



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 12:35 PM BST

PDB ID : 5K2J
Title : Crystal structure of reduced Prx3 in complex with h2o2 from *Vibrio vulnificus*
Authors : Ahn, J.; Ha, N.-C.
Deposited on : 2016-05-19
Resolution : 1.91 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)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

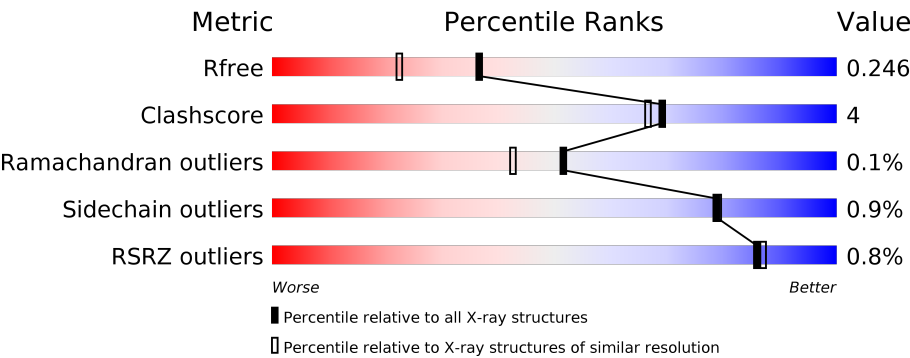
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	164	<div><div>%</div><div>87%10%..</div></div>
1	B	164	<div><div>89%9%.</div></div>
1	C	164	<div><div>%</div><div>88%9%.</div></div>
1	D	164	<div><div>88%8%..</div></div>
1	E	164	<div><div>87%7%5%</div></div>
1	F	164	<div><div>2%</div><div>85%12%..</div></div>

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Mol	Chain	Length	Quality of chain
1	G	164	<div><div><div>%</div><div><div></div><div>88%</div><div>5%</div><div>7%</div></div></div></div>
1	H	164	<div><div><div></div><div>94%</div><div></div><div></div><div></div></div></div>
1	I	164	<div><div><div>3%</div><div><div></div><div>80%</div><div>16%</div><div></div></div></div></div>
1	J	164	<div><div><div></div><div>87%</div><div>9%</div><div></div></div></div>
1	K	164	<div><div><div></div><div>87%</div><div>7%</div><div>7%</div></div></div>
1	L	164	<div><div><div>%</div><div><div></div><div>91%</div><div>9%</div></div></div></div>

2 Entry composition

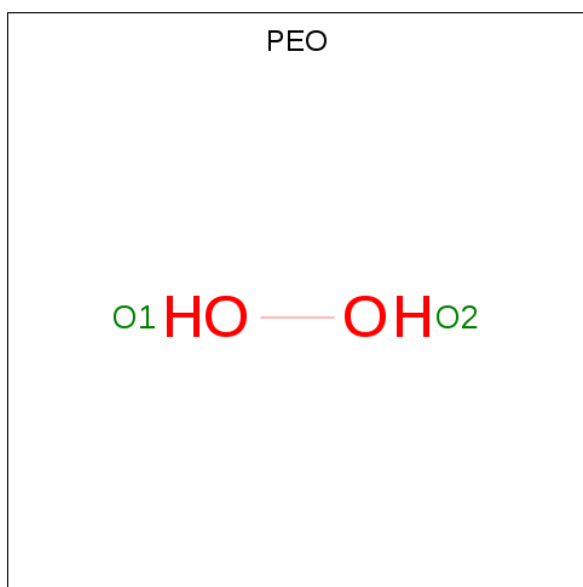
There are 3 unique types of molecules in this entry. The entry contains 14956 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1-Cys peroxiredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	0	0	0
			1203	766	204	227	6			
1	B	160	Total	C	N	O	S	0	0	0
			1192	759	197	230	6			
1	C	160	Total	C	N	O	S	0	0	0
			1192	759	197	230	6			
1	D	159	Total	C	N	O	S	0	0	0
			1193	760	201	226	6			
1	E	155	Total	C	N	O	S	0	0	0
			1150	734	187	223	6			
1	F	161	Total	C	N	O	S	0	0	0
			1204	766	203	229	6			
1	G	153	Total	C	N	O	S	0	0	0
			1134	725	185	218	6			
1	H	158	Total	C	N	O	S	0	0	0
			1172	747	191	228	6			
1	I	157	Total	C	N	O	S	0	0	0
			1173	748	195	224	6			
1	J	157	Total	C	N	O	S	0	0	0
			1163	742	190	225	6			
1	K	153	Total	C	N	O	S	0	0	0
			1134	725	185	218	6			
1	L	164	Total	C	N	O	S	0	0	0
			1233	783	209	235	6			

