2-CB2	-8.65	1.29	1.46
1	A	57	CR2	CG2-CB2	-8.51	1.29	1.46
1	B	57	CR2	CG2-CB2	-8.34	1.29	1.46
1	E	57	CR2	CG2-CB2	-8.28	1.30	1.46
1	A	57	CR2	OH-CZ	-4.82	1.25	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	57	CR2	OH-CZ	-4.75	1.25	1.37
1	C	57	CR2	OH-CZ	-4.64	1.26	1.37
1	B	57	CR2	OH-CZ	-4.55	1.26	1.37
1	F	57	CR2	OH-CZ	-4.47	1.26	1.37
1	E	57	CR2	OH-CZ	-4.46	1.26	1.37
1	C	57	CR2	C2-N3	-2.76	1.33	1.39
1	F	57	CR2	C2-N3	-2.63	1.34	1.39
1	D	57	CR2	C2-N3	-2.56	1.34	1.39
1	E	57	CR2	C2-N3	-2.55	1.34	1.39
1	B	57	CR2	C2-N3	-2.54	1.34	1.39
1	A	57	CR2	C2-N3	-2.46	1.34	1.39
1	E	57	CR2	CA2-N2	-2.43	1.33	1.38
1	C	57	CR2	CA2-N2	-2.37	1.33	1.38
1	F	57	CR2	CA2-N2	-2.11	1.33	1.38
1	A	57	CR2	O2-C2	2.35	1.28	1.23
1	B	57	CR2	O2-C2	2.58	1.28	1.23
1	D	57	CR2	O2-C2	2.58	1.28	1.23
1	E	57	CR2	O2-C2	2.81	1.29	1.23
1	C	57	CR2	O2-C2	2.87	1.29	1.23
1	F	57	CR2	O2-C2	2.90	1.29	1.23

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57	CR2	O2-C2-CA2	-7.04	127.15	130.95
1	F	57	CR2	O2-C2-CA2	-6.90	127.22	130.95
1	E	57	CR2	CB2-CA2-N2	-6.88	116.37	128.67
1	B	57	CR2	CB2-CA2-N2	-6.76	116.58	128.67
1	F	57	CR2	CB2-CA2-N2	-6.61	116.85	128.67
1	D	57	CR2	O2-C2-CA2	-6.57	127.40	130.95
1	A	57	CR2	CB2-CA2-N2	-6.56	116.94	128.67
1	C	57	CR2	O2-C2-CA2	-6.51	127.43	130.95
1	D	57	CR2	CB2-CA2-N2	-6.41	117.22	128.67
1	C	57	CR2	CB2-CA2-N2	-5.90	118.13	128.67
1	B	57	CR2	O2-C2-CA2	-5.50	127.97	130.95
1	E	57	CR2	O2-C2-CA2	-5.05	128.22	130.95
1	D	57	CR2	CD2-CG2-CB2	-2.78	111.71	121.23
1	D	57	CR2	CE1-CD1-CG2	-2.76	117.83	121.29
1	F	57	CR2	CE1-CD1-CG2	-2.76	117.83	121.29
1	F	57	CR2	CD2-CG2-CB2	-2.75	111.82	121.23
1	B	57	CR2	CE2-CD2-CG2	-2.70	117.91	121.29
1	A	57	CR2	C2-CA2-N2	-2.66	106.78	108.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	57	CR2	CD1-CG2-CB2	-2.66	112.14	121.23
1	B	57	CR2	C2-CA2-N2	-2.65	106.79	108.91
1	A	57	CR2	CD1-CG2-CB2	-2.60	112.34	121.23
1	C	57	CR2	C2-CA2-N2	-2.35	107.04	108.91
1	E	57	CR2	CE1-CD1-CG2	-2.32	118.39	121.29
1	E	57	CR2	C2-CA2-N2	-2.28	107.09	108.91
1	E	57	CR2	CD2-CG2-CB2	-2.28	113.44	121.23
1	C	57	CR2	CD2-CG2-CB2	-2.22	113.64	121.23
1	D	57	CR2	C2-CA2-N2	-2.20	107.15	108.91
1	C	57	CR2	CE1-CD1-CG2	-2.04	118.74	121.29
1	B	57	CR2	CD2-CG2-CB2	2.06	128.29	121.23
1	D	57	CR2	CD1-CG2-CB2	2.06	128.29	121.23
1	F	57	CR2	CD1-CG2-CB2	2.07	128.30	121.23
1	F	57	CR2	CA3-N3-C2	2.10	127.41	123.99
1	A	57	CR2	CD2-CG2-CB2	2.18	128.69	121.23
1	B	57	CR2	CA1-C1-N3	2.22	126.03	122.86
1	F	57	CR2	CA1-C1-N3	2.30	126.14	122.86
1	E	57	CR2	CA1-C1-N3	2.37	126.24	122.86
1	A	57	CR2	CA3-N3-C2	2.39	127.89	123.99
1	D	57	CR2	CA3-N3-C2	2.53	128.11	123.99
1	E	57	CR2	CA3-N3-C2	2.60	128.22	123.99
1	C	57	CR2	CA1-C1-N3	2.66	126.65	122.86
1	E	57	CR2	CA2-C2-N3	7.57	107.19	103.40
1	F	57	CR2	CA2-C2-N3	7.62	107.22	103.40
1	D	57	CR2	CA2-C2-N3	7.95	107.39	103.40
1	C	57	CR2	CA2-C2-N3	8.03	107.42	103.40
1	A	57	CR2	CA2-C2-N3	8.36	107.59	103.40
1	B	57	CR2	CA2-C2-N3	8.47	107.64	103.40
1	C	57	CR2	CB2-CA2-C2	8.52	134.83	122.36
1	D	57	CR2	CB2-CA2-C2	9.02	135.57	122.36
1	F	57	CR2	CB2-CA2-C2	9.09	135.67	122.36
1	A	57	CR2	CB2-CA2-C2	9.50	136.28	122.36
1	B	57	CR2	CB2-CA2-C2	9.68	136.53	122.36
1	E	57	CR2	CB2-CA2-C2	9.68	136.53	122.36
1	B	57	CR2	CG2-CB2-CA2	20.93	157.39	130.22
1	A	57	CR2	CG2-CB2-CA2	21.29	157.86	130.22
1	F	57	CR2	CG2-CB2-CA2	22.24	159.10	130.22
1	D	57	CR2	CG2-CB2-CA2	22.33	159.22	130.22
1	E	57	CR2	CG2-CB2-CA2	24.66	162.23	130.22
1	C	57	CR2	CG2-CB2-CA2	26.25	164.31	130.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	57	CR2	1	0
1	C	57	CR2	1	0
1	E	57	CR2	1	0
1	F	57	CR2	1	0

