



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:08 pm GMT

PDB ID : 3NFI
Title : Crystal structure of tandem winged helix domain of RNA polymerase I subunit A49
Authors : Geiger, S.R.; Lorenzen, K.; Schrieck, A.; Hanecker, P.; Kostrewa, D.; Heck, A.J.R.; Cramer, P.
Deposited on : 2010-06-10
Resolution : 1.90 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	:	trunk28620
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)	:	recalc28949

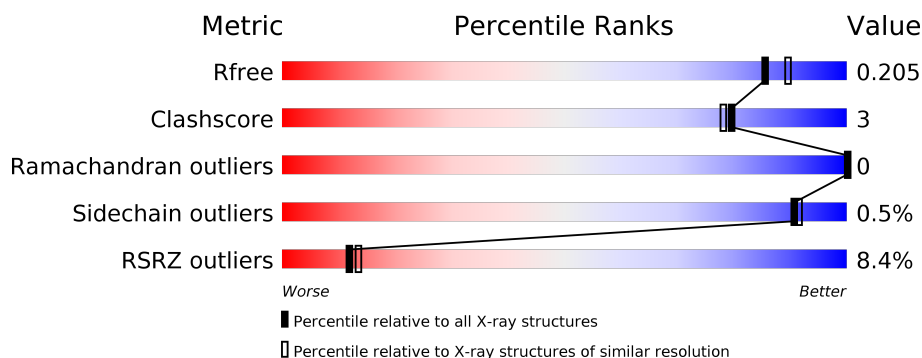
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (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. 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	237	<div> <div>4%</div> <div>84%</div> <div>8%</div> <div>8%</div> </div>
1	B	237	<div> <div>14%</div> <div>89%</div> <div>6%</div> <div>•</div> </div>
1	C	237	<div> <div>8%</div> <div>82%</div> <div>8%</div> <div>10%</div> </div>
1	D	237	<div> <div>3%</div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
1	E	237	<div> <div>9%</div> <div>81%</div> <div>8%</div> <div>11%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9695 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 DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	Se	0	9	0
			1798	1167	296	329	1	5			
1	B	227	Total	C	N	O	S	Se	0	5	0
			1838	1189	304	338	1	6			
1	C	214	Total	C	N	O	S	Se	0	9	0
			1750	1139	285	319	1	6			
1	D	220	Total	C	N	O	S	Se	0	6	0
			1790	1161	296	327	1	5			
1	E	212	Total	C	N	O	S	Se	0	7	0
			1721	1120	278	316	1	6			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	GLY	-	EXPRESSION TAG	UNP Q01080
A	168	SER	-	EXPRESSION TAG	UNP Q01080
A	169	HIS	-	EXPRESSION TAG	UNP Q01080
A	170	MSE	-	EXPRESSION TAG	UNP Q01080
A	178	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
A	261	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
B	167	GLY	-	EXPRESSION TAG	UNP Q01080
B	168	SER	-	EXPRESSION TAG	UNP Q01080
B	169	HIS	-	EXPRESSION TAG	UNP Q01080
B	170	MSE	-	EXPRESSION TAG	UNP Q01080
B	178	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
B	261	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
C	167	GLY	-	EXPRESSION TAG	UNP Q01080
C	168	SER	-	EXPRESSION TAG	UNP Q01080
C	169	HIS	-	EXPRESSION TAG	UNP Q01080
C	170	MSE	-	EXPRESSION TAG	UNP Q01080
C	178	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
C	261	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
D	167	GLY	-	EXPRESSION TAG	UNP Q01080

Continued on next page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	168	SER	-	EXPRESSION TAG	UNP Q01080
D	169	HIS	-	EXPRESSION TAG	UNP Q01080
D	170	MSE	-	EXPRESSION TAG	UNP Q01080
D	178	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
D	261	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
E	167	GLY	-	EXPRESSION TAG	UNP Q01080
E	168	SER	-	EXPRESSION TAG	UNP Q01080
E	169	HIS	-	EXPRESSION TAG	UNP Q01080
E	170	MSE	-	EXPRESSION TAG	UNP Q01080
E	178	MSE	LEU	ENGINEERED MUTATION	UNP Q01080
E	261	MSE	LEU	ENGINEERED MUTATION	UNP Q01080

- # PE4

- Molecule 3 is water.

Continued on next page...