- Molecule 2 is HYDROGEN PEROXIDE (three-letter code: PEO) (formula: H₂O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O 2 2	0	0
2	E	1	Total O 2 2	0	0
2	I	1	Total O 2 2	0	0
2	K	1	Total O 2 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	85	Total O 85 85	0	0
3	B	64	Total O 64 64	0	0
3	C	64	Total O 64 64	0	0
3	D	66	Total O 66 66	0	0
3	E	66	Total O 66 66	0	0
3	F	57	Total O 57 57	0	0
3	G	60	Total O 60 60	0	0
3	H	77	Total O 77 77	0	0

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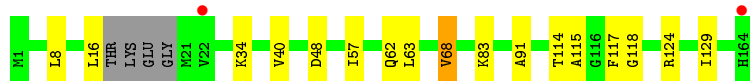
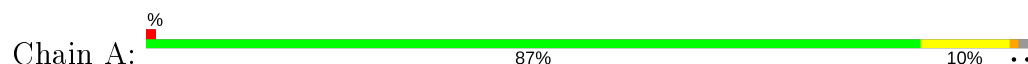
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	59	Total 59	O 59	0	0
3	J	78	Total 78	O 78	0	0
3	K	59	Total 59	O 59	0	0
3	L	70	Total 70	O 70	0	0

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.

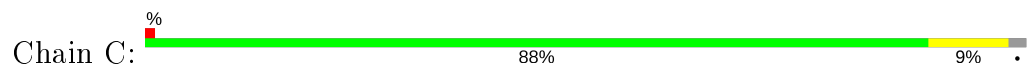
- Molecule 1: 1-Cys peroxiredoxin



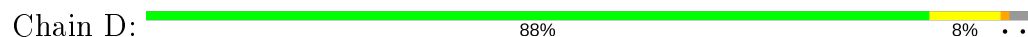
- Molecule 1: 1-Cys peroxiredoxin



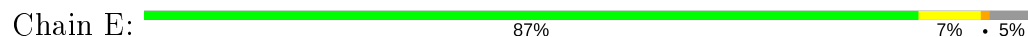
- Molecule 1: 1-Cys peroxiredoxin



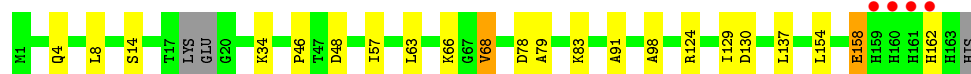
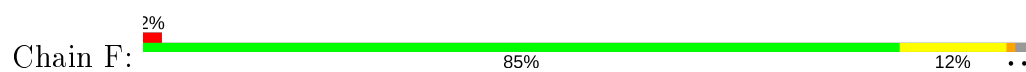
- Molecule 1: 1-Cys peroxiredoxin



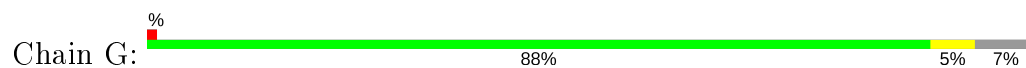
- Molecule 1: 1-Cys peroxiredoxin



- Molecule 1: 1-Cys peroxiredoxin



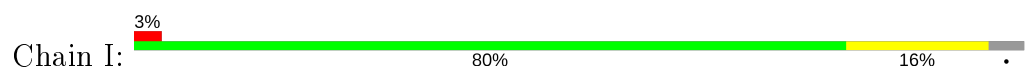
- Molecule 1: 1-Cys peroxiredoxin



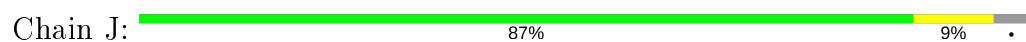
- Molecule 1: 1-Cys peroxiredoxin



- Molecule 1: 1-Cys peroxiredoxin



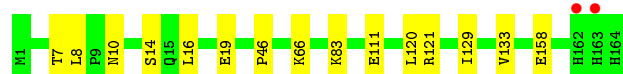
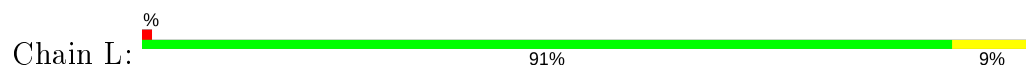
- Molecule 1: 1-Cys peroxiredoxin



