



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:45 AM GMT

PDB ID : 2O3R
Title : Structural Basis for Formation and Hydrolysis of Calcium Messenger Cyclic ADP-ribose by Human CD38
Authors : Liu, Q.; Kriksunov, I.A.; Graeff, R.; Lee, H.C.; Hao, Q.
Deposited on : 2006-12-01
Resolution : 1.75 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

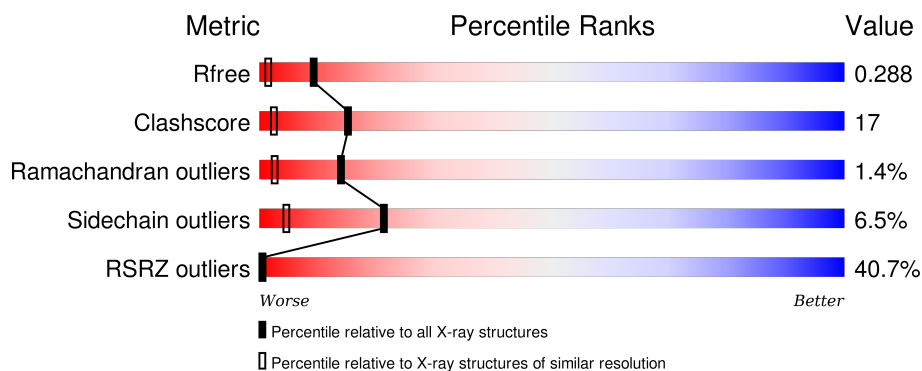
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	262	<div> <div>29%</div> <div>72%</div> <div>19%</div> <div>5%</div> <div>• •</div> </div>
1	B	262	<div> <div>49%</div> <div>60%</div> <div>31%</div> <div>5%</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
2	CXR	A	301	X	-	-	-
2	CXR	B	301	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4484 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.

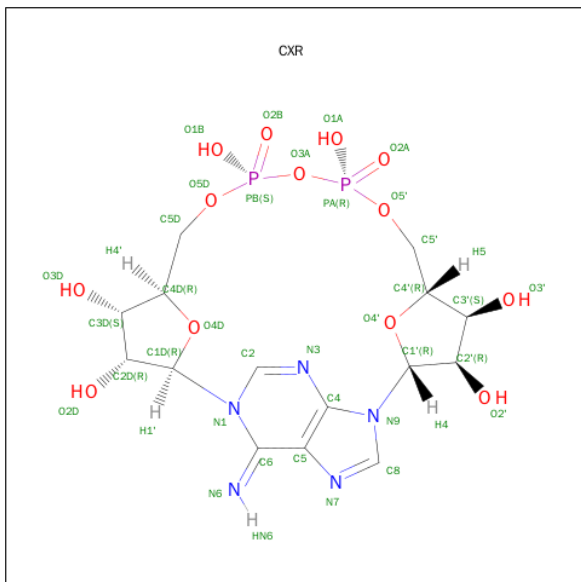
- Molecule 1 is a protein called ADP-ribosyl cyclase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2007	1265	351	375	16			
1	B	252	Total	C	N	O	S	0	0	0
			2007	1265	351	375	16			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LYS	-	CLONING ARTIFACT	UNP P28907
A	40	ARG	-	CLONING ARTIFACT	UNP P28907
A	41	GLU	-	CLONING ARTIFACT	UNP P28907
A	42	ALA	-	CLONING ARTIFACT	UNP P28907
A	43	GLU	-	CLONING ARTIFACT	UNP P28907
A	44	ALA	-	CLONING ARTIFACT	UNP P28907
A	49	THR	GLN	ENGINEERED	UNP P28907
A	100	ASP	ASN	ENGINEERED	UNP P28907
A	164	ASP	ASN	ENGINEERED	UNP P28907
A	209	ASP	ASN	ENGINEERED	UNP P28907
A	219	ASP	ASN	ENGINEERED	UNP P28907
A	226	ASP	GLU	ENGINEERED	UNP P28907
B	39	LYS	-	CLONING ARTIFACT	UNP P28907
B	40	ARG	-	CLONING ARTIFACT	UNP P28907
B	41	GLU	-	CLONING ARTIFACT	UNP P28907
B	42	ALA	-	CLONING ARTIFACT	UNP P28907
B	43	GLU	-	CLONING ARTIFACT	UNP P28907
B	44	ALA	-	CLONING ARTIFACT	UNP P28907
B	49	THR	GLN	ENGINEERED	UNP P28907
B	100	ASP	ASN	ENGINEERED	UNP P28907
B	164	ASP	ASN	ENGINEERED	UNP P28907
B	209	ASP	ASN	ENGINEERED	UNP P28907
B	219	ASP	ASN	ENGINEERED	UNP P28907
B	226	ASP	GLU	ENGINEERED	UNP P28907

