



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:34 PM UTC

PDB ID : 6OE3 / pdb_00006oe3
Title : Crystal Structure of HIV-1 Reverse Transcriptase in Complex with 5-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-7-fluoro-2-naphthonitrile (JLJ635), a Non-nucleoside Inhibitor
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Deposited on : 2019-03-27
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

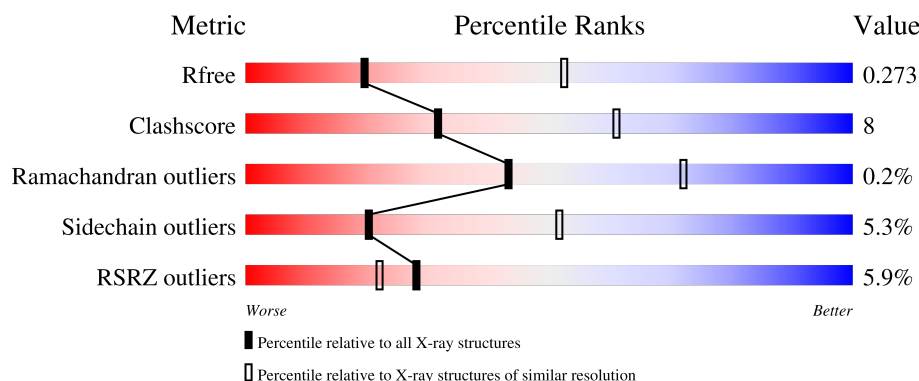
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	557	6% 76% 21% .
2	B	428	6% 72% 21% .

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7600 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 HIV-1 REVERSE TRANSCRIPTASE, P66 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	0	0	0
			4279	2770	699	804	6			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

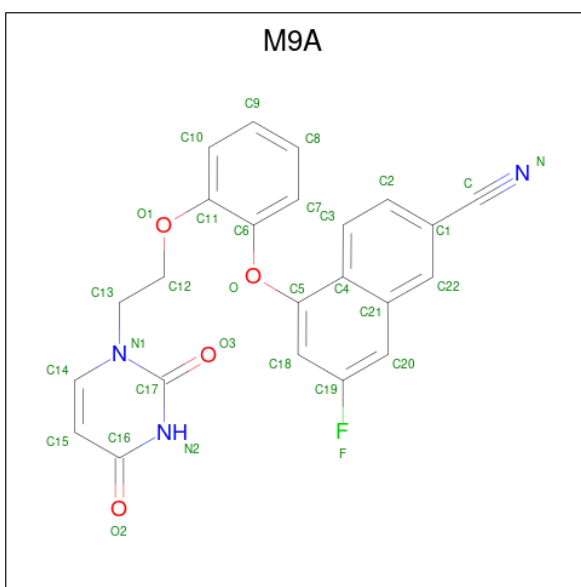
- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE, P51 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	409	Total	C	N	O	S	0	0	0
			3271	2129	533	603	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is 5-{2-[2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy}-7-fluorona phthalene-2-carbonitrile (CCD ID: M9A) (formula: C₂₃H₁₆FN₃O₄).

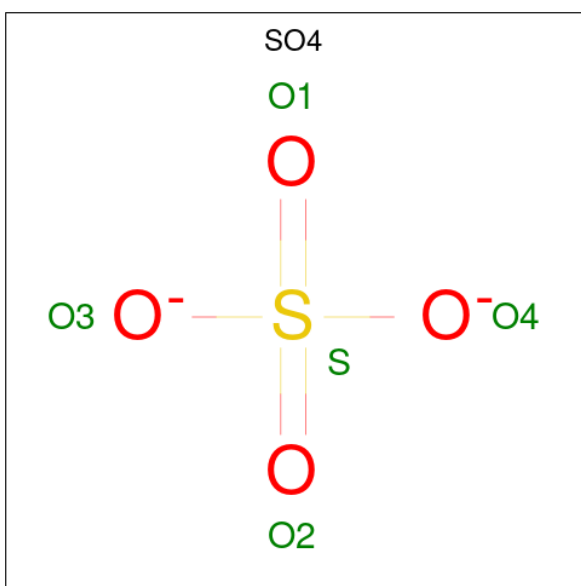


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			31	23	1	3	4		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