- Molecule 1: 1-Cys peroxiredoxin



- Molecule 1: 1-Cys peroxiredoxin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.08Å 97.72Å 97.49Å 78.72° 67.33° 67.34°	Depositor
Resolution (Å)	19.68 – 1.91 23.89 – 1.91	Depositor EDS
% Data completeness (in resolution range)	74.8 (19.68-1.91) 74.8 (23.89-1.91)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.17 (at 1.90Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.195 , 0.244 0.195 , 0.246	Depositor DCC
R_{free} test set	6751 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 23.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.459 for h,h-k,h-l 0.030 for -h,-l,-k 0.029 for -h,-h+l,-h+k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14956	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3496e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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

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	0.26	0/1227	0.49	0/1666
1	B	0.25	0/1213	0.46	0/1647
1	C	0.26	0/1213	0.49	0/1647
1	D	0.26	0/1216	0.47	0/1651
1	E	0.26	0/1168	0.47	0/1586
1	F	0.27	0/1227	0.47	0/1666
1	G	0.30	0/1152	0.49	1/1564 (0.1%)
1	H	0.27	0/1191	0.47	0/1617
1	I	0.26	0/1194	0.47	0/1621
1	J	0.26	0/1182	0.48	0/1605
1	K	0.26	0/1152	0.46	0/1564
1	L	0.27	0/1258	0.47	0/1707
All	All	0.26	0/14393	0.47	1/19541 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	140	GLU	C-N-CA	5.14	134.56	121.70

There are no chirality outliers.

There are no planarity outliers.

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	1203	0	1194	12	0
1	B	1192	0	1196	9	0
1	C	1192	0	1196	9	0
1	D	1193	0	1187	9	0
1	E	1150	0	1159	8	0
1	F	1204	0	1197	12	0
1	G	1134	0	1145	4	0
1	H	1172	0	1182	3	0
1	I	1173	0	1173	16	0
1	J	1163	0	1176	10	0
1	K	1134	0	1146	6	0
1	L	1233	0	1224	8	0
2	A	2	0	0	0	0
2	E	2	0	0	0	0
2	I	2	0	0	0	0
2	K	2	0	0	0	0
3	A	85	0	0	2	0
3	B	64	0	0	2	0
3	C	64	0	0	3	0
3	D	66	0	0	3	0
3	E	66	0	0	3	0
3	F	57	0	0	3	0
3	G	60	0	0	0	0
3	H	77	0	0	0	0
3	I	59	0	0	3	0
3	J	78	0	0	5	0
3	K	59	0	0	1	0
3	L	70	0	0	2	0
All	All	14956	0	14175	104	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 4.

