



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:46 pm GMT

PDB ID : 3UTC
Title : Ec_IspH in complex with (E)-4-hydroxybut-3-enyl diphosphate
Authors : Span, I.; Wang, K.; Wang, W.; Zhang, Y.; Bacher, A.; Eisenreich, W.; Li, K.;
Schulz, C.; Oldfield, E.; Groll, M.
Deposited on : 2011-11-25
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

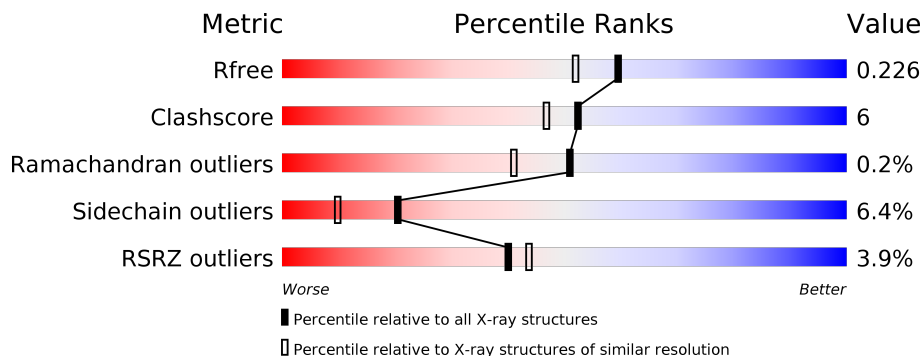
1 Overall quality at a glance

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	324	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>• 5%</div> </div> </div>
1	B	324	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>11%</div> <div>• • •</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5192 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 4-hydroxy-3-methylbut-2-enyl diphosphate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2383	1487	427	459	10			
1	B	310	Total	C	N	O	S	0	0	0
			2390	1492	428	460	10			

There are 16 discrepancies between the modelled and reference sequences:

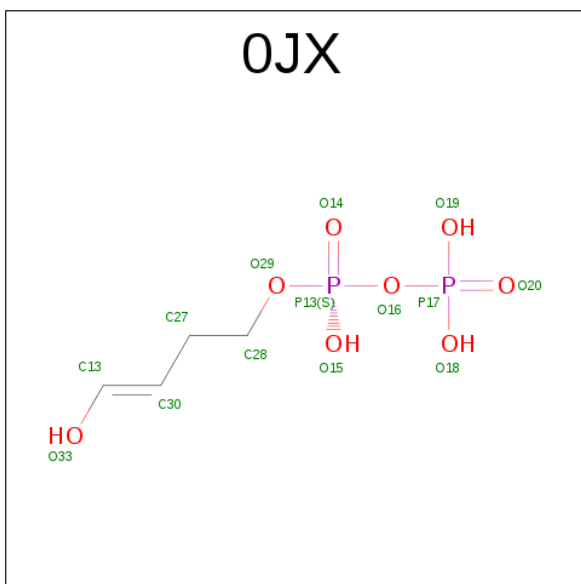
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	EXPRESSION TAG	UNP P62623
A	-6	HIS	-	EXPRESSION TAG	UNP P62623
A	-5	HIS	-	EXPRESSION TAG	UNP P62623
A	-4	HIS	-	EXPRESSION TAG	UNP P62623
A	-3	HIS	-	EXPRESSION TAG	UNP P62623
A	-2	HIS	-	EXPRESSION TAG	UNP P62623
A	-1	GLY	-	EXPRESSION TAG	UNP P62623
A	0	SER	-	EXPRESSION TAG	UNP P62623
B	-7	HIS	-	EXPRESSION TAG	UNP P62623
B	-6	HIS	-	EXPRESSION TAG	UNP P62623
B	-5	HIS	-	EXPRESSION TAG	UNP P62623
B	-4	HIS	-	EXPRESSION TAG	UNP P62623
B	-3	HIS	-	EXPRESSION TAG	UNP P62623
B	-2	HIS	-	EXPRESSION TAG	UNP P62623
B	-1	GLY	-	EXPRESSION TAG	UNP P62623
B	0	SER	-	EXPRESSION TAG	UNP P62623

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is (3E)-4-HYDROXYBUT-3-EN-1-YL TRIHYDROGEN DIPHOSPHATE (three-letter code: 0JX) (formula: $C_4H_{10}O_8P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			14	4	8	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	0
			14	4	8	2		