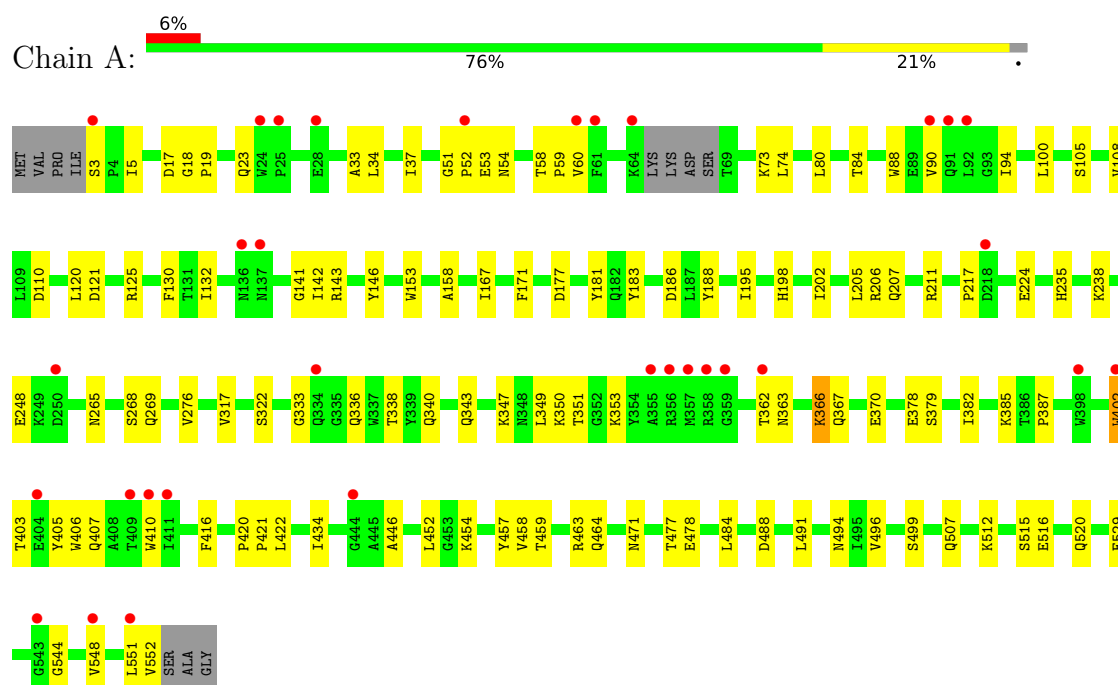
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	O	0	0
			8	8		
6	B	5	Total	O	0	0
			5	5		

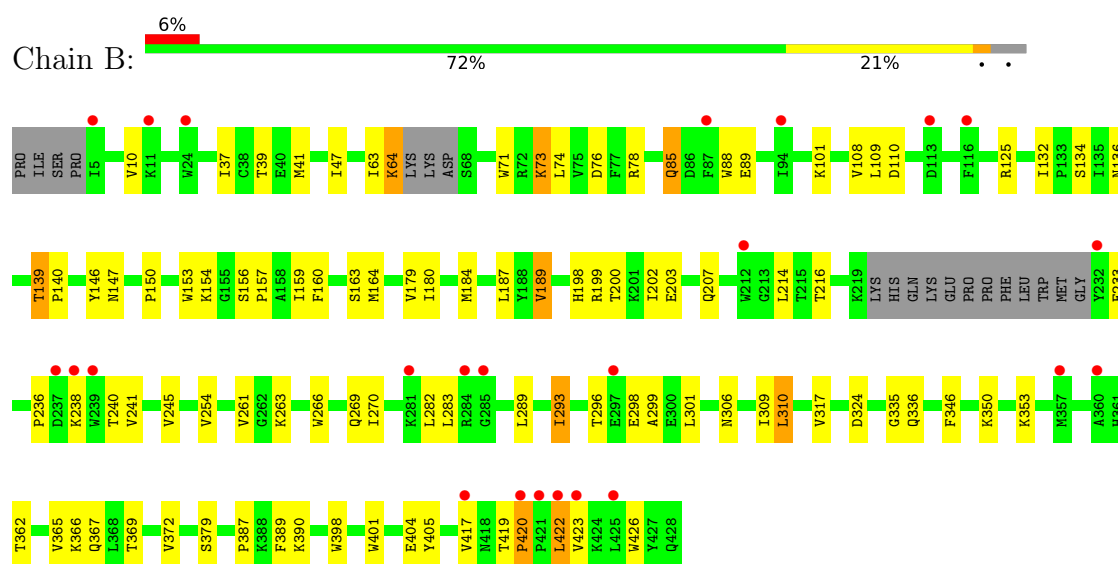
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: HIV-1 REVERSE TRANSCRIPTASE, P66 SUBUNIT



• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE, P51 SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	224.31Å 69.57Å 104.83Å 90.00° 105.79° 90.00°	Depositor
Resolution (Å)	43.17 – 2.90 43.17 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (43.17-2.90) 98.0 (43.17-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 2.90Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.228 , 0.273 0.232 , 0.273	Depositor DCC
R_{free} test set	1709 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	82.9	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7600	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, SO4, M9A

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	0.27	0/4393	0.47	0/6006
2	B	0.28	0/3363	0.48	0/4592
All	All	0.28	0/7756	0.48	0/10598

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	52	PRO	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4279	0	4136	69	0
2	B	3271	0	3199	61	0
3	A	31	0	0	0	0
4	A	1	0	0	0	0
5	A	5	0	0	0	0
6	A	8	0	0	0	0
6	B	5	0	0	0	0
All	All	7600	0	7335	121	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 8.

All (121) 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:B:85:GLN:HA	2:B:88:TRP:HB2	1.60	0.84
1:A:454:LYS:HB2	1:A:552:VAL:HG13	1.61	0.83
1:A:434:ILE:H	1:A:494:ASN:HD21	1.27	0.82
2:B:180:ILE:HG12	2:B:189:VAL:HG12	1.66	0.76
2:B:236:PRO:HA	2:B:238:LYS:HG3	1.69	0.74
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.21	0.73
2:B:390:LYS:HB3	2:B:417:VAL:HG21	1.76	0.68
1:A:382:ILE:HA	2:B:136:ASN:HD22	1.61	0.65
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.80	0.63
1:A:362:THR:HG23	1:A:512:LYS:HD2	1.80	0.62
1:A:458:VAL:HB	1:A:548:VAL:HG22	1.81	0.62
2:B:134:SER:OG	2:B:139:THR:O	2.12	0.60
1:A:51:GLY:O	1:A:53:GLU:N	2.33	0.60
2:B:306:ASN:HA	2:B:309:ILE:HG22	1.85	0.58
2:B:369:THR:HG22	2:B:398:TRP:CH2	2.39	0.58
1:A:350:LYS:NZ	1:A:378:GLU:OE2	2.33	0.57
2:B:296:THR:HB	2:B:299:ALA:H	1.69	0.57
2:B:366:LYS:HD2	2:B:405:TYR:CE1	2.39	0.57
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.86	0.56
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.41	0.56
2:B:254:VAL:HG22	2:B:293:ILE:HD11	1.88	0.56
1:A:317:VAL:HG11	1:A:347:LYS:HD2	1.87	0.56
1:A:478:GLU:HG2	1:A:499:SER:CB	2.36	0.56
