



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2017 – 07:47 PM EST

PDB ID : 5IUK
Title : Crystal structure of the DesK-DesR complex in the phosphotransfer state with high Mg²⁺ (150 mM)
Authors : Trajtenberg, F.; Imelio, J.A.; Larrieux, N.; Buschiazzi, A.
Deposited on : unknown
Resolution : 2.90 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

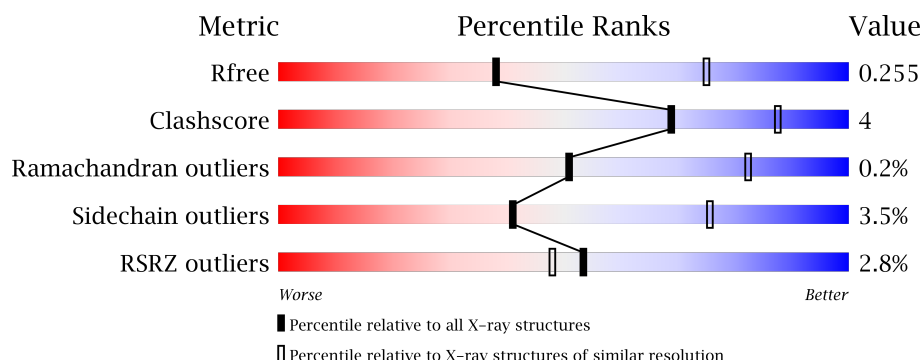
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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. 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	218	<div> <div>5%</div> <div>89%</div> <div>6%</div> <div>•</div> </div>
1	B	218	<div> <div>2%</div> <div>80%</div> <div>14%</div> <div>• 5%</div> </div>
1	D	218	<div> <div>4%</div> <div>84%</div> <div>13%</div> <div>•</div> </div>
1	E	218	<div> <div>•</div> <div>81%</div> <div>11%</div> <div>• 6%</div> </div>
2	C	139	<div> <div>2%</div> <div>80%</div> <div>15%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	139	<div> <div></div> <div>%</div> <div>80%</div> <div>15%</div> <div>• •</div> </div>

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
4	MG	C	201	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8842 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 Sensor histidine kinase DesK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1675	1042	299	327	7			
1	B	207	Total	C	N	O	S	0	0	0
			1652	1026	297	323	6			
1	D	213	Total	C	N	O	S	0	0	0
			1708	1062	303	336	7			
1	E	206	Total	C	N	O	S	0	0	0
			1643	1021	296	320	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	153	GLY	-	expression tag	UNP O34757
A	188	GLU	HIS	engineered mutation	UNP O34757
B	153	GLY	-	expression tag	UNP O34757
B	188	GLU	HIS	engineered mutation	UNP O34757
D	153	GLY	-	expression tag	UNP O34757
D	188	GLU	HIS	engineered mutation	UNP O34757
E	153	GLY	-	expression tag	UNP O34757
E	188	GLU	HIS	engineered mutation	UNP O34757

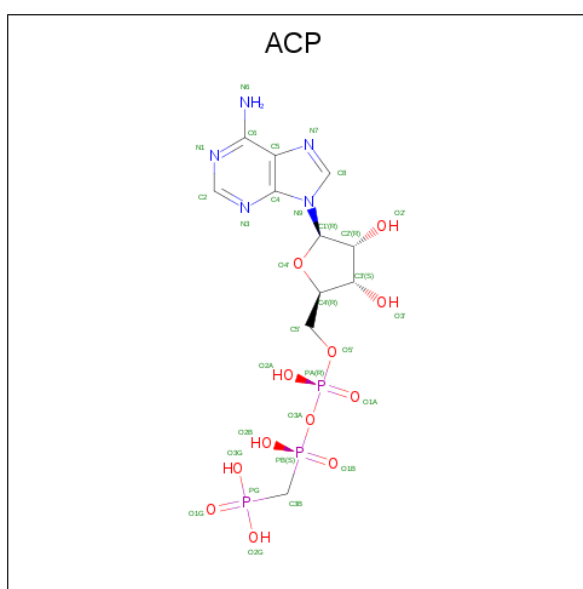
- Molecule 2 is a protein called Transcriptional regulatory protein DesR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	132	Total	C	N	O	S	0	0	0
			1006	635	165	197	9			
2	F	133	Total	C	N	O	S	0	0	0
			1018	644	166	199	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP O34723
C	-2	SER	-	expression tag	UNP O34723
C	-1	GLY	-	expression tag	UNP O34723
C	0	SER	-	expression tag	UNP O34723
F	-3	GLY	-	expression tag	UNP O34723
F	-2	SER	-	expression tag	UNP O34723
F	-1	GLY	-	expression tag	UNP O34723
F	0	SER	-	expression tag	UNP O34723

