



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:46 AM GMT

PDB ID : 3FZY
Title : Crystal Structure of Pre-cleavage Form of Cysteine Protease Domain from *Vibrio cholerae* RtxA Toxin
Authors : Shuvalova, L.; Minasov, G.; Prochazkova, K.; Satchell, K.J.F.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2009-01-26
Resolution : 1.95 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

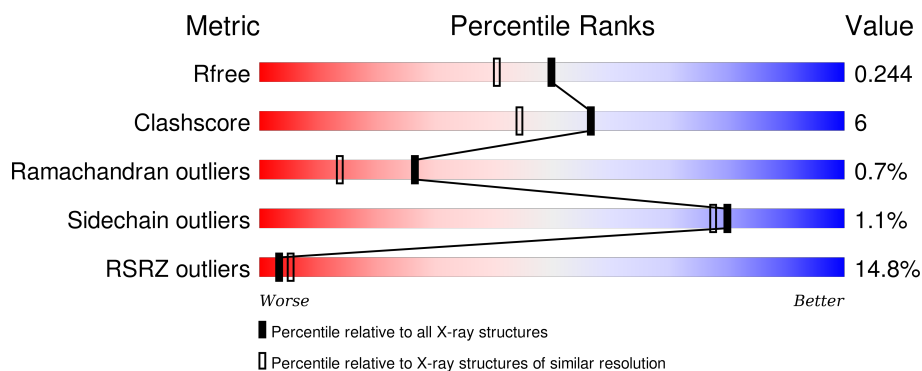
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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	234	 10% 81% 11% • 8%
1	B	234	 17% 80% 10% 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3890 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 RTX toxin RtxA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	17	0
			1794	1101	327	363	3			
1	B	211	Total	C	N	O	S	0	9	0
			1690	1030	313	345	2			

There are 48 discrepancies between the modelled and reference sequences:

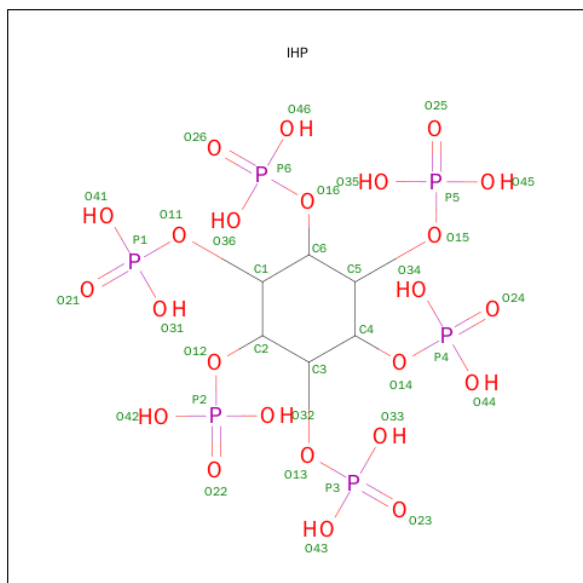
Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	EXPRESSION TAG	UNP Q9KS12
A	-22	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-21	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-20	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-19	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-18	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-17	HIS	-	EXPRESSION TAG	UNP Q9KS12
A	-16	SER	-	EXPRESSION TAG	UNP Q9KS12
A	-15	SER	-	EXPRESSION TAG	UNP Q9KS12
A	-14	GLY	-	EXPRESSION TAG	UNP Q9KS12
A	-13	VAL	-	EXPRESSION TAG	UNP Q9KS12
A	-12	ASP	-	EXPRESSION TAG	UNP Q9KS12
A	-11	LEU	-	EXPRESSION TAG	UNP Q9KS12
A	-10	GLY	-	EXPRESSION TAG	UNP Q9KS12
A	-9	THR	-	EXPRESSION TAG	UNP Q9KS12
A	-8	GLU	-	EXPRESSION TAG	UNP Q9KS12
A	-7	ASN	-	EXPRESSION TAG	UNP Q9KS12
A	-6	LEU	-	EXPRESSION TAG	UNP Q9KS12
A	-5	TYR	-	EXPRESSION TAG	UNP Q9KS12
A	-4	PHE	-	EXPRESSION TAG	UNP Q9KS12
A	-3	GLN	-	EXPRESSION TAG	UNP Q9KS12
A	-2	SER	-	EXPRESSION TAG	UNP Q9KS12
A	-1	ASN	-	EXPRESSION TAG	UNP Q9KS12
A	3568	SER	CYS	ENGINEERED	UNP Q9KS12
B	-23	MET	-	EXPRESSION TAG	UNP Q9KS12