- Molecule 2 is CYCLIC ADENOSINE DIPHOSPHATE-RIBOSE (three-letter code: CXR) (formula: $\text{C}_{15}\text{H}_{21}\text{N}_5\text{O}_{13}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 35	C 15	N 5	O 13	P 2	0	0
2	B	1	Total 35	C 15	N 5	O 13	P 2	0	0

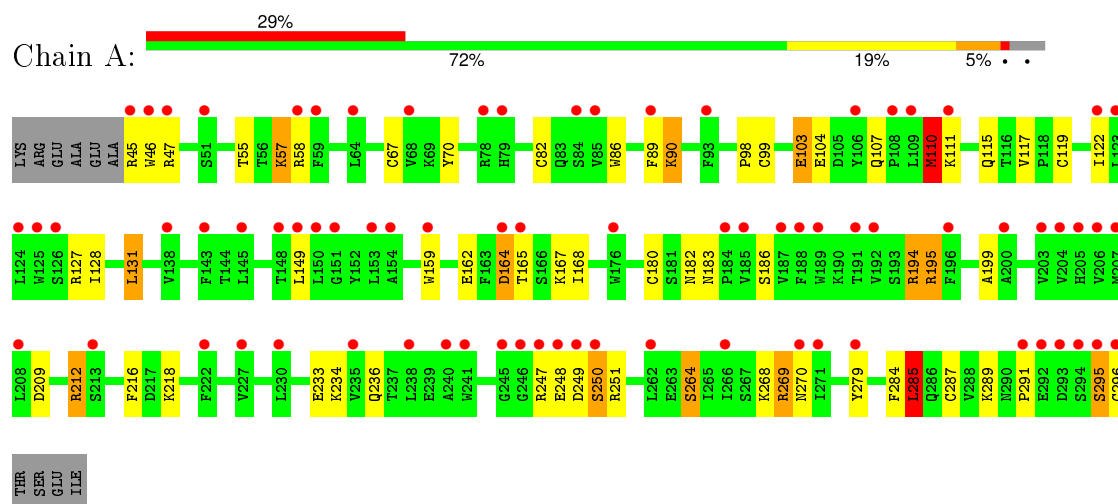
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	223	Total O 223 223	0	0
3	B	177	Total O 177 177	0	0

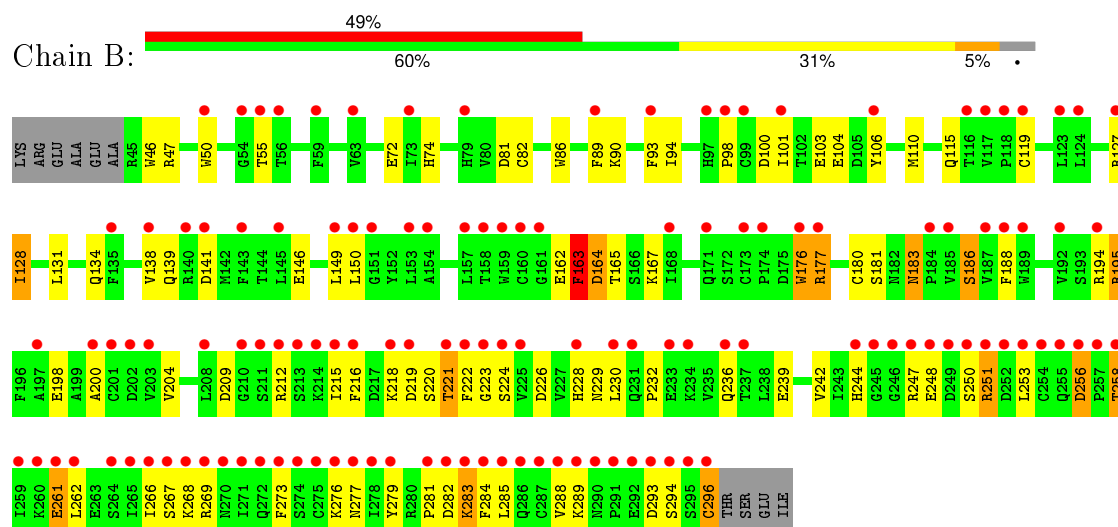
3 Residue-property plots

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: ADP-ribosyl cyclase 1



• Molecule 1: ADP-ribosyl cyclase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	41.72Å 53.00Å 65.94Å 104.96° 91.22° 94.57°	Depositor
Resolution (Å)	20.00 – 1.75 19.86 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.75) 86.7 (19.86-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.183 , 0.229 0.253 , 0.288	Depositor DCC
R_{free} test set	2631 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 74.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 51735 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4484	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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: CXR