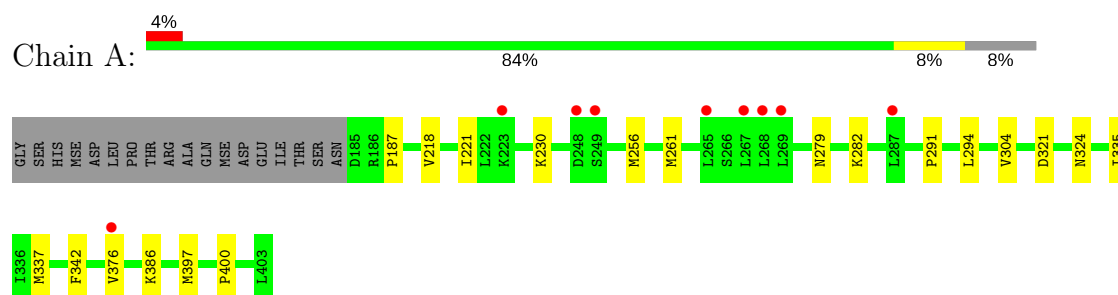
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	116	Total 116	O 116	0	0
3	D	156	Total 156	O 156	0	0
3	E	142	Total 142	O 142	0	0

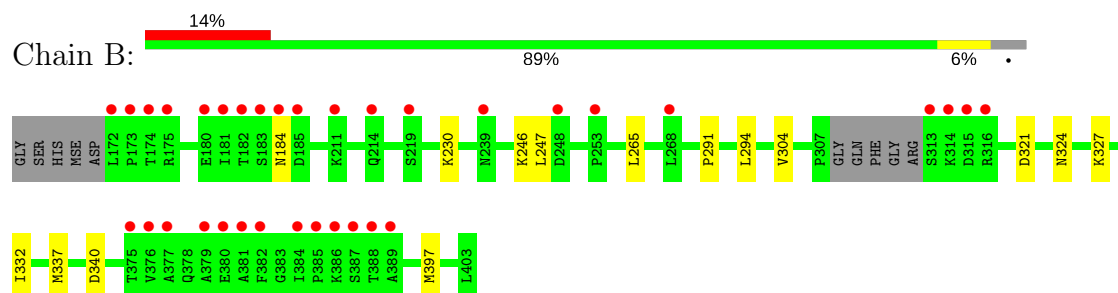
3 Residue-property plots [i](#)

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.

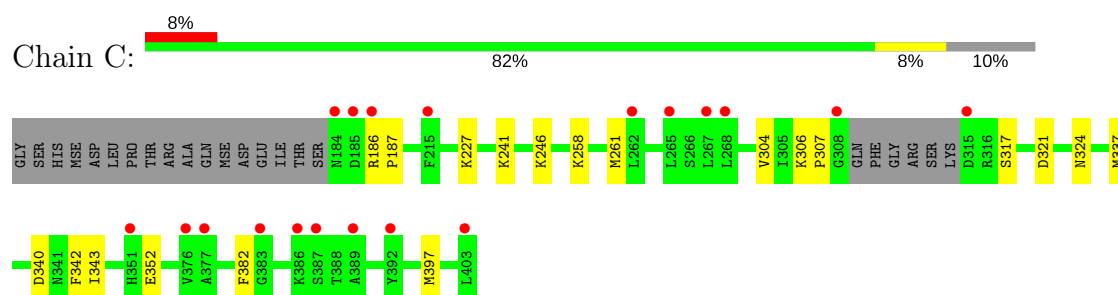
- Molecule 1: DNA-directed RNA polymerase I subunit RPA49



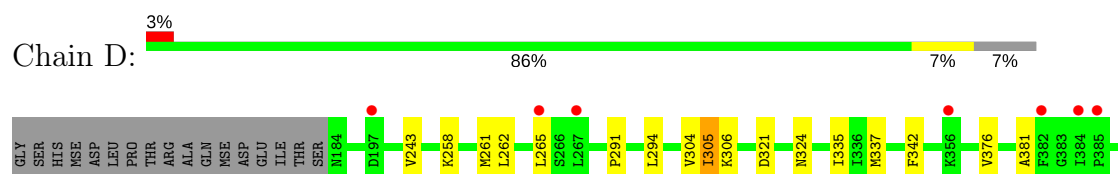
- Molecule 1: DNA-directed RNA polymerase I subunit RPA49