All (104) 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:D:21:MET:SD	3:D:247:HOH:O	2.34	0.85
1:L:66:LYS:HE2	1:L:158:GLU:HG2	1.68	0.76
1:C:9:PRO:O	3:C:201:HOH:O	2.04	0.75
1:G:141:ALA:HB3	1:G:144:SER:HB2	1.71	0.73
1:I:112:MET:SD	3:I:357:HOH:O	2.46	0.72
1:E:16:LEU:HD23	1:E:83:LYS:HD3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:19:GLU:N	1:L:19:GLU:OE2	2.23	0.70
1:F:66:LYS:HE3	1:F:154:LEU:HD11	1.75	0.69
1:F:34:LYS:NZ	1:F:130:ASP:OD1	2.24	0.69
1:L:111:GLU:HB2	1:L:120:LEU:HD21	1.74	0.68
1:A:117:PHE:O	3:A:301:HOH:O	2.14	0.64
1:D:135:THR:HG22	1:D:136:THR:HG23	1.78	0.64
1:E:8:LEU:HD11	1:E:129:ILE:HD13	1.78	0.64
1:F:14:SER:HB2	3:F:254:HOH:O	1.97	0.64
1:L:121:ARG:NH2	3:L:201:HOH:O	2.24	0.63
1:F:8:LEU:HD11	1:F:129:ILE:HD13	1.81	0.62
1:E:9:PRO:O	3:E:301:HOH:O	2.16	0.62
1:I:141:ALA:HB3	1:I:144:SER:HB2	1.84	0.60
1:C:7:THR:HG22	1:C:133:VAL:HG22	1.85	0.59
1:L:16:LEU:HD23	1:L:83:LYS:HD3	1.86	0.57
1:C:144:SER:OG	1:C:146:GLU:OE2	2.18	0.57
1:J:16:LEU:HD23	1:J:83:LYS:HD3	1.87	0.56
1:C:8:LEU:HD11	1:C:129:ILE:HD13	1.86	0.56
1:A:16:LEU:HD23	1:A:83:LYS:HD3	1.87	0.56
1:B:34:LYS:NZ	3:B:202:HOH:O	2.39	0.55
1:I:48:ASP:OD1	1:I:124:ARG:NH1	2.37	0.55
1:B:8:LEU:HD11	1:B:129:ILE:HD13	1.87	0.55
1:D:48:ASP:OD1	1:D:124:ARG:NH1	2.35	0.53
1:L:8:LEU:HD11	1:L:129:ILE:HD13	1.90	0.53
1:C:16:LEU:HD23	1:C:83:LYS:HD3	1.91	0.53
1:K:73:SER:OG	3:K:301:HOH:O	2.18	0.53
1:A:48:ASP:OD1	1:A:124:ARG:NH1	2.36	0.52
1:F:98:ALA:HB3	3:F:254:HOH:O	2.09	0.51
1:J:28:GLU:OE2	3:J:201:HOH:O	2.19	0.51
1:G:66:LYS:HE2	1:G:66:LYS:HA	1.92	0.51
1:D:104:PHE:O	3:D:201:HOH:O	2.19	0.51
1:K:8:LEU:HD11	1:K:129:ILE:HD13	1.92	0.51
1:B:16:LEU:HD23	1:B:83:LYS:HD3	1.94	0.50
1:A:8:LEU:HD11	1:A:129:ILE:HD13	1.93	0.50
1:A:115:ALA:O	1:B:101:ASP:HB3	2.12	0.50
1:C:33:LYS:NZ	3:C:204:HOH:O	2.36	0.50
1:F:79:ALA:HB2	3:F:254:HOH:O	2.12	0.50
1:C:101:ASP:HB3	1:D:115:ALA:O	2.12	0.49
1:J:106:LYS:HE2	1:J:120:LEU:HD13	1.96	0.48
1:J:37:LEU:HD23	1:J:127:MET:HE2	1.96	0.48
1:F:63:LEU:O	1:F:68:VAL:HG13	2.14	0.47
1:K:38:PHE:CZ	1:K:73:SER:HB2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:ILE:HD11	1:D:91:ALA:HB2	1.96	0.47
1:E:137:LEU:N	3:E:302:HOH:O	2.36	0.47
1:C:26:VAL:HB	3:C:201:HOH:O	2.14	0.47
1:H:8:LEU:HD11	1:H:129:ILE:HD13	1.96	0.47
1:D:16:LEU:HD23	1:D:83:LYS:HD3	1.97	0.47
1:K:7:THR:HG22	1:K:133:VAL:HG22	1.96	0.47
1:B:146:GLU:HG3	1:B:147:VAL:HG13	1.97	0.47
1:F:158:GLU:OE1	1:F:162:HIS:NE2	2.49	0.46
1:I:66:LYS:NZ	1:I:158:GLU:HB2	2.30	0.46
1:I:16:LEU:HD13	1:I:83:LYS:HD3	1.97	0.46
1:J:70:LEU:O	3:J:202:HOH:O	2.20	0.46
1:F:4:GLN:NE2	1:F:137:LEU:HB3	2.31	0.46
1:L:7:THR:HG22	1:L:133:VAL:HG22	1.98	0.46
1:G:48:ASP:OD1	1:G:124:ARG:NH1	2.40	0.46
1:E:63:LEU:O	1:E:68:VAL:HG13	2.16	0.45
1:B:18:LYS:H	1:B:18:LYS:HD2	1.80	0.45
1:I:8:LEU:HD11	1:I:129:ILE:HD13	1.97	0.45
1:D:9:PRO:O	3:D:202:HOH:O	2.19	0.45
1:A:63:LEU:O	1:A:68:VAL:HG13	2.17	0.44
1:J:83:LYS:NZ	3:J:205:HOH:O	2.43	0.44