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	1.35	9/2057 (0.4%)	1.31	11/2784 (0.4%)
1	B	1.43	21/2057 (1.0%)	1.14	7/2784 (0.3%)
All	All	1.39	30/4114 (0.7%)	1.23	18/5568 (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	B	0	1

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	283	LYS	CD-CE	12.47	1.82	1.51
1	B	163	PHE	CB-CG	-9.60	1.35	1.51
1	B	239	GLU	CD-OE2	8.29	1.34	1.25
1	B	86	TRP	CE3-CZ3	8.12	1.52	1.38
1	A	70	TYR	CD1-CE1	7.61	1.50	1.39
1	A	110	MET	CG-SD	-7.47	1.61	1.81
1	B	82	CYS	CB-SG	7.28	1.94	1.82
1	B	251	ARG	CZ-NH1	7.26	1.42	1.33
1	B	176	TRP	CB-CG	-7.05	1.37	1.50
1	A	82	CYS	CB-SG	6.89	1.94	1.82
1	B	276	LYS	CE-NZ	6.86	1.66	1.49
1	B	188	PHE	CD2-CE2	6.61	1.52	1.39
1	B	119	CYS	CB-SG	-6.45	1.71	1.82
1	B	296	CYS	C-O	6.42	1.35	1.23
1	B	46	TRP	CE3-CZ3	5.97	1.48	1.38
1	B	72	GLU	CB-CG	5.92	1.63	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	93	PHE	CG-CD2	5.91	1.47	1.38
1	A	284	PHE	C-N	5.74	1.47	1.34
1	B	277	ASN	CG-OD1	5.74	1.36	1.24
1	A	234	LYS	N-CA	5.69	1.57	1.46
1	B	163	PHE	CD2-CE2	-5.53	1.28	1.39
1	B	101	ILE	N-CA	5.46	1.57	1.46
1	B	50	TRP	CG-CD1	5.41	1.44	1.36
1	B	188	PHE	CD1-CE1	5.38	1.50	1.39
1	A	264	SER	CB-OG	-5.20	1.35	1.42
1	B	186	SER	CB-OG	5.17	1.49	1.42
1	B	283	LYS	CE-NZ	5.14	1.61	1.49
1	A	67	CYS	CB-SG	-5.10	1.73	1.81
1	A	159	TRP	CE3-CZ3	5.05	1.47	1.38
1	A	233	GLU	CG-CD	5.02	1.59	1.51

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	NE-CZ-NH1	24.01	132.31	120.30
1	A	269	ARG	NE-CZ-NH2	-23.24	108.68	120.30
1	A	269	ARG	CD-NE-CZ	8.82	135.94	123.60
1	B	251	ARG	NE-CZ-NH1	8.21	124.41	120.30
1	B	251	ARG	NE-CZ-NH2	-7.90	116.35	120.30
1	A	285	LEU	CA-CB-CG	7.48	132.51	115.30
1	B	164	ASP	N-CA-CB	-7.39	97.31	110.60
1	B	81	ASP	CB-CG-OD2	6.63	124.27	118.30
1	B	146	GLU	OE1-CD-OE2	-6.10	115.98	123.30
1	B	55	THR	CA-CB-CG2	-5.99	104.02	112.40
1	A	195	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	234	LYS	CD-CE-NZ	-5.76	98.45	111.70
1	A	90	LYS	CB-CA-C	-5.75	98.91	110.40
1	A	269	ARG	CG-CD-NE	-5.70	99.83	111.80
1	A	99	CYS	CA-CB-SG	-5.23	104.58	114.00
1	A	194	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	A	131	LEU	CB-CG-CD2	5.10	119.67	111.00
1	B	283	LYS	CD-CE-NZ	-5.05	100.08	111.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	164	ASP	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	2007	0	1915	56	0
1	B	2007	0	1915	91	0
2	A	35	0	18	0	0
2	B	35	0	19	7	0
3	A	223	0	0	17	0
3	B	177	0	0	16	0
All	All	4484	0	3867	139	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 17.