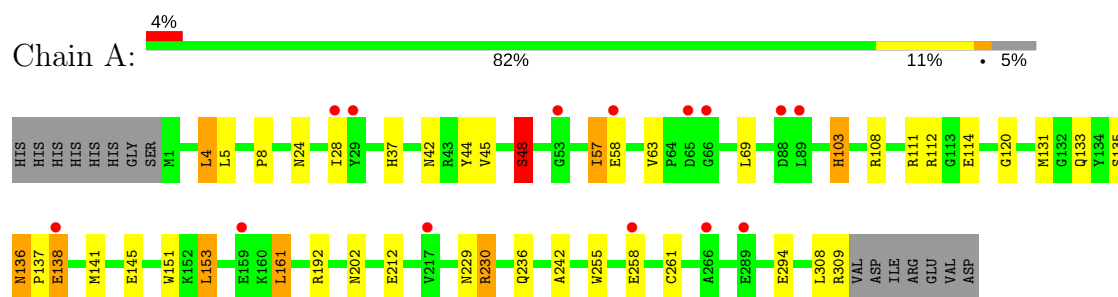
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	183	Total	O	0	0
			183	183		
4	B	192	Total	O	0	0
			192	192		

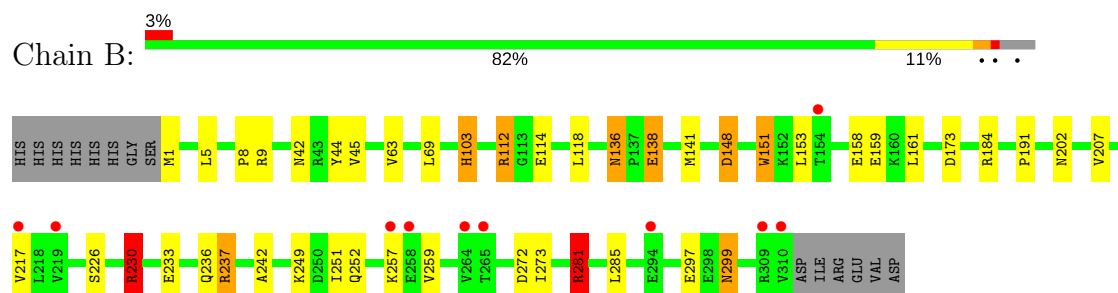
3 Residue-property plots [i](#)

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: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase



- Molecule 1: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.12Å 80.79Å 112.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.85 – 1.90 24.85 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (24.85-1.90) 99.0 (24.85-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.147 , 0.227 0.146 , 0.226	Depositor DCC
R_{free} test set	2524 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.502	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5192	wwPDB-VP
Average B, all atoms (Å ²)	35.0	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 46.77 % 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 1.0914e-04. 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: SF4, OJX

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	0.90	2/2418 (0.1%)	1.04	6/3273 (0.2%)
1	B	0.88	1/2425 (0.0%)	0.98	11/3283 (0.3%)
All	All	0.89	3/4843 (0.1%)	1.01	17/6556 (0.3%)

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	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	151	TRP	CD2-CE2	6.57	1.49	1.41
1	B	151	TRP	CD2-CE2	6.43	1.49	1.41
1	A	255	TRP	CD2-CE2	5.55	1.48	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	ARG	NE-CZ-NH1	-23.01	108.80	120.30
1	A	230	ARG	NE-CZ-NH2	14.93	127.77	120.30
1	B	230	ARG	NE-CZ-NH1	-12.91	113.85	120.30
1	B	230	ARG	NE-CZ-NH2	10.42	125.51	120.30
1	A	230	ARG	CG-CD-NE	-8.98	92.94	111.80
1	B	230	ARG	CG-CD-NE	-8.62	93.69	111.80
1	B	173	ASP	CB-CG-OD2	6.62	124.26	118.30
1	B	281	ARG	NE-CZ-NH1	6.44	123.52	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	ARG	CD-NE-CZ	6.24	132.33	123.60
1	B	184	ARG	NE-CZ-NH1	-5.98	117.31	120.30
1	B	237	ARG	NE-CZ-NH1	-5.65	117.47	120.30
1	B	9	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	A	153	LEU	CA-CB-CG	5.32	127.55	115.30
1	B	237	ARG	CB-CG-CD	5.22	125.18	111.60
1	A	161	LEU	CA-CB-CG	5.16	127.16	115.30
1	B	237	ARG	CA-CB-CG	-5.04	102.31	113.40
1	B	184	ARG	NE-CZ-NH2	5.01	122.81	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	308	LEU	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	2383	0	2395	31	0
1	B	2390	0	2404	30	0
2	A	8	0	0	0	0
2	B	8	0	0	0	0
3	A	14	0	7	1	0
3	B	14	0	8	0	0
4	A	183	0	0	5	1
4	B	192	0	0	7	1
All	All	5192	0	4814	61	1

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 6.