2:B:10:VAL:HG13	2:B:88:TRP:CZ2	2.41	0.55
2:B:101:LYS:O	2:B:236:PRO:HB2	2.06	0.55
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.72	0.55
1:A:382:ILE:HG23	2:B:136:ASN:ND2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:157:PRO:HG3	2:B:184:MET:HA	1.91	0.52
1:A:446:ALA:HB2	1:A:477:THR:HG21	1.92	0.52
2:B:125:ARG:HD3	2:B:147:ASN:HA	1.91	0.52
1:A:17:ASP:OD1	1:A:18:GLY:N	2.42	0.52
2:B:306:ASN:O	2:B:310:LEU:HB2	2.09	0.52
1:A:80:LEU:O	1:A:84:THR:HG23	2.09	0.52
1:A:171:PHE:CZ	1:A:205:LEU:HB2	2.45	0.52
2:B:10:VAL:HA	2:B:88:TRP:HZ2	1.75	0.52
2:B:199:ARG:NE	2:B:233:GLU:OE2	2.43	0.52
2:B:160:PHE:HE2	2:B:164:MET:HE2	1.76	0.51
1:A:207:GLN:O	1:A:211:ARG:HG3	2.11	0.51
1:A:132:ILE:O	1:A:141:GLY:HA3	2.11	0.51
2:B:379:SER:OG	2:B:387:PRO:HD3	2.12	0.50
2:B:110:ASP:O	2:B:216:THR:HG22	2.11	0.50
1:A:110:ASP:O	1:A:217:PRO:HD3	2.10	0.50
1:A:235:HIS:HB2	1:A:238:LYS:O	2.12	0.50
2:B:240:THR:HG23	2:B:350:LYS:HG3	1.93	0.50
1:A:544:GLY:O	1:A:548:VAL:HG23	2.11	0.50
2:B:85:GLN:HG3	2:B:154:LYS:HB3	1.94	0.50
2:B:64:LYS:HD3	2:B:71:TRP:CD2	2.47	0.49
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.76	0.49
2:B:88:TRP:HZ3	2:B:159:ILE:HG13	1.77	0.49
1:A:94:ILE:HG22	1:A:183:TYR:HE1	1.77	0.49
1:A:90:VAL:HG22	1:A:158:ALA:HB2	1.95	0.49
2:B:85:GLN:O	2:B:89:GLU:N	2.45	0.49
2:B:198:HIS:O	2:B:202:ILE:HG12	2.13	0.48
2:B:324:ASP:OD1	2:B:324:ASP:N	2.47	0.48
2:B:245:VAL:O	2:B:263:LYS:NZ	2.43	0.48
2:B:298:GLU:O	2:B:301:LEU:HB2	2.14	0.47
1:A:23:GLN:HE22	1:A:59:PRO:HA	1.77	0.47
1:A:269:GLN:HA	1:A:351:THR:O	2.14	0.47
1:A:410:TRP:HZ3	2:B:405:TYR:HE2	1.61	0.47
2:B:150:PRO:HG2	2:B:153:TRP:HB2	1.96	0.47
2:B:73:LYS:HG3	2:B:74:LEU:N	2.28	0.47
2:B:160:PHE:CE2	2:B:164:MET:HE2	2.51	0.46
1:A:457:TYR:OH	1:A:488:ASP:OD2	2.30	0.46
1:A:416:PHE:HZ	1:A:422:LEU:HD21	1.80	0.46
1:A:496:VAL:HG21	2:B:289:LEU:HD21	1.96	0.46
1:A:340:GLN:HG3	1:A:351:THR:HG22	1.97	0.46
1:A:516:GLU:O	1:A:520:GLN:HG3	2.16	0.45
1:A:88:TRP:CH2	2:B:140:PRO:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:GLU:HG2	1:A:499:SER:HB3	1.99	0.45
2:B:266:TRP:O	2:B:269:GLN:HG2	2.16	0.45
1:A:379:SER:CB	1:A:387:PRO:HD3	2.46	0.45
1:A:100:LEU:HD22	1:A:181:TYR:HE2	1.81	0.45
1:A:177:ASP:OD1	1:A:177:ASP:N	2.43	0.45