All (139) 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:283:LYS:CE	1:B:283:LYS:CD	1.82	1.56
1:B:221:THR:HG21	2:B:301:CXR:C5D	1.71	1.20
1:B:221:THR:CG2	2:B:301:CXR:H12	1.78	1.13
1:A:270:ASN:HB2	3:A:523:HOH:O	1.53	1.06
1:A:165:THR:HG23	1:A:167:LYS:H	1.19	1.05
1:B:221:THR:HG21	2:B:301:CXR:H12	1.06	1.04
1:B:195:ARG:HH11	1:B:195:ARG:HG3	1.20	1.04
1:B:176:TRP:HD1	1:B:177:ARG:HG3	1.26	0.97
1:B:266:ILE:HD11	1:B:273:PHE:HB2	1.49	0.91
1:A:269:ARG:HD2	3:B:413:HOH:O	1.70	0.91
1:B:74:HIS:HD2	3:B:437:HOH:O	1.55	0.89
1:B:165:THR:HG23	1:B:167:LYS:H	1.40	0.86
1:B:115:GLN:HE22	1:B:149:LEU:H	1.30	0.80
1:A:115:GLN:HE22	1:A:149:LEU:H	1.29	0.79
1:B:177:ARG:HH11	1:B:177:ARG:CB	1.95	0.79
1:B:74:HIS:CD2	3:B:437:HOH:O	2.34	0.79
1:A:291:PRO:CA	3:A:449:HOH:O	2.34	0.76
1:B:177:ARG:HB3	1:B:177:ARG:NH1	2.00	0.75
1:B:198:GLU:HG3	1:B:229:ASN:HB3	1.68	0.75
1:B:177:ARG:HH11	1:B:177:ARG:HB3	1.52	0.74
1:A:269:ARG:HD3	1:B:100:ASP:CG	2.07	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:THR:HG21	2:B:301:CXR:H11	1.69	0.73
1:A:268:LYS:HD2	1:B:163:PHE:HE1	1.54	0.73
1:B:103:GLU:CD	1:B:194:ARG:HH21	1.93	0.71
1:B:195:ARG:HG3	1:B:195:ARG:NH1	1.98	0.71
1:B:236:GLN:HB3	3:B:365:HOH:O	1.92	0.70
1:B:244:HIS:HB2	1:B:279:TYR:O	1.92	0.70
1:B:176:TRP:CD1	1:B:177:ARG:HG3	2.18	0.69
1:A:268:LYS:CD	1:B:163:PHE:HE1	2.06	0.68
1:A:270:ASN:HB2	3:A:522:HOH:O	1.91	0.68
1:A:268:LYS:HD2	1:B:163:PHE:CE1	2.28	0.68
1:B:195:ARG:N	1:B:195:ARG:HD2	2.10	0.67
1:B:162:GLU:HB2	1:B:165:THR:HG22	1.75	0.67
1:A:122:ILE:CD1	3:A:444:HOH:O	2.43	0.66
1:A:199:ALA:HB3	3:A:444:HOH:O	1.94	0.66
1:A:270:ASN:CG	3:A:461:HOH:O	2.34	0.65
1:A:122:ILE:HD11	3:A:444:HOH:O	1.96	0.65
1:B:138:VAL:CG1	1:B:289:LYS:HA	2.26	0.65
1:A:110:MET:SD	1:A:195:ARG:HD2	2.37	0.65
1:A:165:THR:HG23	1:A:167:LYS:N	2.03	0.65
1:A:295:SER:C	1:A:296:CYS:SG	2.76	0.64
1:A:119:CYS:HB3	3:A:357:HOH:O	1.98	0.63
1:B:228:HIS:HD2	1:B:269:ARG:HH21	1.47	0.63
1:A:268:LYS:CD	1:B:163:PHE:CE1	2.82	0.62
1:B:90:LYS:HG2	1:B:94:ILE:HG13	1.81	0.62
1:A:183:ASN:ND2	1:A:186:SER:H	1.98	0.62
1:B:283:LYS:CE	1:B:283:LYS:CG	2.75	0.62
1:A:270:ASN:CB	3:A:522:HOH:O	2.47	0.61
1:B:138:VAL:HG13	1:B:289:LYS:HA	1.82	0.61
1:A:285:LEU:HD13	1:A:289:LYS:HE3	1.83	0.61
1:B:283:LYS:CD	1:B:283:LYS:NZ	2.64	0.60
1:A:269:ARG:HD3	1:B:100:ASP:CB	2.30	0.60
1:A:162:GLU:HB2	1:A:165:THR:HG22	1.83	0.60
1:A:269:ARG:HD3	1:B:100:ASP:HB3	1.84	0.60
1:B:209:ASP:OD2	1:B:212:ARG:NE	2.32	0.60
1:A:209:ASP:HB3	1:A:212:ARG:HG3	1.84	0.59
1:B:251:ARG:H	1:B:251:ARG:HD3	1.67	0.59
1:B:222:PHE:HA	1:B:226:ASP:HB2	1.84	0.59
1:B:195:ARG:NH1	3:B:416:HOH:O	2.36	0.58
2:B:301:CXR:O5D	2:B:301:CXR:H3	2.03	0.58
1:B:221:THR:HB	2:B:301:CXR:O2B	2.04	0.57
1:B:216:PHE:HB3	1:B:258:THR:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:ASP:OD2	1:A:164:ASP:N	2.38	0.57
1:B:253:LEU:HD22	3:B:445:HOH:O	2.04	0.56
1:B:244:HIS:NE2	1:B:279:TYR:HD1	2.03	0.56
1:B:228:HIS:HD2	1:B:269:ARG:NH2	2.04	0.55
1:B:266:ILE:HD11	1:B:273:PHE:CB	2.30	0.55
1:B:104:GLU:HG3	3:B:415:HOH:O	2.06	0.55
1:A:182:ASN:HB2	3:A:505:HOH:O	2.06	0.55
1:A:194:ARG:CZ	3:A:435:HOH:O	2.55	0.54