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Mg 1	0	0
4	D	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0
4	E	1	Total 1	Mg 1	0	0

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total 1	K 1	0	0
5	F	1	Total 1	K 1	0	0

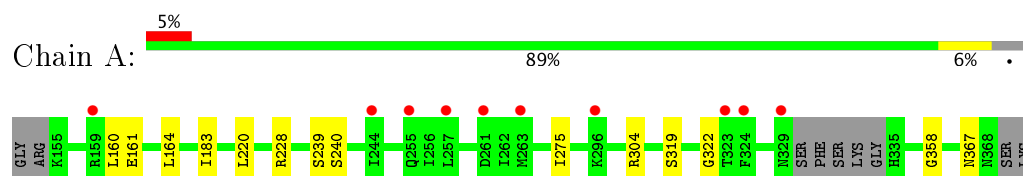
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	O 1	0	0
6	B	2	Total 2	O 2	0	0
6	D	1	Total 1	O 1	0	0
6	E	1	Total 1	O 1	0	0
6	C	2	Total 2	O 2	0	0
6	F	2	Total 2	O 2	0	0

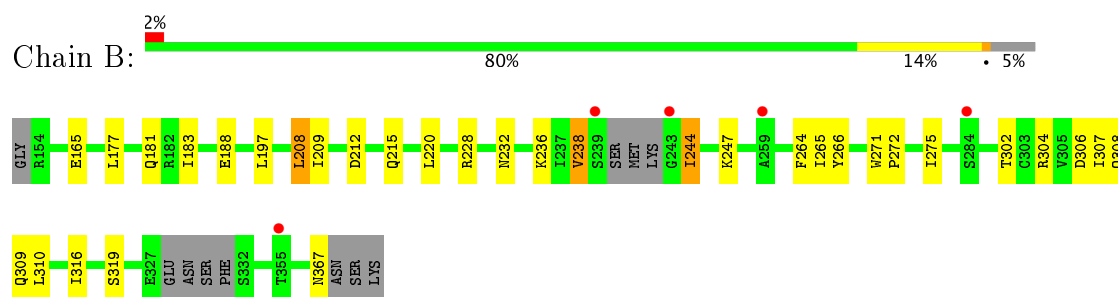
3 Residue-property plots [i](#)

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.

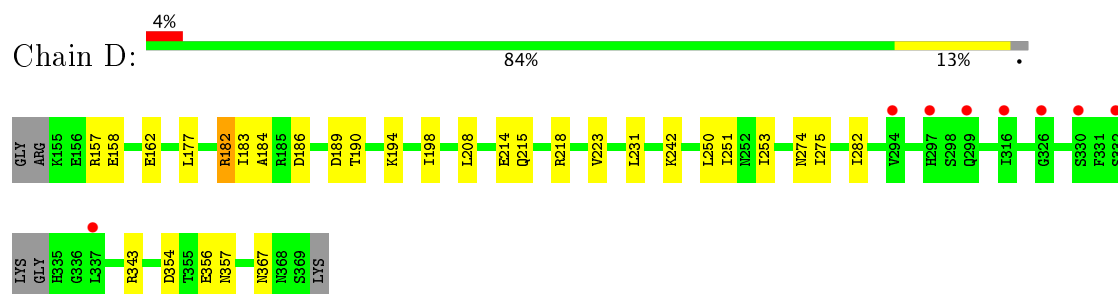
- Molecule 1: Sensor histidine kinase DesK