- Molecule 1: DNA-directed RNA polymerase I subunit RPA49

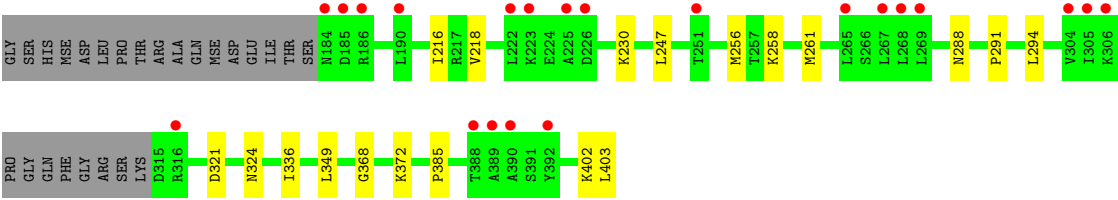
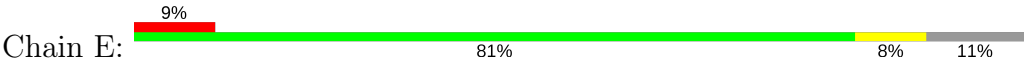


- Molecule 1: DNA-directed RNA polymerase I subunit RPA49



L403

● Molecule 1: DNA-directed RNA polymerase I subunit RPA49



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.11Å 78.10Å 100.67Å 90.00° 113.39° 90.00°	Depositor
Resolution (Å)	27.82 – 1.90 30.87 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (27.82-1.90) 98.3 (30.87-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 1.89Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.189 , 0.224 0.203 , 0.205	Depositor DCC
R_{free} test set	4564 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9695	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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: PE4

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	0.50	0/1852	0.61	0/2496
1	B	0.46	0/1878	0.59	0/2531
1	C	0.47	0/1805	0.62	0/2433
1	D	0.51	0/1834	0.62	0/2471
1	E	0.64	1/1768 (0.1%)	0.60	0/2383
All	All	0.52	1/9137 (0.0%)	0.61	0/12314

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	403	LEU	C-OXT	-15.93	0.93	1.23

There are no bond angle outliers.

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	1798	0	1902	15	0
1	B	1838	0	1936	11	0
1	C	1750	0	1861	13	0
1	D	1790	0	1890	9	0
1	E	1721	0	1817	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	12	0	14	1	0
3	A	226	0	0	1	0
3	B	146	0	0	0	0
3	C	116	0	0	0	0
3	D	156	0	0	0	0
3	E	142	0	0	1	0
All	All	9695	0	9420	58	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 3.

