Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 06:59 PM GMT

PDB ID	:	1DIT
Title	:	COMPLEX OF A DIVALENT INHIBITOR WITH THROMBIN
Authors	:	Tulinsky, A.; Krishnan, R.
Deposited on	:	1995-07-20
Resolution	:	2.30 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

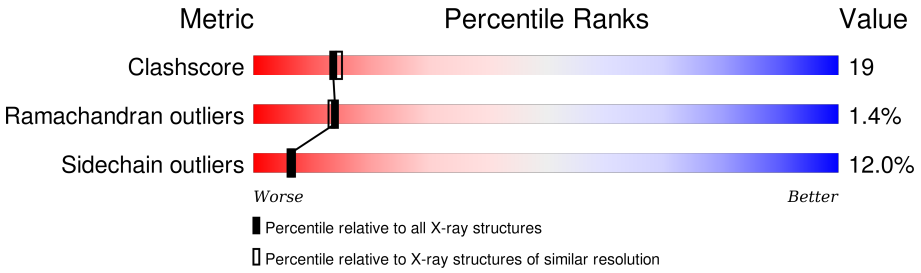
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	36	50% 19% 8% • 19%
2	H	259	52% 29% 14% • •
3	P	20	45% 20% 15% 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2530 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 ALPHA-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	29	Total	C	N	O	S	0	0	0
			235	147	38	49	1			

- Molecule 2 is a protein called ALPHA-THROMBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	251	Total	C	N	O	S	0	0	0
			2016	1287	352	363	14			

- Molecule 3 is a protein called PEPTIDE INHIBITOR CVS995.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	16	Total	C	N	O	0	0	0
			114	69	19	26			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	20	Total	O	0	0
			20	20		
4	H	138	Total	O	0	0
			138	138		
4	P	7	Total	O	0	0
			7	7		

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 (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.

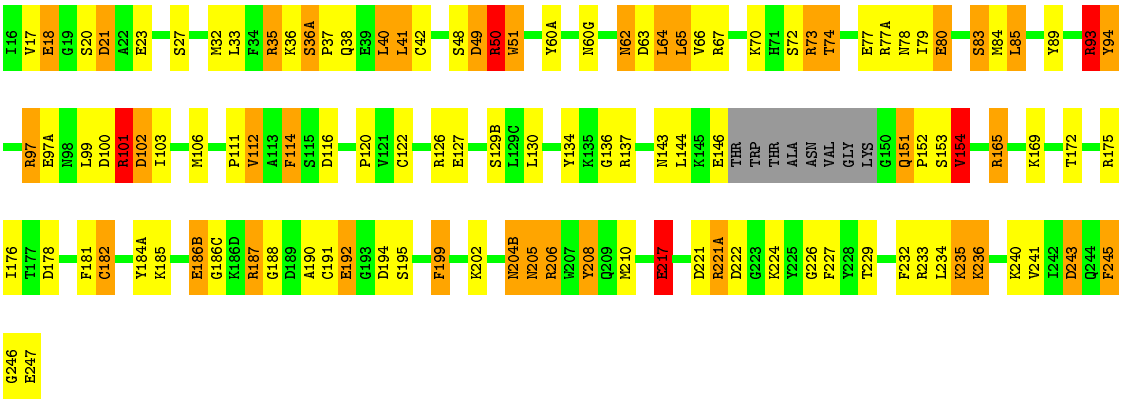
Note EDS was not executed.

- Molecule 1: ALPHA-THROMBIN

Chain L:

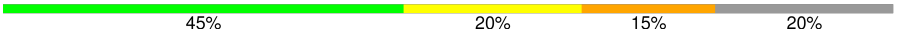
- Molecule 2: ALPHA-THROMBIN

Chain H:



- Molecule 3: PEPTIDE INHIBITOR CVS995

Chain P:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	70.90Å 72.20Å 73.20Å 90.00° 100.90° 90.00°	Depositor
Resolution (Å)	7.00 – 2.30	Depositor
% Data completeness (in resolution range)	75.0 (7.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2530	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2PP, 0MG