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-21	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-20	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-19	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-18	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-17	HIS	-	EXPRESSION TAG	UNP Q9KS12
B	-16	SER	-	EXPRESSION TAG	UNP Q9KS12
B	-15	SER	-	EXPRESSION TAG	UNP Q9KS12
B	-14	GLY	-	EXPRESSION TAG	UNP Q9KS12
B	-13	VAL	-	EXPRESSION TAG	UNP Q9KS12
B	-12	ASP	-	EXPRESSION TAG	UNP Q9KS12
B	-11	LEU	-	EXPRESSION TAG	UNP Q9KS12
B	-10	GLY	-	EXPRESSION TAG	UNP Q9KS12
B	-9	THR	-	EXPRESSION TAG	UNP Q9KS12
B	-8	GLU	-	EXPRESSION TAG	UNP Q9KS12
B	-7	ASN	-	EXPRESSION TAG	UNP Q9KS12
B	-6	LEU	-	EXPRESSION TAG	UNP Q9KS12
B	-5	TYR	-	EXPRESSION TAG	UNP Q9KS12
B	-4	PHE	-	EXPRESSION TAG	UNP Q9KS12
B	-3	GLN	-	EXPRESSION TAG	UNP Q9KS12
B	-2	SER	-	EXPRESSION TAG	UNP Q9KS12
B	-1	ASN	-	EXPRESSION TAG	UNP Q9KS12
B	3568	SER	CYS	ENGINEERED	UNP Q9KS12

- Molecule 2 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			36	6	24	6		
2	B	1	Total	C	O	P	0	0
			36	6	24	6		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	X	0	0
			12	12		

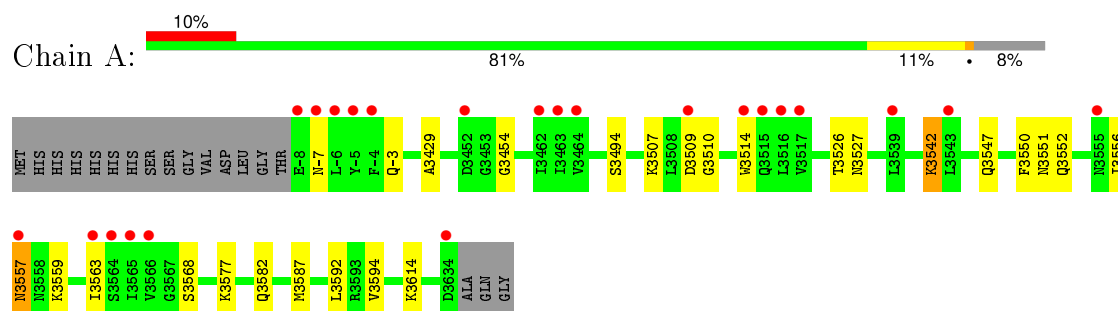
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	178	Total	O	0	11
			183	183		
5	B	135	Total	O	0	6
			138	138		