1:A:57:LYS:O	1:A:58:ARG:HG2	2.08	0.54
1:A:165:THR:CG2	1:A:167:LYS:H	2.08	0.53
1:A:57:LYS:C	1:A:58:ARG:HG2	2.28	0.53
1:A:162:GLU:OE2	1:A:165:THR:HG21	2.09	0.53
1:A:127:ARG:HB3	1:A:212:ARG:NE	2.24	0.53
1:B:183:ASN:ND2	1:B:186:SER:H	2.06	0.53
1:A:115:GLN:NE2	1:A:149:LEU:H	2.04	0.53
1:B:220:SER:O	1:B:223:GLY:N	2.42	0.52
1:B:177:ARG:CB	1:B:177:ARG:NH1	2.64	0.52
1:A:98:PRO:O	1:A:183:ASN:HA	2.10	0.52
1:B:47:ARG:CZ	3:B:442:HOH:O	2.56	0.52
1:B:293:ASP:H	1:B:296:CYS:HB2	1.73	0.52
1:A:104:GLU:HG2	3:A:456:HOH:O	2.09	0.52
1:B:47:ARG:NE	3:B:442:HOH:O	2.42	0.52
1:B:244:HIS:CE1	1:B:279:TYR:CD1	2.98	0.52
1:A:128:ILE:O	1:A:128:ILE:HG23	2.08	0.51
1:B:139:GLN:C	1:B:141:ASP:H	2.12	0.51
1:B:221:THR:HG22	3:B:390:HOH:O	2.11	0.51
1:B:98:PRO:O	1:B:183:ASN:HA	2.11	0.50
1:B:228:HIS:CD2	1:B:269:ARG:HH21	2.28	0.50
1:B:279:TYR:O	1:B:281:PRO:HD3	2.11	0.50
1:B:261:GLU:HG3	1:B:261:GLU:O	2.13	0.49
1:B:216:PHE:CD2	1:B:262:LEU:HB2	2.47	0.49
1:A:122:ILE:HD13	3:A:444:HOH:O	2.11	0.48
1:B:127:ARG:HE	1:B:212:ARG:HH11	1.61	0.48
1:A:55:THR:HG21	1:A:168:ILE:HG21	1.95	0.48
1:A:268:LYS:HD3	1:B:163:PHE:CE1	2.48	0.47
1:B:128:ILE:HB	1:B:209:ASP:HB2	1.96	0.47
1:B:296:CYS:HA	3:B:434:HOH:O	2.13	0.47
1:A:183:ASN:HD21	1:A:186:SER:H	1.60	0.47
1:A:249:ASP:CA	1:A:279:TYR:CD1	2.97	0.47
1:A:86:TRP:CE2	1:A:90:LYS:HG3	2.50	0.47
1:B:221:THR:HG22	2:B:301:CXR:H12	1.86	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:GLN:NE2	1:B:149:LEU:H	2.08	0.46
1:A:57:LYS:H	1:A:57:LYS:HG3	1.25	0.46
1:B:141:ASP:HB3	3:B:401:HOH:O	2.15	0.46
1:B:200:ALA:HB1	1:B:204:VAL:HG22	1.98	0.46
1:A:107:GLN:HA	1:A:110:MET:HG3	1.98	0.46
1:B:106:TYR:O	1:B:110:MET:HG2	2.16	0.46
1:B:244:HIS:NE2	1:B:279:TYR:CD1	2.83	0.45
1:B:266:ILE:HG13	1:B:267:SER:N	2.32	0.45
1:A:117:VAL:HG12	3:A:415:HOH:O	2.15	0.45
1:B:176:TRP:CH2	3:B:409:HOH:O	2.69	0.45
1:A:216:PHE:CE2	1:A:218:LYS:HG2	2.52	0.44
1:B:176:TRP:CZ3	1:B:181:SER:HB2	2.52	0.44
1:B:195:ARG:HD2	1:B:195:ARG:H	1.79	0.44
1:B:244:HIS:CG	1:B:279:TYR:HA	2.53	0.44
1:B:110:MET:HE1	1:B:150:LEU:HD13	2.00	0.44
1:B:215:ILE:HD12	1:B:256:ASP:CG	2.39	0.43
1:B:139:GLN:C	1:B:141:ASP:N	2.72	0.43
1:A:103:GLU:HG2	3:A:320:HOH:O	2.18	0.43
1:B:134:GLN:OE1	1:B:285:LEU:HD11	2.18	0.43
1:B:176:TRP:C	1:B:176:TRP:CD1	2.89	0.43
1:A:55:THR:HG21	1:A:168:ILE:CG2	2.49	0.42
1:A:47:ARG:O	1:A:47:ARG:HG2	2.18	0.42
1:B:228:HIS:CE1	3:B:456:HOH:O	2.73	0.42
1:A:180:CYS:HB2	3:A:505:HOH:O	2.20	0.42
1:B:176:TRP:HD1	1:B:177:ARG:CG	2.13	0.41
1:A:287:CYS:HB3	1:A:296:CYS:HB3	1.80	0.41
1:A:45:ARG:HB2	1:A:46:TRP:H	1.75	0.41
1:B:110:MET:CE	1:B:150:LEU:HD13	2.51	0.41
1:B:180:CYS:HB2	3:B:325:HOH:O	2.21	0.41
1:B:244:HIS:CD2	1:B:250:SER:HB2	2.56	0.41
1:B:284:PHE:O	1:B:288:VAL:HG23	2.21	0.40
1:B:176:TRP:CZ3	3:B:409:HOH:O	2.58	0.40
1:A:264:SER:CB	1:B:163:PHE:HZ	2.34	0.40
1:A:295:SER:CA	3:A:341:HOH:O	2.69	0.40
1:B:230:LEU:O	1:B:232:PRO:HD3	2.21	0.40
1:B:127:ARG:NE	1:B:212:ARG:HH11	2.18	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	250/262 (95%)	235 (94%)	11 (4%)	4 (2%)	12	2
1	B	250/262 (95%)	233 (93%)	14 (6%)	3 (1%)	16	3
All	All	500/524 (95%)	468 (94%)	25 (5%)	7 (1%)	14	2