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	L	1.30	1/237 (0.4%)	2.08	9/315 (2.9%)
2	H	1.40	6/2068 (0.3%)	2.54	111/2794 (4.0%)
3	P	1.29	0/92	1.62	0/120
All	All	1.38	7/2397 (0.3%)	2.47	120/3229 (3.7%)

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	L	0	1
2	H	0	7
3	P	0	1
All	All	0	9

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	101	ARG	C-N	-21.57	0.84	1.34
2	H	191	CYS	C-N	12.12	1.61	1.34
1	L	12	LEU	C-N	-7.57	1.16	1.34
2	H	192	GLU	C-N	7.52	1.46	1.33
2	H	78	ASN	N-CA	6.97	1.60	1.46
2	H	93	ARG	CD-NE	6.00	1.56	1.46
2	H	100	ASP	C-N	5.73	1.47	1.34

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	67	ARG	CD-NE-CZ	32.54	169.16	123.60
2	H	67	ARG	NE-CZ-NH1	25.78	133.19	120.30
2	H	93	ARG	NE-CZ-NH1	23.34	131.97	120.30
2	H	35	ARG	NE-CZ-NH2	-22.64	108.98	120.30
2	H	97	ARG	NE-CZ-NH2	-19.98	110.31	120.30
2	H	175	ARG	NE-CZ-NH1	-15.31	112.64	120.30
2	H	93	ARG	NE-CZ-NH2	-15.09	112.76	120.30
2	H	192	GLU	OE1-CD-OE2	-13.86	106.67	123.30
2	H	77(A)	ARG	NE-CZ-NH2	-13.72	113.44	120.30
1	L	9	LYS	CB-CG-CD	13.56	146.85	111.60
2	H	67	ARG	CG-CD-NE	13.41	139.97	111.80
2	H	67	ARG	NE-CZ-NH2	-12.85	113.88	120.30
2	H	93	ARG	CD-NE-CZ	-12.30	106.38	123.60
2	H	50	ARG	NE-CZ-NH2	-12.28	114.16	120.30
2	H	233	ARG	NE-CZ-NH1	-11.47	114.57	120.30
2	H	206	ARG	NE-CZ-NH2	-10.50	115.05	120.30
2	H	101	ARG	O-C-N	-10.21	106.36	122.70
2	H	243	ASP	CB-CG-OD1	10.21	127.49	118.30
2	H	178	ASP	CB-CG-OD2	-9.20	110.02	118.30
2	H	192	GLU	CB-CG-CD	8.98	138.44	114.20
2	H	63	ASP	CB-CG-OD2	8.96	126.36	118.30
2	H	77(A)	ARG	CA-C-N	8.81	136.58	117.20
2	H	184(A)	TYR	CB-CG-CD1	-8.73	115.76	121.00
1	L	1(D)	GLY	O-C-N	8.67	136.56	122.70
2	H	35	ARG	NE-CZ-NH1	8.66	124.63	120.30
2	H	205	ASN	OD1-CG-ND2	8.64	141.76	121.90
2	H	233	ARG	NE-CZ-NH2	8.52	124.56	120.30
2	H	208	TYR	CB-CG-CD2	-8.43	115.94	121.00
2	H	175	ARG	NE-CZ-NH2	8.32	124.46	120.30
2	H	245	PHE	CA-C-N	8.30	132.80	116.20
2	H	97	ARG	NH1-CZ-NH2	8.24	128.47	119.40
2	H	205	ASN	CB-CG-OD1	-8.18	105.24	121.60
2	H	97(A)	GLU	OE1-CD-OE2	8.05	132.97	123.30
2	H	93	ARG	CB-CG-CD	8.00	132.40	111.60
2	H	101	ARG	NE-CZ-NH2	7.97	124.28	120.30
2	H	93	ARG	CG-CD-NE	-7.94	95.13	111.80
2	H	60(A)	TYR	CB-CG-CD1	-7.78	116.33	121.00
2	H	27	SER	N-CA-CB	-7.74	98.89	110.50
2	H	77	GLU	CA-C-O	7.59	136.04	120.10
2	H	101	ARG	CB-CA-C	7.53	125.46	110.40
1	L	14(D)	ARG	NE-CZ-NH2	7.52	124.06	120.30
2	H	83	SER	O-C-N	7.46	134.63	122.70
2	H	245	PHE	CA-C-O	-7.42	104.51	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	116	ASP	CB-CG-OD1	7.39	124.95	118.30
2	H	21	ASP	CB-CG-OD1	7.38	124.94	118.30
2	H	77(A)	ARG	C-N-CA	-7.14	103.85	121.70
2	H	63	ASP	CB-CG-OD1	-7.08	111.92	118.30
2	H	114	PHE	CB-CG-CD1	-7.07	115.85	120.80
2	H	126	ARG	N-CA-CB	7.05	123.29	110.60
2	H	137	ARG	NE-CZ-NH2	7.04	123.82	120.30
2	H	85	LEU	O-C-N	6.97	133.85	122.70
1	L	12	LEU	O-C-N	-6.96	111.56	122.70