All (61) 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:B:112:ARG:HG3	1:B:112:ARG:HH21	1.25	0.99
1:A:24:ASN:O	1:A:28:ILE:HG12	1.76	0.86
1:A:42:ASN:HD22	1:A:45:VAL:H	1.26	0.82
1:B:42:ASN:HD22	1:B:45:VAL:H	1.28	0.82
1:A:4:LEU:HD22	1:A:261:CYS:SG	2.22	0.80
1:B:112:ARG:CB	1:B:114:GLU:HG3	2.26	0.66
1:B:272:ASP:OD2	4:B:580:HOH:O	2.13	0.66
1:B:236:GLN:HG2	4:B:404:HOH:O	1.96	0.66
1:B:112:ARG:HB3	1:B:114:GLU:HG3	1.79	0.65
1:A:57:ILE:HD12	1:A:63:VAL:HG22	1.81	0.62
1:B:103:HIS:HE1	4:B:328:HOH:O	1.84	0.59
1:A:57:ILE:HD12	1:A:63:VAL:CG2	2.32	0.59
1:A:103:HIS:HE1	4:A:322:HOH:O	1.86	0.58
1:B:42:ASN:ND2	1:B:45:VAL:H	2.01	0.57
1:B:112:ARG:CG	1:B:112:ARG:HH21	2.07	0.56
1:A:136:ASN:ND2	1:A:138:GLU:HB2	2.20	0.56
1:B:112:ARG:HG3	1:B:112:ARG:NH2	2.04	0.55
1:A:42:ASN:ND2	1:A:45:VAL:H	2.01	0.55
1:A:136:ASN:HD21	1:A:138:GLU:HB2	1.72	0.54
1:B:118:LEU:HB2	1:B:141:MET:CE	2.38	0.54
1:B:136:ASN:ND2	1:B:138:GLU:H	2.06	0.54
1:B:252:GLN:OE1	4:B:528:HOH:O	2.18	0.53
3:A:318:0JX:H7	3:A:318:0JX:O16	2.08	0.52
1:B:251:ILE:HD12	1:B:281:ARG:HG2	1.91	0.52
1:A:131:MET:HA	1:A:141:MET:HE3	1.92	0.52
1:A:37:HIS:CD2	1:A:58:GLU:HA	2.45	0.52
1:A:44:TYR:O	1:A:48:SER:HB2	2.09	0.51
1:B:1:MET:HG3	1:B:259:VAL:O	2.10	0.51
1:A:103:HIS:CE1	4:A:322:HOH:O	2.61	0.51
1:B:112:ARG:HB2	1:B:114:GLU:HG3	1.94	0.50
1:A:131:MET:HA	1:A:141:MET:CE	2.43	0.49
1:B:297:GLU:HG3	4:B:460:HOH:O	2.12	0.49
1:B:103:HIS:CE1	4:B:328:HOH:O	2.63	0.48
1:A:112:ARG:HB2	1:A:114:GLU:HG3	1.96	0.47
1:B:136:ASN:C	1:B:136:ASN:HD22	2.18	0.47
1:B:8:PRO:HG2	1:B:202:ASN:HB3	1.97	0.46
1:A:212:GLU:HG3	4:A:521:HOH:O	2.16	0.46
1:A:37:HIS:HD2	1:A:58:GLU:HA	1.79	0.45
1:A:4:LEU:CD2	1:A:261:CYS:SG	3.00	0.45
1:A:108:ARG:NH1	1:A:108:ARG:HB2	2.31	0.45
1:B:158:GLU:HG3	4:B:364:HOH:O	2.17	0.45
1:A:192:ARG:NH2	1:B:191:PRO:HD3	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:ILE:CD1	1:A:63:VAL:CG2	2.94	0.44
1:A:135:SER:O	1:A:137:PRO:HD3	2.18	0.44
1:A:108:ARG:O	1:A:112:ARG:HG3	2.19	0.43
1:A:120:GLY:O	1:A:145:GLU:HG2	2.18	0.43
1:B:112:ARG:CG	1:B:112:ARG:NH2	2.72	0.43
1:A:136:ASN:ND2	1:A:138:GLU:H	2.16	0.43
1:A:136:ASN:HD22	1:A:136:ASN:C	2.21	0.43
1:A:8:PRO:HG2	1:A:202:ASN:HB3	1.99	0.43
1:B:233:GLU:O	1:B:237:ARG:HG3	2.18	0.43
1:B:63:VAL:HG21	1:B:69:LEU:HD13	2.01	0.42
1:B:230:ARG:HD3	1:B:230:ARG:HA	1.83	0.42
1:B:217:VAL:O	1:B:242:ALA:HA	2.19	0.42
1:A:236:GLN:HG3	1:A:242:ALA:HB3	2.01	0.42
1:B:299:ASN:HD22	1:B:299:ASN:C	2.23	0.42
1:B:148:ASP:HA	1:B:151:TRP:CD1	2.55	0.42
1:A:42:ASN:HD21	1:A:44:TYR:HB3	1.85	0.41
1:A:133:GLN:NE2	4:A:420:HOH:O	2.54	0.41
1:B:42:ASN:HD21	1:B:44:TYR:HB3	1.85	0.41
1:A:111:ARG:NH1	4:A:414:HOH:O	2.53	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:320:HOH:O	4:B:503:HOH:O[2_454]	1.59	0.61