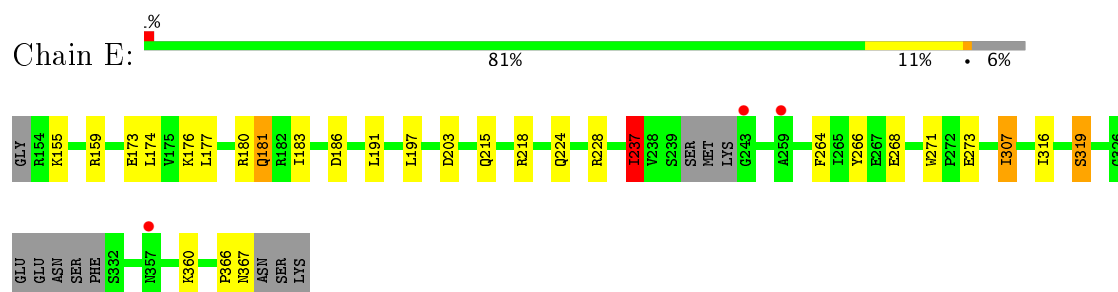
- Molecule 1: Sensor histidine kinase DesK



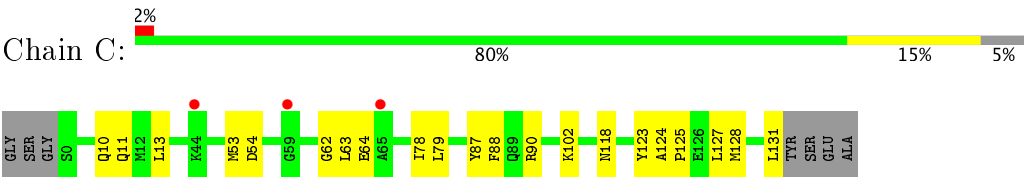
- Molecule 1: Sensor histidine kinase DesK



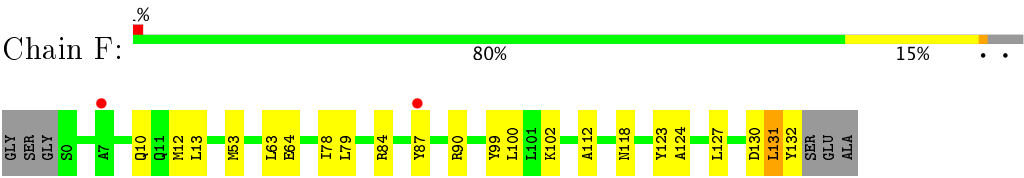
- Molecule 1: Sensor histidine kinase DesK



● Molecule 2: Transcriptional regulatory protein DesR



● Molecule 2: Transcriptional regulatory protein DesR



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.93Å 115.61Å 91.59Å 90.00° 116.71° 90.00°	Depositor
Resolution (Å)	39.27 – 2.90 39.27 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (39.27-2.90) 97.3 (39.27-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.90Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.2	Depositor
R, R_{free}	0.195 , 0.239 0.211 , 0.255	Depositor DCC
R_{free} test set	1720 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	82.9	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 74.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8842	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: K, ACP, MG