2	H	154	VAL	N-CA-CB	-6.91	96.30	111.50
1	L	4	ARG	NE-CZ-NH2	6.86	123.73	120.30
1	L	10	LYS	CA-CB-CG	6.73	128.21	113.40
2	H	221(A)	ARG	CD-NE-CZ	-6.68	114.25	123.60
2	H	77(A)	ARG	CA-C-O	-6.61	106.21	120.10
2	H	42	CYS	N-CA-CB	-6.54	98.82	110.60
2	H	205	ASN	CA-CB-CG	-6.46	99.18	113.40
2	H	49	ASP	CB-CG-OD1	6.45	124.10	118.30
1	L	1(D)	GLY	CA-C-N	-6.36	103.21	117.20
2	H	192	GLU	CB-CA-C	6.33	123.07	110.40
2	H	74	THR	N-CA-CB	-6.33	98.27	110.30
2	H	205	ASN	N-CA-CB	-6.28	99.29	110.60
2	H	80	GLU	CG-CD-OE1	-6.26	105.79	118.30
2	H	77(A)	ARG	CD-NE-CZ	6.22	132.30	123.60
2	H	20	SER	O-C-N	6.17	132.58	122.70
2	H	186(B)	GLU	CB-CG-CD	6.16	130.83	114.20
2	H	83	SER	N-CA-CB	6.11	119.67	110.50
2	H	85	LEU	CB-CG-CD2	-6.09	100.64	111.00
2	H	35	ARG	NH1-CZ-NH2	6.04	126.04	119.40
2	H	181	PHE	CB-CG-CD1	-6.03	116.58	120.80
2	H	50	ARG	NH1-CZ-NH2	6.00	126.00	119.40
2	H	221(A)	ARG	NE-CZ-NH1	-5.96	117.32	120.30
2	H	67	ARG	NH1-CZ-NH2	-5.94	112.87	119.40
2	H	80	GLU	OE1-CD-OE2	5.88	130.36	123.30
2	H	199	PHE	CB-CA-C	5.86	122.13	110.40
2	H	243	ASP	CB-CG-OD2	-5.68	113.19	118.30
2	H	64	LEU	N-CA-CB	-5.67	99.06	110.40
2	H	120	PRO	N-CA-CB	5.60	110.02	103.30
2	H	210	MET	CA-CB-CG	5.60	122.82	113.30
1	L	14(G)	LEU	CB-CG-CD1	5.57	120.46	111.00
2	H	60(G)	ASN	CB-CG-ND2	5.55	130.02	116.70
2	H	84	MET	CA-CB-CG	-5.53	103.89	113.30
2	H	192	GLU	CG-CD-OE2	5.51	129.31	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	112	VAL	O-C-N	5.44	131.41	122.70
2	H	186(B)	GLU	OE1-CD-OE2	-5.44	116.77	123.30
2	H	221	ASP	CB-CA-C	5.44	121.27	110.40
2	H	222	ASP	CB-CG-OD2	5.41	123.17	118.30
2	H	186(C)	GLY	C-N-CA	5.40	135.19	121.70
2	H	222	ASP	C-N-CA	5.39	133.61	122.30
2	H	137	ARG	O-C-N	5.39	131.32	122.70
2	H	101	ARG	CD-NE-CZ	5.36	131.11	123.60
2	H	130	LEU	CA-CB-CG	5.36	127.61	115.30
2	H	187	ARG	CD-NE-CZ	-5.34	116.12	123.60
2	H	154	VAL	CB-CA-C	5.33	121.53	111.40
2	H	134	TYR	CG-CD1-CE1	5.31	125.55	121.30
2	H	51	TRP	CD2-CE3-CZ3	-5.28	111.93	118.80
2	H	33	LEU	CA-CB-CG	5.27	127.43	115.30
2	H	151	GLN	CB-CA-C	5.24	120.87	110.40
2	H	190	ALA	N-CA-CB	5.23	117.43	110.10
2	H	144	LEU	O-C-N	5.22	131.06	122.70
2	H	246	GLY	N-CA-C	5.22	126.15	113.10
2	H	221(A)	ARG	NH1-CZ-NH2	-5.22	113.66	119.40
2	H	35	ARG	CB-CG-CD	-5.22	98.04	111.60
2	H	181	PHE	CG-CD1-CE1	-5.21	115.06	120.80
2	H	184(A)	TYR	CG-CD2-CE2	-5.21	117.13	121.30
2	H	94	TYR	N-CA-CB	-5.19	101.25	110.60
2	H	74	THR	OG1-CB-CG2	5.17	121.90	110.00
2	H	100	ASP	CB-CG-OD1	5.17	122.95	118.30
2	H	143	ASN	CA-C-N	-5.16	105.85	117.20
2	H	93	ARG	CA-CB-CG	-5.14	102.09	113.40
2	H	51	TRP	CH2-CZ2-CE2	-5.13	112.27	117.40
2	H	221(A)	ARG	NE-CZ-NH2	5.12	122.86	120.30
1	L	12	LEU	CA-C-N	5.11	128.44	117.20
2	H	18	GLU	C-N-CA	5.11	133.02	122.30
2	H	217	GLU	O-C-N	5.09	131.85	123.20
2	H	217	GLU	N-CA-CB	5.06	119.71	110.60
2	H	89	TYR	CB-CG-CD2	-5.04	117.97	121.00
2	H	206	ARG	O-C-N	5.02	130.73	122.70