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	GLU
1	A	295	SER
1	B	248	GLU
1	A	250	SER
1	A	247	ARG
1	B	294	SER
1	B	247	ARG

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	223/241 (92%)	211 (95%)	12 (5%)	27	7
1	B	223/241 (92%)	206 (92%)	17 (8%)	16	3
All	All	446/482 (92%)	417 (94%)	29 (6%)	21	4

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LYS
1	A	89	PHE
1	A	103	GLU
1	A	110	MET
1	A	111	LYS
1	A	131	LEU
1	A	164	ASP
1	A	212	ARG
1	A	236	GLN
1	A	250	SER
1	A	251	ARG
1	A	285	LEU
1	B	89	PHE
1	B	128	ILE
1	B	131	LEU
1	B	163	PHE
1	B	177	ARG
1	B	183	ASN
1	B	195	ARG
1	B	218	LYS
1	B	219	ASP
1	B	221	THR
1	B	224	SER
1	B	242	VAL
1	B	256	ASP
1	B	258	THR
1	B	261	GLU
1	B	268	LYS
1	B	282	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	115	GLN
1	A	134	GLN
1	A	139	GLN
1	A	171	GLN
1	A	183	ASN
1	A	270	ASN
1	B	115	GLN
1	B	171	GLN
1	B	183	ASN

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Mol	Chain	Res	Type
1	B	228	HIS
1	B	286	GLN

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 ⓘ

2 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	CXR	A	301	-	28,39,39	3.23	15 (53%)	37,62,62	1.73	8 (21%)
2	CXR	B	301	-	28,39,39	3.61	11 (39%)	37,62,62	1.82	7 (18%)

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	CXR	A	301	-	1/1/10/10	0/18/58/58	0/0/5/5
2	CXR	B	301	-	1/1/10/10	0/18/58/58	0/0/5/5

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	CXR	C6-C5	-4.96	1.31	1.41
2	B	301	CXR	C2D-C3D	-4.52	1.41	1.53
2	B	301	CXR	C4-N3	-3.36	1.30	1.35
2	A	301	CXR	C2D-C3D	-2.61	1.46	1.53
2	A	301	CXR	O5'-C5'	-2.36	1.35	1.44
2	A	301	CXR	PB-O1B	-2.20	1.45	1.54
2	A	301	CXR	O4'-C4'	2.26	1.50	1.45
2	A	301	CXR	PA-O2A	2.27	1.59	1.51
2	B	301	CXR	O3'-C3'	2.31	1.48	1.43
2	B	301	CXR	PB-O5D	2.38	1.69	1.59
2	A	301	CXR	C5-C4	2.49	1.46	1.40
2	A	301	CXR	O3D-C3D	2.75	1.49	1.43
2	A	301	CXR	C2-N3	2.77	1.35	1.30
2	B	301	CXR	O4'-C4'	2.79	1.51	1.45
2	A	301	CXR	PA-O5'	2.83	1.72	1.59
2	B	301	CXR	C8-N7	3.15	1.40	1.34
2	A	301	CXR	C6-N6	3.34	1.35	1.29
2	A	301	CXR	C4-N3	3.75	1.41	1.35
2	A	301	CXR	O2D-C2D	4.70	1.54	1.43
2	B	301	CXR	O4'-C1'	5.48	1.48	1.41
2	B	301	CXR	C5-C4	5.49	1.52	1.40
2	B	301	CXR	O2D-C2D	5.71	1.56	1.43
2	A	301	CXR	O4D-C1D	6.94	1.50	1.41
2	A	301	CXR	O4'-C1'	7.92	1.51	1.41
2	A	301	CXR	C8-N7	8.21	1.50	1.34
2	B	301	CXR	C6-N6	12.97	1.52	1.29