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	0.49	0/1688	0.71	0/2263
1	B	0.52	0/1662	0.77	1/2224 (0.0%)
1	D	0.50	0/1722	0.72	0/2308
1	E	0.52	0/1653	0.77	1/2212 (0.0%)
2	C	0.55	0/1017	0.73	0/1366
2	F	0.52	0/1030	0.70	0/1384
All	All	0.51	0/8772	0.74	2/11757 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	244	ILE	C-N-CA	6.34	137.56	121.70
1	E	366	PRO	C-N-CA	5.58	135.64	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1675	0	1724	6	0
1	B	1652	0	1708	21	0
1	D	1708	0	1752	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1643	0	1702	18	0
2	C	1006	0	1033	12	0
2	F	1018	0	1042	17	0
3	A	31	0	14	0	0
3	B	31	0	14	0	0
3	D	31	0	14	0	0
3	E	31	0	14	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
5	C	1	0	0	0	0
5	F	1	0	0	0	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
6	C	2	0	0	1	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	2	0	0	0	0
All	All	8842	0	9017	77	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 (77) 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:319:SER:HB3	1:E:360:LYS:HG2	1.64	0.80
1:E:197:LEU:HD21	2:F:12:MET:HG2	1.70	0.73
1:B:308:GLN:HB2	1:B:310:LEU:HD21	1.71	0.72
1:E:271:TRP:HA	1:E:307:ILE:HG21	1.74	0.69
2:F:10:GLN:HB2	2:F:13:LEU:HD12	1.81	0.63
2:C:64:GLU:HG3	2:C:90:ARG:HH22	1.64	0.62
2:F:64:GLU:HG3	2:F:90:ARG:HH22	1.65	0.62
1:B:308:GLN:HB2	1:B:310:LEU:CD2	2.30	0.61
1:E:307:ILE:HG13	1:E:316:ILE:HG12	1.82	0.60
1:B:197:LEU:HD13	2:C:13:LEU:HD12	1.82	0.60
2:F:99:TYR:CE2	2:F:127:LEU:HB3	2.36	0.60
1:D:354:ASP:OD1	1:D:356:GLU:HG2	2.02	0.59
2:F:84:ARG:HB2	2:F:87:TYR:CD2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:99:TYR:HE2	2:F:127:LEU:HB3	1.68	0.58
1:B:307:ILE:HG13	1:B:316:ILE:HG12	1.86	0.58
1:E:264:PHE:CE2	1:E:266:TYR:CD1	2.93	0.56
1:D:242:LYS:HA	1:E:181:GLN:HE22	1.71	0.55
1:E:155:LYS:HE3	1:E:159:ARG:HB2	1.87	0.55
1:D:183:ILE:HG21	1:E:183:ILE:HG21	1.88	0.54
1:A:161:GLU:HA	1:A:164:LEU:HD12	1.91	0.53
1:D:343:ARG:HG2	1:E:174:LEU:HD11	1.90	0.53
1:B:264:PHE:CE2	1:B:266:TYR:CD1	2.97	0.52
1:B:244:ILE:HG22	1:B:247:LYS:H	1.75	0.52
1:E:173:GLU:HA	1:E:176:LYS:HE3	1.93	0.51
1:B:265:ILE:HD13	1:B:302:THR:HG23	1.93	0.50
2:C:124:ALA:HB3	2:C:127:LEU:HD12	1.94	0.49
1:D:214:GLU:HB3	1:D:218:ARG:HH22	1.78	0.49
2:C:53:MET:HB3	2:C:78:ILE:HD13	1.94	0.49
2:C:63:LEU:HD13	2:C:90:ARG:HD3	1.94	0.48
2:C:64:GLU:HG3	2:C:90:ARG:NH2	2.29	0.48
1:D:356:GLU:HG3	1:D:357:ASN:H	1.78	0.48
1:D:251:ILE:HD13	2:F:132:TYR:HA	1.96	0.48
2:F:64:GLU:HG3	2:F:90:ARG:NH2	2.27	0.48
1:B:308:GLN:CB	1:B:310:LEU:HD21	2.40	0.48
1:D:158:GLU:O	1:D:162:GLU:HG2	2.14	0.48
2:F:63:LEU:HD13	2:F:90:ARG:HD3	1.98	0.46
1:B:177:LEU:O	1:B:181:GLN:HG2	2.14	0.46
1:D:186:ASP:O	1:D:190:THR:HG23	2.15	0.46
1:E:271:TRP:HA	1:E:307:ILE:CG2	2.43	0.46
1:B:275:ILE:HA	1:B:367:ASN:OD1	2.16	0.46
1:D:184:ALA:HB2	1:E:237:ILE:HG13	1.98	0.45
2:F:100:LEU:HD11	2:F:112:ALA:CB	2.47	0.45
1:B:232:ASN:O	1:B:236:LYS:HB2	2.17	0.45
1:B:272:PRO:HB3	1:B:309:GLN:OE1	2.17	0.45
1:B:272:PRO:HD2	1:B:307:ILE:HG12	1.99	0.45
2:F:124:ALA:HB3	2:F:127:LEU:HD12	1.99	0.45
1:E:215:GLN:HA	1:E:218:ARG:HD2	1.99	0.44
1:B:212:ASP:OD2	1:B:215:GLN:HB2	2.17	0.44
1:D:275:ILE:HA	1:D:367:ASN:OD1	2.18	0.44
2:C:88:PHE:CE1	2:C:123:TYR:HD2	2.36	0.44
1:E:224:GLN:O	1:E:228:ARG:HG2	2.18	0.44
2:C:125:PRO:HB3	2:F:123:TYR:HE2	1.83	0.44
1:B:208:LEU:HD13	1:B:212:ASP:HB3	2.00	0.43
1:A:183:ILE:HG21	1:B:183:ILE:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:268:GLU:HA	1:E:271:TRP:CD1	2.54	0.43
1:A:275:ILE:HA	1:A:367:ASN:OD1	2.19	0.43
1:D:198:ILE:HG23	1:D:223:VAL:HG13	2.00	0.43
1:A:322:GLY:O	1:A:358:GLY:HA2	2.18	0.42
1:D:250:LEU:HD12	1:D:253:ILE:HD11	2.01	0.42
1:B:271:TRP:HA	1:B:307:ILE:CG2	2.49	0.42
1:D:208:LEU:HD13	1:D:215:GLN:HB3	2.02	0.42
1:E:173:GLU:O	1:E:177:LEU:HG	2.20	0.42
2:F:130:ASP:C	2:F:131:LEU:HG	2.40	0.42
2:C:10:GLN:HG3	6:C:301:HOH:O	2.20	0.42
2:C:125:PRO:HB3	2:F:123:TYR:CE2	2.54	0.42
1:D:182:ARG:HH21	1:E:180:ARG:NH2	2.18	0.42
1:A:220:LEU:CD2	1:B:220:LEU:HD21	2.50	0.41
1:A:220:LEU:HD12	1:B:209:ILE:HD11	2.01	0.41
2:C:79:LEU:HB3	2:C:102:LYS:HG2	2.03	0.41
2:C:54:ASP:O	2:C:62:GLY:HA3	2.20	0.41
2:F:53:MET:HB3	2:F:78:ILE:HD13	2.01	0.41
2:F:84:ARG:HD2	2:F:87:TYR:CE2	2.56	0.41
1:D:274:ASN:O	1:D:367:ASN:ND2	2.49	0.41
1:B:304:ARG:HB3	1:B:319:SER:OG	2.20	0.40
1:D:282:ILE:HG12	1:E:174:LEU:HD22	2.03	0.40
1:B:271:TRP:CG	1:B:307:ILE:HG21	2.56	0.40
2:F:79:LEU:HB3	2:F:102:LYS:HG3	2.04	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	205/218 (94%)	200 (98%)	5 (2%)	0	100	100
1	B	201/218 (92%)	195 (97%)	5 (2%)	1 (0%)	32	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	209/218 (96%)	204 (98%)	5 (2%)	0	100	100
1	E	200/218 (92%)	193 (96%)	6 (3%)	1 (0%)	32	68
2	C	130/139 (94%)	127 (98%)	3 (2%)	0	100	100
2	F	131/139 (94%)	129 (98%)	2 (2%)	0	100	100
All	All	1076/1150 (94%)	1048 (97%)	26 (2%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	237	ILE
1	B	238	VAL