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	101	ARG	Sidechain,Mainchain
2	H	192	GLU	Mainchain

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Mol	Chain	Res	Type	Group
2	H	221(A)	ARG	Sidechain
2	H	50	ARG	Sidechain
2	H	73	ARG	Sidechain
2	H	93	ARG	Sidechain
1	L	4	ARG	Sidechain
3	P	4	0MG	Mainchain

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	L	235	0	233	5	0
2	H	2016	0	1974	78	0
3	P	114	0	96	8	0
4	H	138	0	0	5	0
4	L	20	0	0	1	0
4	P	7	0	0	0	0
All	All	2530	0	2303	82	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 19.

All (82) 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)
2:H:101:ARG:O	2:H:102:ASP:N	1.67	1.22
2:H:101:ARG:C	2:H:102:ASP:CA	2.09	1.21
2:H:101:ARG:CA	2:H:102:ASP:N	2.13	1.12
2:H:236:LYS:HD2	2:H:236:LYS:H	0.93	1.04
2:H:236:LYS:H	2:H:236:LYS:CD	1.74	1.00
2:H:236:LYS:N	2:H:236:LYS:HD2	1.77	1.00
2:H:101:ARG:O	2:H:102:ASP:CA	2.09	0.96
2:H:101:ARG:C	2:H:102:ASP:N	0.84	0.89
2:H:217:GLU:HG3	2:H:224:LYS:HD2	1.56	0.87
2:H:101:ARG:O	2:H:103:ILE:N	2.12	0.82
2:H:50:ARG:HD3	2:H:111:PRO:HD3	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:151:GLN:NE2	3:P:7:GLY:O	2.12	0.81
2:H:50:ARG:HD3	2:H:111:PRO:CD	2.12	0.79
2:H:36:LYS:HE2	2:H:62:ASN:O	1.82	0.79
2:H:85:LEU:HD11	2:H:106:MET:HE1	1.67	0.76
2:H:93:ARG:O	2:H:101:ARG:HD3	1.86	0.75
2:H:73:ARG:NH2	4:H:565:HOH:O	1.87	0.73
2:H:50:ARG:HG2	2:H:111:PRO:HA	1.72	0.72
2:H:235:LYS:HB3	2:H:236:LYS:HE3	1.71	0.71
2:H:172:THR:O	4:H:420:HOH:O	2.08	0.70
2:H:101:ARG:O	2:H:102:ASP:C	2.33	0.67
2:H:204(B):ASN:C	2:H:204(B):ASN:HD22	1.98	0.67
2:H:195:SER:OG	3:P:4:0MG:C	2.44	0.65
2:H:235:LYS:CB	2:H:236:LYS:HE3	2.28	0.64
2:H:36(A):SER:HA	2:H:37:PRO:C	2.17	0.63
2:H:70:LYS:HE3	2:H:72:SER:O	1.99	0.62
2:H:195:SER:CB	3:P:4:0MG:C2	2.76	0.62
2:H:93:ARG:O	2:H:101:ARG:CD	2.48	0.62
2:H:85:LEU:HD13	2:H:106:MET:HE2	1.81	0.61
2:H:36:LYS:O	2:H:38:GLN:HG2	2.01	0.60
2:H:165:ARG:HD3	2:H:169:LYS:NZ	2.16	0.60
2:H:17:VAL:O	2:H:188:GLY:HA2	2.01	0.60
2:H:85:LEU:HD11	2:H:106:MET:CE	2.30	0.59
2:H:136:GLY:HA3	2:H:199:PHE:CZ	2.38	0.58
2:H:17:VAL:O	2:H:18:GLU:HB2	2.04	0.57
2:H:32:MET:HG3	2:H:40:LEU:HD23	1.85	0.57
2:H:236:LYS:N	2:H:236:LYS:CD	2.49	0.56
2:H:85:LEU:CD1	2:H:106:MET:CE	2.84	0.56