All (58) 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:218:VAL:HG23	1:A:256:MSE:SE	2.30	0.80
1:A:337[B]:MSE:SE	1:A:397:MSE:HG3	2.32	0.79
1:C:337[B]:MSE:SE	1:C:397:MSE:SE	3.03	0.77
1:A:187:PRO:HB2	3:A:781:HOH:O	1.85	0.77
1:C:337[B]:MSE:SE	1:C:397:MSE:HG3	2.36	0.76
1:B:184:ASN:HA	1:B:327:LYS:HZ2	1.51	0.75
1:A:337[B]:MSE:SE	1:A:397:MSE:SE	3.05	0.74
1:B:184:ASN:HA	1:B:327:LYS:NZ	2.04	0.72
1:A:304:VAL:HG23	1:A:324:ASN:HD21	1.55	0.70
1:B:304:VAL:HG23	1:B:324:ASN:HD21	1.55	0.70
1:E:218:VAL:HG23	1:E:256[B]:MSE:SE	2.47	0.65
1:B:337[B]:MSE:SE	1:B:397:MSE:SE	3.16	0.63
1:D:304:VAL:HG23	1:D:324:ASN:HD21	1.64	0.62
1:C:304:VAL:HG23	1:C:324:ASN:HD21	1.67	0.60
1:A:337[B]:MSE:SE	1:A:397:MSE:CG	2.99	0.60
1:E:372:LYS:HA	2:E:1:PE4:H121	1.82	0.60
1:E:368:GLY:CA	1:E:402:LYS:HE3	2.32	0.59
1:C:241:LYS:HB2	1:C:352:GLU:OE1	2.03	0.58
1:E:368:GLY:HA2	1:E:402:LYS:HE3	1.84	0.58
1:C:337[B]:MSE:SE	1:C:397:MSE:CG	3.01	0.58
1:A:321:ASP:H	1:A:324:ASN:HD22	1.53	0.55
1:A:218:VAL:CG2	1:A:256:MSE:SE	3.02	0.55
1:D:321:ASP:H	1:D:324:ASN:HD22	1.54	0.54
1:B:321:ASP:H	1:B:324:ASN:HD22	1.55	0.54
1:E:321:ASP:H	1:E:324:ASN:HD22	1.56	0.53
1:A:400:PRO:HB3	1:C:307:PRO:HB2	1.90	0.52
1:A:221:ILE:HG23	1:A:230:LYS:HG2	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:MSE:HB3	1:A:335:ILE:HG23	1.94	0.50
1:D:305:ILE:HG12	1:D:306:LYS:N	2.27	0.49
1:B:265[B]:LEU:HD11	1:B:332:ILE:HG23	1.96	0.47
1:C:343:ILE:HG12	1:C:382:PHE:HZ	1.79	0.47
1:D:337:MSE:SE	1:D:342:PHE:HA	2.65	0.47
1:A:337[A]:MSE:SE	1:A:342:PHE:HA	2.65	0.46
1:C:337[A]:MSE:SE	1:C:342:PHE:HA	2.65	0.46
1:D:381:ALA:HA	1:E:385:PRO:HB3	1.98	0.45
1:D:265:LEU:HB2	1:D:335:ILE:HG21	1.98	0.45
1:E:288:ASN:ND2	3:E:503:HOH:O	2.50	0.45
1:B:246:LYS:HE3	1:B:340:ASP:OD1	2.17	0.45
1:D:291:PRO:HD2	1:D:294:LEU:HD12	1.98	0.45
1:E:336:ILE:HD13	1:E:349:LEU:HD11	1.99	0.44
1:D:243:VAL:HA	1:D:262:LEU:HD11	1.99	0.44
1:B:265[B]:LEU:CD1	1:B:332:ILE:HG23	2.47	0.44
1:C:246:LYS:HE3	1:C:340:ASP:OD1	2.18	0.44
1:C:186:ARG:HG3	1:C:187:PRO:HD2	1.99	0.44
1:A:291:PRO:HD2	1:A:294:LEU:HD12	2.00	0.44
1:C:306:LYS:HG3	1:C:317:SER:HB3	1.99	0.43
1:C:258:LYS:HA	1:C:261:MSE:HE3	2.00	0.43
1:E:216:ILE:HG12	1:E:294:LEU:HD11	2.01	0.43
1:E:230:LYS:HB3	1:E:247:LEU:HD21	2.01	0.43
1:B:230:LYS:HB3	1:B:247:LEU:HD21	2.01	0.42
1:C:321:ASP:H	1:C:324:ASN:HD22	1.67	0.42
1:A:337[B]:MSE:CE	1:A:397:MSE:HG3	2.49	0.42
1:D:258:LYS:HA	1:D:261:MSE:HE3	2.02	0.41
1:A:279:ASN:HD21	1:A:282:LYS:HD2	1.85	0.41
1:B:291:PRO:HD2	1:B:294:LEU:HD12	2.02	0.41
1:E:291:PRO:HD2	1:E:294:LEU:HD12	2.02	0.41
1:E:258:LYS:HA	1:E:261:MSE:HE3	2.02	0.40
1:B:337[B]:MSE:SE	1:B:397:MSE:HG3	2.72	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	226/237 (95%)	221 (98%)	5 (2%)	0	100	100
1	B	228/237 (96%)	227 (100%)	1 (0%)	0	100	100
1	C	219/237 (92%)	217 (99%)	2 (1%)	0	100	100
1	D	224/237 (94%)	219 (98%)	5 (2%)	0	100	100
1	E	215/237 (91%)	213 (99%)	2 (1%)	0	100	100
All	All	1112/1185 (94%)	1097 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	207/208 (100%)	205 (99%)	2 (1%)	80	80
1	B	211/208 (101%)	211 (100%)	0	100	100
1	C	203/208 (98%)	202 (100%)	1 (0%)	91	91
1	D	205/208 (99%)	203 (99%)	2 (1%)	80	80
1	E	197/208 (95%)	197 (100%)	0	100	100
All	All	1023/1040 (98%)	1018 (100%)	5 (0%)	91	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	376	VAL
1	A	386	LYS
1	C	227	LYS
1	D	305	ILE
1	D	376	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	200	GLN
1	A	278	ASN
1	A	324	ASN
1	B	237	GLN
1	B	324	ASN
1	B	341	ASN
1	C	238	ASN
1	C	252	GLN
1	C	324	ASN
1	D	324	ASN
1	D	341	ASN
1	E	252	GLN
1	E	324	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	PE4	E	1	-	11,11,23	1.06	0	10,10,22	1.77	3 (30%)