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 [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 ⓘ

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	211/220 (95%)	0.45	10 (4%)	35 44	35, 39, 43, 48	0
1	B	212/220 (96%)	0.60	16 (7%)	17 23	34, 39, 45, 57	0
1	C	215/220 (97%)	0.83	26 (12%)	6 7	35, 39, 42, 48	0
1	D	215/220 (97%)	0.84	29 (13%)	4 6	36, 39, 42, 48	0
1	E	215/220 (97%)	0.95	27 (12%)	5 6	35, 39, 41, 48	0
1	F	215/220 (97%)	0.79	32 (14%)	3 5	35, 39, 42, 48	0
All	All	1283/1320 (97%)	0.75	140 (10%)	7 10	34, 39, 42, 57	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	179	ALA	18.4
1	B	180	ILE	13.0
1	B	219	ILE	10.7
1	E	219	ILE	9.6
1	F	180	ILE	9.2
1	E	180	ILE	7.2
1	C	178	SER	7.0
1	C	219	ILE	6.9
1	D	180	ILE	6.6
1	D	183	SER	6.5
1	C	180	ILE	6.2
1	D	2	PRO	6.0
1	E	181	HIS	6.0
1	F	2	PRO	5.9
1	D	79	ASN	5.9
1	F	147	ASP	5.8
1	D	179	ALA	5.8
1	D	219	ILE	5.7
1	E	187	ASN	5.7