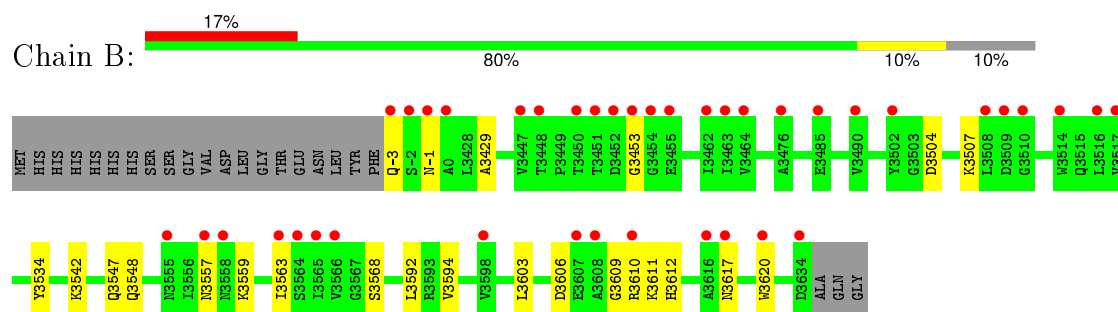
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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: RTX toxin RtxA



- Molecule 1: RTX toxin RtxA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.05Å 66.37Å 137.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.67 – 1.95 23.67 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.6 (23.67-1.95) 99.6 (23.67-1.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0051	Depositor
R, R_{free}	0.169 , 0.216 0.196 , 0.244	Depositor DCC
R_{free} test set	1584 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 31517 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3890	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 5.48% 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: UNX, IHP, CL

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	0.69	0/1823	0.80	0/2467
1	B	0.58	0/1717	0.74	0/2324
All	All	0.64	0/3540	0.77	0/4791

There are no bond length outliers.

There are no bond angle outliers.

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	1794	0	1711	24	0
1	B	1690	0	1609	17	0
2	A	36	0	6	1	0
2	B	36	0	6	1	0
3	A	1	0	0	0	0
4	A	12	0	0	0	0
5	A	183	0	0	2	0
5	B	138	0	0	1	0
All	All	3890	0	3332	42	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 6.

All (42) 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:3547:GLN:OE1	1:A:3592[A]:LEU:HD21	1.52	1.07
1:A:3526:THR:HG22	1:A:3577[A]:LYS:HE2	1.66	0.76
1:A:3587:MET:HE3	1:A:3592[B]:LEU:HD23	1.69	0.73
1:B:3429:ALA:HB2	1:B:3568:SER:HB2	1.78	0.66
1:A:3547:GLN:OE1	1:A:3592[A]:LEU:CD2	2.39	0.65
1:A:-3[B]:GLN:HE22	1:A:3614:LYS:HZ2	1.42	0.65
1:A:3542:LYS:NZ	1:A:3542:LYS:HB2	2.12	0.64
1:A:3587:MET:CE	1:A:3592[B]:LEU:HD23	2.29	0.63
1:A:3494:SER:HA	1:A:3542:LYS:HE2	1.81	0.62