1:A:114:THR:OG1	1:A:118:GLY:HA2	2.17	0.44
1:I:104:PHE:O	3:I:301:HOH:O	2.20	0.44
1:I:16:LEU:HB3	1:I:83:LYS:HD2	1.99	0.44
1:E:11:ALA:HB3	1:E:104:PHE:HD1	1.83	0.43
1:H:37:LEU:HD23	1:H:127:MET:HE2	2.00	0.43
1:A:57:ILE:HD11	1:A:91:ALA:HB2	2.01	0.43
1:I:7:THR:HG22	1:I:133:VAL:HG22	2.00	0.43
1:J:77:ASN:O	1:J:98:ALA:HB1	2.18	0.43
1:K:48:ASP:OD1	1:K:124:ARG:NH1	2.44	0.42
1:I:57:ILE:HD11	1:I:91:ALA:HB2	2.01	0.42
1:J:34:LYS:NZ	1:J:130:ASP:OD1	2.44	0.42
1:A:34:LYS:HG2	1:A:68:VAL:HA	2.01	0.42
1:B:147:VAL:O	3:B:201:HOH:O	2.21	0.42
1:J:33:LYS:NZ	3:J:211:HOH:O	2.51	0.42
1:H:127:MET:HE3	1:H:129:ILE:HD11	2.02	0.42
1:I:128:ILE:HD11	1:I:153:ILE:HG23	2.02	0.42
1:I:25:PRO:HB2	1:I:28:GLU:HB2	2.02	0.42
1:J:60:ALA:HB1	3:J:255:HOH:O	2.19	0.42
1:K:16:LEU:HD23	1:K:83:LYS:HD3	2.01	0.42
1:F:57:ILE:HD11	1:F:91:ALA:HB2	2.02	0.42
1:A:40:VAL:HB	1:A:48:ASP:CG	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ASP:OD1	1:B:124:ARG:NH1	2.46	0.41
1:E:34:LYS:HG2	1:E:68:VAL:HA	2.01	0.41
1:A:117:PHE:N	1:A:118:GLY:HA3	2.35	0.41
3:E:345:HOH:O	1:F:78:ASP:HA	2.20	0.41
1:D:29:LEU:HD21	1:D:95:LEU:HD21	2.03	0.41
1:E:66:LYS:HD3	1:E:66:LYS:HA	1.89	0.41
1:I:124:ARG:HD2	1:I:140:GLU:HG3	2.03	0.41
1:C:48:ASP:OD1	1:C:124:ARG:NH1	2.45	0.41
1:F:48:ASP:OD1	1:F:124:ARG:NH1	2.47	0.41
1:L:14:SER:HB2	3:L:265:HOH:O	2.21	0.41
1:G:40:VAL:HB	1:G:48:ASP:CG	2.41	0.40
1:I:132:GLY:O	3:I:302:HOH:O	2.22	0.40
1:A:62:GLN:OE1	3:A:302:HOH:O	2.21	0.40
1:B:12:THR:HG21	1:B:23:HIS:HB3	2.03	0.40
1:I:38:PHE:CZ	1:I:73:SER:HB2	2.56	0.40
1:I:128:ILE:HB	1:I:136:THR:HB	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	156/164 (95%)	143 (92%)	13 (8%)	0	100	100
1	B	158/164 (96%)	148 (94%)	10 (6%)	0	100	100
1	C	158/164 (96%)	148 (94%)	10 (6%)	0	100	100
1	D	155/164 (94%)	145 (94%)	10 (6%)	0	100	100
1	E	151/164 (92%)	142 (94%)	9 (6%)	0	100	100
1	F	157/164 (96%)	148 (94%)	8 (5%)	1 (1%)	25	15
1	G	149/164 (91%)	140 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	156/164 (95%)	146 (94%)	10 (6%)	0	100	100
1	I	153/164 (93%)	144 (94%)	9 (6%)	0	100	100
1	J	155/164 (94%)	145 (94%)	10 (6%)	0	100	100
1	K	149/164 (91%)	137 (92%)	12 (8%)	0	100	100
1	L	162/164 (99%)	152 (94%)	9 (6%)	1 (1%)	25	15
All	All	1859/1968 (94%)	1738 (94%)	119 (6%)	2 (0%)	51	43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	46	PRO
1	F	46	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	126/129 (98%)	125 (99%)	1 (1%)	81	82
1	B	125/129 (97%)	124 (99%)	1 (1%)	81	82
1	C	125/129 (97%)	124 (99%)	1 (1%)	81	82
1	D	125/129 (97%)	124 (99%)	1 (1%)	81	82
1	E	121/129 (94%)	119 (98%)	2 (2%)	60	57
1	F	126/129 (98%)	123 (98%)	3 (2%)	49	43
1	G	119/129 (92%)	118 (99%)	1 (1%)	81	82
1	H	123/129 (95%)	123 (100%)	0	100	100
1	I	123/129 (95%)	122 (99%)	1 (1%)	81	82
1	J	122/129 (95%)	121 (99%)	1 (1%)	81	82
1	K	119/129 (92%)	118 (99%)	1 (1%)	81	82
1	L	129/129 (100%)	128 (99%)	1 (1%)	81	82
All	All	1483/1548 (96%)	1469 (99%)	14 (1%)	78	79