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	CXR	PA-O3A-PB	-3.95	121.64	132.73
2	A	301	CXR	O3A-PA-O5'	-3.91	92.57	102.94
2	B	301	CXR	PA-O3A-PB	-3.56	122.75	132.73
2	B	301	CXR	O2'-C2'-C3'	-3.29	101.14	111.83
2	B	301	CXR	C6-N1-C1D	-3.25	115.90	120.53
2	B	301	CXR	C4D-O4D-C1D	-3.03	106.39	109.72
2	B	301	CXR	O4'-C1'-N9	-2.77	102.30	108.10
2	A	301	CXR	C6-N1-C1D	-2.71	116.67	120.53
2	A	301	CXR	C2'-C1'-N9	-2.41	110.62	114.29
2	A	301	CXR	C4'-O4'-C1'	-2.30	107.20	109.72
2	B	301	CXR	O4'-C4'-C5'	2.58	118.56	109.32
2	A	301	CXR	O1B-PB-O2B	2.84	127.92	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	CXR	C2'-C3'-C4'	3.03	108.83	102.61
2	A	301	CXR	C6-C5-C4	3.67	119.67	116.78
2	B	301	CXR	C2-N3-C4	5.39	124.75	116.40

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	301	CXR	C3'
2	A	301	CXR	C3'

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	CXR	7	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	252/262 (96%)	1.77	76 (30%) 1 1	36, 43, 60, 71	0
1	B	252/262 (96%)	2.71	129 (51%) 0 0	33, 47, 69, 78	0
All	All	504/524 (96%)	2.24	205 (40%) 0 0	33, 44, 67, 78	0

All (205) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	249	ASP	13.1
1	B	294	SER	12.7
1	B	296	CYS	11.7
1	B	295	SER	11.7
1	B	246	GLY	11.4
1	B	249	ASP	11.3
1	A	248	GLU	11.0
1	A	292	GLU	10.6
1	B	254	CYS	10.1
1	A	291	PRO	9.9
1	A	296	CYS	8.4
1	B	279	TYR	8.4
1	A	246	GLY	7.8
1	B	245	GLY	7.8
1	B	253	LEU	7.7
1	B	255	GLN	7.7
1	B	291	PRO	7.6
1	B	259	ILE	7.6
1	B	159	TRP	7.5
1	B	213	SER	7.5
1	A	124	LEU	7.5
1	B	266	ILE	7.3
1	B	248	GLU	7.2
1	B	225	VAL	7.0