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	186/194 (96%)	180 (97%)	6 (3%)	44	78
1	B	183/194 (94%)	177 (97%)	6 (3%)	43	77
1	D	191/194 (98%)	185 (97%)	6 (3%)	45	79
1	E	182/194 (94%)	173 (95%)	9 (5%)	29	63
2	C	109/113 (96%)	104 (95%)	5 (5%)	31	65
2	F	110/113 (97%)	108 (98%)	2 (2%)	64	89
All	All	961/1002 (96%)	927 (96%)	34 (4%)	41	75

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	160	LEU
1	A	228	ARG
1	A	239	SER
1	A	240	SER
1	A	304	ARG

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Mol	Chain	Res	Type
1	A	319	SER
1	B	165	GLU
1	B	188	GLU
1	B	208	LEU
1	B	228	ARG
1	B	238	VAL
1	B	306	ASP
1	D	157	ARG
1	D	177	LEU
1	D	182	ARG
1	D	189	ASP
1	D	194	LYS
1	D	231	LEU
1	E	181	GLN
1	E	186	ASP
1	E	191	LEU
1	E	203	ASP
1	E	237	ILE
1	E	273	GLU
1	E	307	ILE
1	E	319	SER
1	E	367	ASN
2	C	11	GLN
2	C	87	TYR
2	C	118	ASN
2	C	128	MET
2	C	131	LEU
2	F	118	ASN
2	F	131	LEU

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

Mol	Chain	Res	Type
1	D	224	GLN
1	E	181	GLN
1	E	225	GLN
1	E	255	GLN
1	E	274	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 7 are monoatomic - leaving 4 for Mogul analysis.