1:B:3606[A]:ASP:OD1	1:B:3612:HIS:NE2	2.31	0.62
1:A:3592[B]:LEU:HG	1:A:3594:VAL:HG13	1.83	0.60
1:A:3547:GLN:HE22	1:A:3559:LYS:HB3	1.67	0.58
1:B:3610:ARG:NH2	2:B:8001:IHP:O21	2.40	0.55
1:B:3547:GLN:OE1	1:B:3592:LEU:HD21	2.07	0.54
1:B:-3:GLN:HG3	1:B:-1:ASN:H	1.73	0.54
1:A:3557:ASN:H	1:A:3557:ASN:HD22	1.58	0.50
1:B:3534:TYR:CZ	1:B:3542:LYS:HE3	2.47	0.50
1:A:3557:ASN:N	1:A:3557:ASN:HD22	2.11	0.49
1:A:-7:ASN:O	1:A:-3[B]:GLN:HG2	2.13	0.49
1:A:3547:GLN:NE2	1:A:3559:LYS:HB3	2.28	0.47
1:A:3509[B]:ASP:OD1	1:A:3510:GLY:N	2.46	0.47
1:A:3542:LYS:HZ3	1:A:3542:LYS:HB2	1.78	0.47
1:A:3507[B]:LYS:O	1:A:3507[B]:LYS:CG	2.63	0.47
1:A:3550:PHE:CE2	1:A:3556:ILE:HD12	2.50	0.46
1:A:3556:ILE:HG22	1:A:3557:ASN:N	2.31	0.46
1:A:3582:GLN:NE2	5:A:191:HOH:O	2.49	0.46
1:B:3606[B]:ASP:OD1	1:B:3606[B]:ASP:C	2.54	0.45
1:B:3617[B]:ASN:O	1:B:3617[B]:ASN:OD1	2.35	0.45
1:B:3547:GLN:NE2	1:B:3559:LYS:HG2	2.31	0.45
1:A:3429:ALA:HB2	1:A:3568:SER:HB2	1.98	0.45
1:A:3514:TRP:HB2	1:A:3563[B]:ILE:HD13	1.99	0.44
1:B:-3:GLN:HB3	1:B:3620:TRP:CZ2	2.52	0.44
1:B:3611:LYS:HD2	5:B:50:HOH:O	2.18	0.44
1:B:3606[B]:ASP:OD1	1:B:3609:GLY:N	2.52	0.43
1:B:3603:LEU:HD11	1:B:3611:LYS:HG2	2.01	0.42
1:B:3563:ILE:HD12	1:B:3594:VAL:HG21	2.01	0.42
2:A:8000:IHP:O23	2:A:8000:IHP:O24	2.37	0.42
1:A:3551:ASN:HB3	5:A:188:HOH:O	2.19	0.41
1:B:3548[B]:GLN:NE2	1:B:3548[B]:GLN:HA	2.35	0.41
1:A:3563[A]:ILE:HD12	1:A:3594:VAL:HG21	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3504:ASP:HB3	1:B:3507:LYS:HD3	2.02	0.40
1:B:3547:GLN:HE21	1:B:3559:LYS:HA	1.87	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	231/234 (99%)	219 (95%)	10 (4%)	2 (1%)	21	9
1	B	218/234 (93%)	199 (91%)	18 (8%)	1 (0%)	34	21
All	All	449/468 (96%)	418 (93%)	28 (6%)	3 (1%)	26	14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3454	GLY
1	B	3453	GLY
1	A	3527	ASN