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	307/324 (95%)	302 (98%)	4 (1%)	1 (0%)	44 34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	308/324 (95%)	306 (99%)	2 (1%)	0	100	100
All	All	615/648 (95%)	608 (99%)	6 (1%)	1 (0%)	51	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	SER

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	257/271 (95%)	242 (94%)	15 (6%)	23	12
1	B	258/271 (95%)	240 (93%)	18 (7%)	18	8
All	All	515/542 (95%)	482 (94%)	33 (6%)	20	10

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	5	LEU
1	A	48	SER
1	A	57	ILE
1	A	69	LEU
1	A	103	HIS
1	A	136	ASN
1	A	138	GLU
1	A	153	LEU
1	A	161	LEU
1	A	229	ASN
1	A	230	ARG
1	A	258	GLU
1	A	294	GLU
1	A	309	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	5	LEU
1	B	103	HIS
1	B	112	ARG
1	B	136	ASN
1	B	138	GLU
1	B	148	ASP
1	B	153	LEU
1	B	159	GLU
1	B	161	LEU
1	B	207	VAL
1	B	226	SER
1	B	230	ARG
1	B	249	LYS
1	B	257	LYS
1	B	273	ILE
1	B	281	ARG
1	B	285	LEU
1	B	299	ASN

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	37	HIS
1	A	42	ASN
1	A	59	GLN
1	A	78	GLN
1	A	103	HIS
1	A	133	GLN
1	A	136	ASN
1	A	236	GLN
1	A	277	ASN
1	A	283	GLN
1	B	2	GLN
1	B	42	ASN
1	B	78	GLN
1	B	103	HIS
1	B	133	GLN
1	B	136	ASN
1	B	213	GLN
1	B	283	GLN
1	B	299	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 ⓘ

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	SF4	A	317	1,3	0,12,12	0.00	-	0,24,24	0.00	-
3	OJX	A	318	2	11,13,13	1.20	1 (9%)	11,18,18	1.71	2 (18%)
2	SF4	B	317	1,3	0,12,12	0.00	-	0,24,24	0.00	-
3	OJX	B	318	2	11,13,13	1.24	1 (9%)	11,18,18	2.09	1 (9%)

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	SF4	A	317	1,3	-	0/0/48/48	0/6/5/5
3	OJX	A	318	2	-	0/12/13/13	0/0/0/0
2	SF4	B	317	1,3	-	0/0/48/48	0/6/5/5
3	OJX	B	318	2	-	0/12/13/13	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	318	OJX	P17-O19	-2.50	1.44	1.54
3	A	318	OJX	P17-O18	-2.31	1.45	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	318	OJX	C27-C30-C13	-6.14	101.59	125.64
3	A	318	OJX	C27-C30-C13	-4.62	107.56	125.64
3	A	318	OJX	O18-P17-O19	2.06	115.94	107.61

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
3	A	318	OJX	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	309/324 (95%)	-0.01	14 (4%) 34 37	17, 32, 61, 77	0
1	B	310/324 (95%)	-0.00	10 (3%) 48 51	18, 32, 58, 75	0
All	All	619/648 (95%)	-0.00	24 (3%) 40 44	17, 32, 60, 77	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	310	VAL	4.8
1	B	217	VAL	3.0
1	A	159	GLU	2.9
1	B	258	GLU	2.9
1	A	65	ASP	2.8
1	B	154	THR	2.7
1	A	138	GLU	2.7
1	A	88	ASP	2.7
1	B	257	LYS	2.5
1	A	258	GLU	2.5
1	B	294	GLU	2.4
1	A	289	GLU	2.4
1	B	265	THR	2.4
1	B	219	VAL	2.4
1	A	28	ILE	2.3
1	B	309	ARG	2.3
1	B	264	VAL	2.3
1	A	66	GLY	2.2
1	A	266	ALA	2.2
1	A	58	GLU	2.2
1	A	217	VAL	2.2
1	A	53	GLY	2.1
1	A	29	TYR	2.0
1	A	89	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(\AA^2)	Q<0.9
2	SF4	A	317	8/8	1.00	0.11	-0.21	18,20,21,26	0
2	SF4	B	317	8/8	1.00	0.10	-0.35	19,20,22,26	0
3	OJX	A	318	14/14	0.99	0.08	-1.13	14,20,24,28	0
3	OJX	B	318	14/14	0.99	0.07	-1.34	14,20,24,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.