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Mol	Chain	Res	Type	RSRZ
1	B	244	HIS	7.0
1	B	290	ASN	6.8
1	B	293	ASP	6.5
1	B	275	CYS	6.5
1	B	287	CYS	6.5
1	B	264	SER	6.4
1	B	250	SER	6.3
1	B	236	GLN	6.2
1	A	123	LEU	6.0
1	A	150	LEU	5.9
1	B	269	ARG	5.8
1	B	188	PHE	5.7
1	A	294	SER	5.5
1	B	212	ARG	5.4
1	B	247	ARG	5.4
1	A	247	ARG	5.3
1	A	208	LEU	5.2
1	B	268	LYS	5.1
1	A	245	GLY	5.1
1	A	204	VAL	5.0
1	B	215	ILE	5.0
1	B	265	ILE	5.0
1	B	153	LEU	4.9
1	A	206	VAL	4.9
1	B	214	LYS	4.9
1	B	289	LYS	4.8
1	B	160	CYS	4.8
1	B	273	PHE	4.8
1	B	185	VAL	4.7
1	B	224	SER	4.7
1	B	201	CYS	4.6
1	A	176	TRP	4.6
1	A	222	PHE	4.5
1	B	184	PRO	4.5
1	B	89	PHE	4.4
1	B	260	LYS	4.4
1	B	252	ASP	4.4
1	B	101	ILE	4.4
1	A	47	ARG	4.3
1	B	211	SER	4.3
1	B	210	GLY	4.3
1	A	79	HIS	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	140	ARG	4.3
1	B	117	VAL	4.2
1	A	250	SER	4.2
1	B	127	ARG	4.2
1	B	99	CYS	4.2
1	B	55	THR	4.1
1	B	59	PHE	4.1
1	A	295	SER	4.1
1	B	277	ASN	4.1
1	A	153	LEU	4.1
1	A	230	LEU	4.1
1	B	157	LEU	4.1
1	B	219	ASP	4.1
1	A	196	PHE	4.0
1	A	159	TRP	4.0
1	B	278	ILE	4.0
1	A	235	VAL	4.0
1	A	227	VAL	3.9
1	A	241	TRP	3.9
1	B	106	TYR	3.9
1	A	46	TRP	3.9
1	B	176	TRP	3.9
1	B	93	PHE	3.9
1	A	165	THR	3.9
1	A	192	VAL	3.9
1	B	228	HIS	3.9
1	B	119	CYS	3.8
1	B	141	ASP	3.8
1	B	257	PRO	3.8
1	B	218	LYS	3.7
1	A	145	LEU	3.7
1	B	116	THR	3.7
1	B	158	THR	3.7
1	B	267	SER	3.7
1	A	238	LEU	3.6
1	B	221	THR	3.6
1	B	216	PHE	3.6
1	B	272	GLN	3.6
1	A	122	ILE	3.6
1	A	213	SER	3.6
1	B	222	PHE	3.6
1	B	98	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	188	PHE	3.5
1	B	258	THR	3.5
1	B	282	ASP	3.5
1	A	149	LEU	3.5
1	B	138	VAL	3.5
1	B	261	GLU	3.5
1	B	271	ILE	3.5
1	B	237	THR	3.5
1	B	149	LEU	3.4
1	B	161	GLY	3.4
1	B	73	ILE	3.4
1	A	78	ARG	3.3
1	B	286	GLN	3.3
1	A	189	TRP	3.3
1	B	262	LEU	3.3
1	B	173	CYS	3.3
1	B	233	GLU	3.2
1	A	148	THR	3.2
1	B	283	LYS	3.2
1	B	202	ASP	3.2
1	B	187	VAL	3.2
1	B	231	GLN	3.2
1	A	164	ASP	3.2
1	B	150	LEU	3.2
1	A	125	TRP	3.1
1	A	207	MET	3.1
1	A	109	LEU	3.1
1	B	234	LYS	3.1
1	B	256	ASP	3.1
1	A	154	ALA	3.1
1	B	63	VAL	3.0
1	B	177	ARG	3.0
1	B	189	TRP	2.9
1	B	50	TRP	2.9
1	B	288	VAL	2.9
1	B	270	ASN	2.9
1	B	192	VAL	2.9
1	A	271	ILE	2.9
1	B	97	HIS	2.8
1	A	185	VAL	2.8
1	A	106	TYR	2.7
1	A	89	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	93	PHE	2.7
1	B	118	PRO	2.7
1	B	194	ARG	2.7
1	A	151	GLY	2.6
1	B	285	LEU	2.6
1	B	54	GLY	2.6
1	A	240	ALA	2.6
1	A	187	VAL	2.6
1	A	58	ARG	2.6
1	A	85	VAL	2.6
1	A	138	VAL	2.6
1	A	203	VAL	2.5
1	A	45	ARG	2.5
1	B	123	LEU	2.5
1	B	292	GLU	2.5
1	A	200	ALA	2.4
1	B	251	ARG	2.4
1	B	203	VAL	2.4
1	B	200	ALA	2.4
1	A	191	THR	2.4
1	B	208	LEU	2.4
1	B	230	LEU	2.4
1	A	293	ASP	2.4
1	B	281	PRO	2.4
1	A	205	HIS	2.4
1	A	59	PHE	2.3
1	B	284	PHE	2.3
1	B	154	ALA	2.3
1	A	84	SER	2.3
1	A	266	ILE	2.3
1	B	168	ILE	2.3
1	A	126	SER	2.3
1	B	276	LYS	2.3
1	B	274	SER	2.3
1	A	64	LEU	2.2
1	B	171	GLN	2.2
1	A	270	ASN	2.2
1	B	151	GLY	2.2
1	B	56	THR	2.2
1	B	174	PRO	2.1
1	A	111	LYS	2.1
1	B	79	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	184	PRO	2.1
1	A	108	PRO	2.1
1	B	145	LEU	2.1
1	B	223	GLY	2.1
1	A	68	VAL	2.1
1	A	279	TYR	2.1
1	B	197	ALA	2.1
1	A	262	LEU	2.1
1	B	124	LEU	2.1
1	A	143	PHE	2.0
1	A	51	SER	2.0
1	B	135	PHE	2.0
1	B	143	PHE	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	CXR	B	301	35/35	0.85	0.17	-0.26	33,45,69,71	0
2	CXR	A	301	35/35	0.91	0.15	-0.44	30,36,53,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.