2:H:32:MET:HG3	2:H:40:LEU:CD2	2.36	0.56
1:L:8:GLU:OE2	2:H:202:LYS:NZ	2.30	0.55
2:H:195:SER:HG	3:P:4:0MG:C2	2.13	0.54
2:H:129(B):SER:HB2	4:H:550:HOH:O	2.07	0.54
3:P:11:GLY:O	3:P:13:PHE:N	2.33	0.53
2:H:85:LEU:CD1	2:H:106:MET:HE2	2.39	0.53
2:H:50:ARG:HD3	2:H:111:PRO:N	2.23	0.52
2:H:18:GLU:HG3	2:H:187:ARG:HB2	1.91	0.52
2:H:112:VAL:HG13	2:H:114:PHE:CE1	2.44	0.52
2:H:41:LEU:HD23	2:H:64:LEU:CD2	2.39	0.51
2:H:241:VAL:O	2:H:245:PHE:HD1	1.93	0.51
2:H:165:ARG:HD3	2:H:169:LYS:HZ2	1.74	0.51
3:P:9:GLY:C	3:P:11:GLY:N	2.63	0.50
2:H:112:VAL:CG1	2:H:114:PHE:HE1	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:112:VAL:HG13	2:H:114:PHE:HE1	1.75	0.50
2:H:37:PRO:HB2	3:P:10:ASN:OD1	2.12	0.50
2:H:36:LYS:CE	2:H:62:ASN:O	2.57	0.49
2:H:204(B):ASN:ND2	2:H:204(B):ASN:C	2.66	0.49
2:H:176:ILE:HD12	2:H:227:PHE:CE2	2.48	0.49
2:H:185:LYS:O	2:H:186(B):GLU:HB2	2.13	0.48
2:H:37:PRO:CB	3:P:10:ASN:OD1	2.62	0.48
1:L:5:PRO:HA	1:L:9:LYS:HE3	1.96	0.48
1:L:14(J):TYR:HE2	2:H:202:LYS:O	1.96	0.48
2:H:194:ASP:O	2:H:195:SER:C	2.52	0.47
2:H:70:LYS:NZ	2:H:80:GLU:OE2	2.37	0.47
2:H:21:ASP:HB3	2:H:154:VAL:CG1	2.45	0.47
2:H:229:THR:HG22	2:H:234:LEU:HD12	1.96	0.47
2:H:35:ARG:O	2:H:38:GLN:HA	2.16	0.46
2:H:50:ARG:HG2	2:H:111:PRO:CA	2.45	0.45
2:H:122:CYS:HB2	2:H:208:TYR:CD1	2.52	0.45
2:H:70:LYS:CE	2:H:72:SER:O	2.65	0.44
2:H:151:GLN:HA	2:H:152:PRO:HD3	1.91	0.44
2:H:85:LEU:HD22	2:H:106:MET:HB3	2.00	0.43
2:H:114:PHE:CD1	2:H:114:PHE:N	2.84	0.42
2:H:204(B):ASN:HD21	2:H:206:ARG:HB2	1.85	0.41
2:H:36(A):SER:CA	2:H:37:PRO:C	2.86	0.41
2:H:97:ARG:HG3	4:H:452:HOH:O	2.21	0.41
2:H:182:CYS:HA	2:H:226:GLY:O	2.21	0.41
2:H:65:LEU:HA	2:H:65:LEU:HD12	1.72	0.41
1:L:10:LYS:HE2	4:L:777:HOH:O	2.20	0.41
2:H:232:PHE:O	2:H:235:LYS:HB2	2.20	0.41
2:H:49:ASP:HA	2:H:112:VAL:HG12	2.03	0.40
2:H:146:GLU:C	4:H:519:HOH:O	2.59	0.40
1:L:14:ASP:HB2	2:H:23:GLU:OE2	2.22	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	L	27/36 (75%)	23 (85%)	3 (11%)	1 (4%)	4 2
2	H	247/259 (95%)	233 (94%)	13 (5%)	1 (0%)	39 48
3	P	12/20 (60%)	6 (50%)	4 (33%)	2 (17%)	0 0
All	All	286/315 (91%)	262 (92%)	20 (7%)	4 (1%)	14 13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	102	ASP
3	P	12	ASP
1	L	14(J)	TYR
3	P	9	GLY