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
3	ACP	A	401	4	27,33,33	0.80	1 (3%)	30,52,52	0.78	1 (3%)
3	ACP	B	401	4	27,33,33	0.62	0	30,52,52	0.93	1 (3%)
3	ACP	D	401	4	27,33,33	0.98	1 (3%)	30,52,52	0.72	1 (3%)
3	ACP	E	401	4	27,33,33	0.59	0	30,52,52	0.96	1 (3%)

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
3	ACP	A	401	4	-	0/15/38/38	0/3/3/3
3	ACP	B	401	4	-	0/15/38/38	0/3/3/3
3	ACP	D	401	4	-	0/15/38/38	0/3/3/3
3	ACP	E	401	4	-	0/15/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	ACP	PB-O3A	3.25	1.62	1.58
3	D	401	ACP	PB-O3A	4.27	1.63	1.58

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	D	401	ACP	O1B-PB-C3B	2.79	115.88	108.97
3	A	401	ACP	O1B-PB-C3B	3.26	117.04	108.97
3	B	401	ACP	O1B-PB-C3B	3.71	118.13	108.97
3	E	401	ACP	O1B-PB-C3B	4.28	119.55	108.97

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	209/218 (95%)	0.21	10 (4%) 31 27	57, 94, 153, 189	0
1	B	207/218 (94%)	0.14	5 (2%) 59 55	65, 100, 142, 175	0
1	D	213/218 (97%)	0.26	8 (3%) 41 35	63, 94, 155, 182	0
1	E	206/218 (94%)	0.13	3 (1%) 74 72	67, 98, 138, 163	0
2	C	132/139 (94%)	0.10	3 (2%) 61 57	61, 91, 122, 138	0
2	F	133/139 (95%)	0.28	2 (1%) 74 72	65, 98, 132, 159	0
All	All	1100/1150 (95%)	0.19	31 (2%) 53 48	57, 96, 146, 189	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	239	SER	3.6
1	A	329	ASN	3.4
1	B	243	GLY	3.3
2	F	7	ALA	3.3
1	D	330	SER	3.2
1	D	337	LEU	3.0
1	A	159	ARG	3.0
2	C	44	LYS	2.7
1	A	296	LYS	2.7
1	A	261	ASP	2.7
1	A	324	PHE	2.7
2	F	87	TYR	2.6
1	E	243	GLY	2.4
1	A	263	MET	2.4
1	D	332	SER	2.4
1	A	257	LEU	2.3
1	A	323	THR	2.3
1	D	326	GLY	2.2
2	C	59	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	299	GLN	2.2
1	D	294	VAL	2.2
1	A	244	ILE	2.2
1	B	259	ALA	2.2
1	D	316	ILE	2.2
1	E	357	ASN	2.1
1	B	284	SER	2.1
2	C	65	ALA	2.1
1	A	255	GLN	2.0
1	B	355	THR	2.0
1	E	259	ALA	2.0
1	D	297	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 carbohydrates 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. 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
4	MG	C	201	1/1	0.70	0.32	2.43	62,62,62,62	1
3	ACP	E	401	31/31	0.98	0.11	-1.07	99,111,127,133	0
3	ACP	B	401	31/31	0.97	0.12	-1.15	102,130,140,144	0
3	ACP	A	401	31/31	0.94	0.17	-1.23	116,127,139,140	0
3	ACP	D	401	31/31	0.93	0.17	-1.43	141,149,160,163	0
5	K	C	202	1/1	0.74	0.13	-1.60	109,109,109,109	0
5	K	F	201	1/1	0.86	0.10	-2.61	121,121,121,121	0
4	MG	A	402	1/1	0.96	0.08	-	127,127,127,127	0
4	MG	D	402	1/1	0.98	0.13	-	159,159,159,159	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	MG	E	402	1/1	0.95	0.05	-	126,126,126,126	0
4	MG	B	402	1/1	0.92	0.04	-	99,99,99,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.