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	PE4	E	1	-	-	0/9/9/21	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	PE4	O5-C8-C7	-2.53	98.48	110.15
2	E	1	PE4	C11-O6-C10	2.49	124.07	113.30
2	E	1	PE4	O7-C12-C11	2.92	123.81	110.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	PE4	1	0

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	215/237 (90%)	0.05	9 (4%) 37 40	21, 31, 58, 79	0
1	B	222/237 (93%)	0.68	34 (15%) 2 2	22, 40, 100, 131	0
1	C	210/237 (88%)	0.31	19 (9%) 10 11	24, 40, 70, 100	0
1	D	216/237 (91%)	0.03	7 (3%) 48 51	18, 31, 59, 84	0
1	E	208/237 (87%)	0.27	21 (10%) 8 8	22, 34, 65, 103	0
All	All	1071/1185 (90%)	0.27	90 (8%) 12 13	18, 35, 75, 131	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	174	THR	9.9
1	B	314	LYS	8.3
1	B	313	SER	7.4
1	E	184	ASN	6.4
1	B	315	ASP	6.3
1	B	182	THR	5.5
1	B	386	LYS	5.4
1	E	185	ASP	5.3
1	B	384	ILE	5.1
1	B	253	PRO	5.1
1	B	376	VAL	4.7
1	E	305	ILE	4.6
1	C	389	ALA	4.6
1	C	392	TYR	4.3
1	C	387	SER	4.0
1	B	183	SER	4.0
1	B	175	ARG	3.9
1	C	308	GLY	3.9
1	B	173	PRO	3.8
1	B	316	ARG	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	316	ARG	3.6
1	E	225	ALA	3.5
1	E	388	THR	3.5
1	D	384	ILE	3.4
1	C	376	VAL	3.4
1	C	351[A]	HIS	3.4
1	B	219	SER	3.3
1	C	268	LEU	3.3
1	C	185	ASP	3.2
1	B	214	GLN	3.1
1	B	379	ALA	3.0
1	B	180	GLU	3.0
1	B	385	PRO	3.0
1	E	222	LEU	3.0
1	E	269	LEU	2.9
1	E	251	THR	2.9
1	B	381	ALA	2.9
1	B	380	GLU	2.8
1	E	392	TYR	2.8
1	A	267	LEU	2.8
1	B	375	THR	2.8
1	E	389	ALA	2.8
1	A	268	LEU	2.8
1	E	226	ASP	2.7
1	C	265[A]	LEU	2.7
1	B	181	ILE	2.7
1	B	248	ASP	2.7
1	B	211	LYS	2.7
1	B	185	ASP	2.6
1	B	239	ASN	2.6
1	B	172	LEU	2.6
1	B	184	ASN	2.6
1	E	306	LYS	2.6
1	D	197[A]	ASP	2.6
1	C	215	PHE	2.5
1	E	265	LEU	2.5
1	C	184	ASN	2.5
1	C	267	LEU	2.5
1	A	376	VAL	2.5
1	D	356	LYS	2.5
1	C	186	ARG	2.5
1	E	304	VAL	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	377	ALA	2.4
1	D	267	LEU	2.4
1	E	267	LEU	2.4
1	C	383	GLY	2.4
1	C	386	LYS	2.4
1	A	265	LEU	2.4
1	B	388	THR	2.4
1	A	287	LEU	2.4
1	A	223	LYS	2.3
1	A	248	ASP	2.3
1	A	269	LEU	2.2
1	C	377	ALA	2.2
1	C	315	ASP	2.2
1	A	249	SER	2.2
1	B	387	SER	2.2
1	B	389	ALA	2.2
1	D	385	PRO	2.1
1	C	262	LEU	2.1
1	C	403	LEU	2.1
1	D	265	LEU	2.1
1	D	382	PHE	2.1
1	B	382	PHE	2.1
1	E	190	LEU	2.1
1	E	186	ARG	2.0
1	E	390	ALA	2.0
1	E	268	LEU	2.0
1	E	223	LYS	2.0
1	B	268	LEU	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
2	PE4	E	1	12/24	0.94	0.17	0.49	32,36,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.