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Mol	Chain	Res	Type	RSRZ
1	E	2	PRO	5.6
1	F	179	ALA	5.3
1	D	75	LEU	5.2
1	F	219	ILE	5.0
1	C	79	ASN	4.9
1	D	188	GLY	4.9
1	C	182	PRO	4.9
1	F	80	ASN	4.9
1	D	107	ALA	4.8
1	E	218	PRO	4.8
1	B	107	ALA	4.8
1	C	80	ASN	4.7
1	E	77	ALA	4.7
1	F	81	GLY	4.5
1	F	107	ALA	4.5
1	C	78	ILE	4.4
1	F	181	HIS	4.4
1	E	177	LYS	4.3
1	F	43	GLY	4.3
1	D	149	VAL	4.2
1	D	177	LYS	4.2
1	F	77	ALA	4.1
1	D	181	HIS	4.0
1	C	181	HIS	4.0
1	B	181	HIS	4.0
1	B	74	PHE	4.0
1	F	183	SER	4.0
1	F	187	ASN	3.9
1	C	43	GLY	3.9
1	B	79	ASN	3.8
1	C	122	PRO	3.8
1	E	185	LEU	3.8
1	C	177	LYS	3.8
1	E	79	ASN	3.8
1	D	81	GLY	3.8
1	C	185	LEU	3.7
1	A	107	ALA	3.7
1	E	124	ASP	3.6
1	F	177	LYS	3.6
1	C	81	GLY	3.5
1	F	178	SER	3.4
1	F	78	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	E	178	SER	3.3
1	D	176	PHE	3.3
1	D	182	PRO	3.3
1	E	179	ALA	3.3
1	D	185	LEU	3.3
1	D	178	SER	3.3
1	B	78	ILE	3.2
1	C	187	ASN	3.2
1	D	108	GLY	3.2
1	F	82	GLY	3.1
1	B	77	ALA	3.1
1	E	81	GLY	3.1
1	D	68	SER	3.0
1	C	16	GLY	3.0
1	A	145	MET	3.0
1	E	126	VAL	3.0
1	C	125	SER	3.0
1	E	78	ILE	2.9
1	A	185	LEU	2.9
1	D	82	GLY	2.8
1	E	184	ILE	2.8
1	B	218	PRO	2.8
1	F	76	HIS	2.8
1	E	14	LEU	2.7
1	A	180	ILE	2.7
1	B	129	THR	2.7
1	B	178	SER	2.7
1	E	182	PRO	2.6
1	C	30	GLU	2.6
1	D	78	ILE	2.6
1	D	129	THR	2.6
1	F	149	VAL	2.6
1	B	28	THR	2.5
1	B	82	GLY	2.5
1	B	69	GLY	2.5
1	D	145	MET	2.5
1	B	179	ALA	2.5
1	A	131	LYS	2.5
1	C	127	ILE	2.5
1	F	186	GLN	2.4
1	C	28	THR	2.4
1	E	16	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	43	GLY	2.4
1	F	185	LEU	2.4
1	A	68	SER	2.4
1	B	184	ILE	2.4
1	D	125	SER	2.4
1	E	110	VAL	2.4
1	A	124	ASP	2.3
1	E	147	ASP	2.3
1	E	112	GLY	2.3
1	F	108	GLY	2.3
1	C	202	SER	2.3
1	F	4	MET	2.3
1	D	111	ILE	2.3
1	F	162	ASP	2.3
1	C	69	GLY	2.3
1	C	107	ALA	2.3
1	F	63	PHE	2.3
1	F	74	PHE	2.3
1	F	115	LYS	2.3
1	D	46	THR	2.2
1	A	177	LYS	2.2
1	C	14	LEU	2.2
1	D	80	ASN	2.2
1	E	105	TYR	2.2
1	F	111	ILE	2.2
1	D	162	ASP	2.1
1	E	80	ASN	2.1
1	F	79	ASN	2.1
1	A	21	LEU	2.1
1	F	182	PRO	2.1
1	C	183	SER	2.1
1	F	70	TYR	2.1
1	E	75	LEU	2.1
1	F	106	GLU	2.1
1	D	187	ASN	2.1
1	C	188	GLY	2.0
1	A	4	MET	2.0

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

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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	CR2	E	57	19/20	0.87	0.20	-	32,35,38,39	0
1	CR2	D	57	19/20	0.93	0.10	-	30,33,37,37	0
1	CR2	F	57	19/20	0.92	0.11	-	30,34,37,39	0
1	CR2	A	57	19/20	0.94	0.12	-	22,25,33,33	0
1	CR2	C	57	19/20	0.92	0.15	-	32,35,38,38	0
1	CR2	B	57	19/20	0.89	0.17	-	21,26,34,34	0

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.