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	L	26/31 (84%)	25 (96%)	1 (4%)	40 54
2	H	216/225 (96%)	188 (87%)	28 (13%)	5 5
3	P	8/12 (67%)	7 (88%)	1 (12%)	6 6
All	All	250/268 (93%)	220 (88%)	30 (12%)	6 6

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	9	LYS
2	H	36(A)	SER
2	H	40	LEU
2	H	41	LEU
2	H	48	SER
2	H	50	ARG

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Mol	Chain	Res	Type
2	H	51	TRP
2	H	62	ASN
2	H	65	LEU
2	H	66	VAL
2	H	74	THR
2	H	79	ILE
2	H	83	SER
2	H	94	TYR
2	H	99	LEU
2	H	101	ARG
2	H	127	GLU
2	H	153	SER
2	H	154	VAL
2	H	165	ARG
2	H	182	CYS
2	H	204(B)	ASN
2	H	205	ASN
2	H	217	GLU
2	H	235	LYS
2	H	236	LYS
2	H	240	LYS
2	H	243	ASP
2	H	247	GLU
3	P	10	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	156	GLN
2	H	204(B)	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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	$\#\|Z\| > 2$
3	0MG	P	4	3,2	9,12,13	3.13	4 (44%)	8,14,16	2.99	3 (37%)

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	0MG	P	4	3,2	-	0/7/13/15	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	4	0MG	C5-N2	-3.81	1.39	1.47
3	P	4	0MG	C4-C5	-2.74	1.39	1.51
3	P	4	0MG	O1-C2	5.22	1.30	1.22
3	P	4	0MG	C-C2	5.78	1.55	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	P	4	0MG	O1-C2-C	-4.08	112.62	123.56
3	P	4	0MG	C3-CA-N	4.21	118.63	109.81
3	P	4	0MG	C3-C4-C5	5.33	128.57	112.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	4	0MG	3	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.