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	195/194 (100%)	192 (98%)	3 (2%)	72	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	184/194 (95%)	183 (100%)	1 (0%)	92	91
All	All	379/388 (98%)	375 (99%)	4 (1%)	80	77

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3542	LYS
1	A	3552	GLN
1	A	3557	ASN
1	B	3557	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	ASN
1	A	3552	GLN
1	A	3557	ASN
1	B	3552	GLN

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](#)

Of 15 ligands modelled in this entry, 12 are unknown and 1 is monoatomic - leaving 2 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	$\# Z > 2$
2	IHP	A	8000	-	36,36,36	0.78	0	48,60,60	1.42	9 (18%)
2	IHP	B	8001	-	36,36,36	0.77	0	48,60,60	1.59	7 (14%)

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	IHP	A	8000	-	-	0/30/54/54	0/1/1/1
2	IHP	B	8001	-	-	0/30/54/54	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	8001	IHP	O11-P1-O21	-5.30	93.87	107.11
2	A	8000	IHP	O13-P3-O23	-3.44	98.51	107.11
2	A	8000	IHP	O11-P1-O21	-3.38	98.67	107.11
2	B	8001	IHP	C5-C4-C3	-2.63	104.62	110.43
2	A	8000	IHP	O15-P5-O25	-2.32	101.31	107.11
2	A	8000	IHP	O12-P2-O22	-2.09	101.89	107.11
2	A	8000	IHP	P1-O11-C1	2.06	126.50	121.56
2	A	8000	IHP	P2-O12-C2	2.19	126.82	121.56
2	A	8000	IHP	O46-P6-O36	2.29	116.10	107.38
2	B	8001	IHP	O12-C2-C3	2.37	113.97	108.47
2	A	8000	IHP	O15-C5-C6	2.40	114.03	108.47
2	B	8001	IHP	O15-C5-C4	2.40	114.04	108.47
2	B	8001	IHP	O41-P1-O21	2.44	118.42	110.58
2	B	8001	IHP	O41-P1-O31	2.49	116.85	107.38
2	A	8000	IHP	O41-P1-O31	2.64	117.45	107.38
2	B	8001	IHP	O43-P3-O33	3.30	119.95	107.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	8000	IHP	1	0
2	B	8001	IHP	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	216/234 (92%)	0.63	23 (10%) 8 13	30, 37, 55, 68	0
1	B	211/234 (90%)	1.09	40 (18%) 2 2	30, 38, 59, 64	0
All	All	427/468 (91%)	0.86	63 (14%) 3 5	30, 38, 58, 68	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3453	GLY	9.3
1	A	-6	LEU	7.4
1	B	-2	SER	6.9
1	B	3451	THR	6.9
1	B	3454	GLY	6.8
1	B	3516	LEU	6.2
1	B	3557	ASN	5.7
1	A	-7	ASN	5.6
1	B	3464	VAL	5.6
1	B	3463	ILE	5.2
1	B	3565	ILE	5.2
1	A	3634	ASP	5.1
1	A	-8	GLU	4.9
1	B	3455	GLU	4.9
1	B	3566	VAL	4.8
1	A	3516	LEU	4.5
1	B	3452	ASP	4.2
1	A	3464	VAL	4.1
1	A	3563[A]	ILE	4.1
1	A	3543	LEU	4.0
1	B	3617[A]	ASN	4.0
1	A	3557	ASN	3.8
1	B	3517	VAL	3.8
1	A	3565	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	3566	VAL	3.7
1	B	3558	ASN	3.5
1	B	3555	ASN	3.4
1	B	-1	ASN	3.4
1	B	3598	VAL	3.4
1	B	3490	VAL	3.4
1	B	3450	THR	3.4
1	A	3463	ILE	3.3
1	B	3510	GLY	3.3
1	A	3514	TRP	3.1
1	B	3514	TRP	3.1
1	A	3564	SER	3.0
1	B	3485	GLU	3.0
1	B	3634	ASP	3.0
1	B	3462	ILE	3.0
1	B	3448	THR	3.0
1	B	-3	GLN	2.9
1	B	3563	ILE	2.8
1	A	3517	VAL	2.8
1	B	3502	TYR	2.8
1	A	3452	ASP	2.7
1	B	3620	TRP	2.7
1	B	3608	ALA	2.7
1	A	-5	TYR	2.6
1	B	3509	ASP	2.6
1	B	3607	GLU	2.6
1	B	3564	SER	2.5
1	A	3515	GLN	2.5
1	B	3447	VAL	2.5
1	A	3539	LEU	2.4
1	A	3555[A]	ASN	2.4
1	B	3508	LEU	2.4
1	A	3462	ILE	2.3
1	A	-4	PHE	2.3
1	B	3476	ALA	2.1
1	B	3616	ALA	2.1
1	A	3509[A]	ASP	2.1
1	B	3610	ARG	2.1
1	B	0	ALA	2.1

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	IHP	A	8000	36/36	0.98	0.09	-0.93	35,41,43,46	0
2	IHP	B	8001	36/36	0.93	0.10	-0.96	41,51,58,68	0
4	UNX	A	326	1/1	0.66	0.28	-	60,60,60,60	0
4	UNX	A	328	1/1	0.92	0.08	-	59,59,59,59	0
4	UNX	A	324	1/1	0.89	0.19	-	65,65,65,65	0
4	UNX	A	323	1/1	0.93	0.20	-	57,57,57,57	0
4	UNX	A	330	1/1	0.73	0.21	-	64,64,64,64	0
4	UNX	A	325	1/1	0.91	0.14	-	50,50,50,50	0
4	UNX	A	327	1/1	0.93	0.15	-	56,56,56,56	0
4	UNX	A	331	1/1	0.79	0.20	-	68,68,68,68	0
4	UNX	A	333	1/1	0.87	0.26	-	63,63,63,63	0
4	UNX	A	334	1/1	0.91	0.22	-	47,47,47,47	0
4	UNX	A	329	1/1	0.80	0.27	-	58,58,58,58	0
3	CL	A	1	1/1	0.95	0.10	-	60,60,60,60	1
4	UNX	A	332	1/1	0.84	0.38	-	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.