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	VAL
1	B	4	GLN
1	C	10	ASN
1	D	135	THR
1	E	64	LYS
1	E	68	VAL
1	F	68	VAL
1	F	83	LYS
1	F	158	GLU
1	G	142	PRO
1	I	26	VAL
1	J	18	LYS
1	K	4	GLN
1	L	10	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	10	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands 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	PEO	K	201	-	1,1,1	0.13	0	-		
2	PEO	I	201	-	1,1,1	0.12	0	-		
2	PEO	A	201	-	1,1,1	0.13	0	-		
2	PEO	E	201	-	1,1,1	0.14	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 ⓘ

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	160/164 (97%)	-0.06	2 (1%) 77 79	13, 25, 45, 76	0
1	B	160/164 (97%)	-0.12	0 100 100	13, 23, 48, 72	0
1	C	160/164 (97%)	-0.04	2 (1%) 77 79	11, 23, 50, 89	0
1	D	159/164 (96%)	-0.04	0 100 100	13, 25, 47, 59	0
1	E	155/164 (94%)	-0.18	0 100 100	13, 24, 45, 66	0
1	F	161/164 (98%)	-0.03	4 (2%) 57 60	13, 25, 46, 82	0
1	G	153/164 (93%)	-0.22	1 (0%) 87 88	11, 24, 46, 57	0
1	H	158/164 (96%)	-0.09	0 100 100	13, 25, 47, 79	0
1	I	157/164 (95%)	-0.10	5 (3%) 47 50	12, 24, 51, 93	0
1	J	157/164 (95%)	-0.17	0 100 100	12, 24, 44, 71	0
1	K	153/164 (93%)	-0.21	0 100 100	12, 24, 43, 53	0
1	L	164/164 (100%)	-0.07	2 (1%) 79 81	13, 25, 57, 76	0
All	All	1897/1968 (96%)	-0.11	16 (0%) 86 87	11, 24, 47, 93	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	HIS	4.3
1	F	159	HIS	4.0
1	I	161	HIS	3.9
1	L	162	HIS	3.7
1	I	159	HIS	3.4
1	C	19	GLU	3.3
1	F	161	HIS	3.2
1	F	162	HIS	3.2
1	F	160	HIS	3.1
1	G	143	LYS	2.9
1	A	22	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	I	160	HIS	2.4
1	I	143	LYS	2.2
1	C	17	THR	2.2
1	I	158	GLU	2.1
1	L	163	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	PEO	I	201	2/2	0.91	0.12	43,43,43,49	0
2	PEO	A	201	2/2	0.92	0.15	46,46,46,49	0
2	PEO	E	201	2/2	0.92	0.15	39,39,39,49	0
2	PEO	K	201	2/2	0.95	0.13	36,36,36,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.