1:A:121:ASP:O	1:A:125:ARG:HG3	2.17	0.45
1:A:108:VAL:HG13	1:A:188:TYR:CE1	2.52	0.45
1:A:3:SER:N	1:A:5:ILE:HD12	2.32	0.45
2:B:108:VAL:O	2:B:109:LEU:HD23	2.16	0.45
1:A:198:HIS:O	1:A:202:ILE:HG12	2.17	0.44
2:B:422:LEU:HD21	2:B:426:TRP:CZ3	2.52	0.44
1:A:265:ASN:O	1:A:268:SER:OG	2.25	0.44
1:A:406:TRP:CE3	2:B:420:PRO:HD3	2.52	0.44
1:A:350:LYS:HE3	1:A:350:LYS:HB2	1.88	0.44
1:A:382:ILE:HG23	2:B:136:ASN:HD21	1.82	0.44
1:A:54:ASN:OD1	1:A:143:ARG:NH1	2.50	0.44
1:A:402:TRP:CD1	1:A:402:TRP:C	2.96	0.44
1:A:5:ILE:HG12	1:A:167:ILE:HD11	2.00	0.43
2:B:336:GLN:HE21	2:B:353:LYS:HD3	1.82	0.43
1:A:333:GLY:O	1:A:336:GLN:NE2	2.35	0.43
1:A:202:ILE:O	1:A:206:ARG:HG3	2.19	0.43
1:A:458:VAL:HG22	1:A:464:GLN:HG2	2.00	0.43
1:A:420:PRO:HA	1:A:421:PRO:C	2.44	0.43
1:A:478:GLU:HG2	1:A:499:SER:HB2	2.00	0.43
1:A:186:ASP:HB3	1:A:188:TYR:CE1	2.53	0.43
1:A:434:ILE:N	1:A:494:ASN:HD21	2.05	0.43
2:B:63:ILE:HD13	2:B:74:LEU:HD22	2.00	0.43
1:A:60:VAL:HG21	1:A:130:PHE:CD2	2.54	0.42
1:A:94:ILE:HG22	1:A:183:TYR:CE1	2.54	0.42
1:A:19:PRO:HG3	1:A:80:LEU:HB2	2.01	0.42
2:B:372:VAL:HG13	2:B:389:PHE:CZ	2.55	0.42
2:B:335:GLY:HA2	2:B:367:GLN:HE22	1.84	0.42
2:B:179:VAL:O	2:B:189:VAL:HA	2.20	0.42
1:A:362:THR:OG1	1:A:363:ASN:N	2.51	0.41
1:A:491:LEU:O	1:A:529:GLU:N	2.52	0.41
2:B:365:VAL:O	2:B:369:THR:HG23	2.19	0.41
2:B:401:TRP:CE3	2:B:404:GLU:HG3	2.53	0.41
2:B:85:GLN:C	2:B:88:TRP:H	2.29	0.41
1:A:366:LYS:O	1:A:370:GLU:HG3	2.21	0.41
1:A:406:TRP:CE2	2:B:419:THR:HG22	2.56	0.41
1:A:105:SER:HB2	1:A:198:HIS:ND1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:GLN:HE22	1:A:512:LYS:NZ	2.19	0.41
1:A:406:TRP:CZ2	2:B:419:THR:HG22	2.56	0.41
2:B:37:ILE:O	2:B:41:MET:HG3	2.21	0.41
1:A:120:LEU:HD12	1:A:121:ASP:H	1.86	0.40
2:B:156:SER:N	2:B:157:PRO:HD2	2.36	0.40
2:B:310:LEU:HA	2:B:310:LEU:HD12	1.85	0.40
1:A:34:LEU:HD23	1:A:34:LEU:HA	1.83	0.40
2:B:270:ILE:HG12	2:B:346:PHE:HB3	2.02	0.40
2:B:76:ASP:OD2	2:B:78:ARG:NE	2.54	0.40
1:A:33:ALA:O	1:A:37:ILE:HG13	2.21	0.40
2:B:64:LYS:HD3	2:B:71:TRP:CE2	2.56	0.40
2:B:203:GLU:O	2:B:207:GLN:HG2	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	A	542/557 (97%)	529 (98%)	13 (2%)	0	100	100
2	B	403/428 (94%)	384 (95%)	17 (4%)	2 (0%)	24	54
All	All	945/985 (96%)	913 (97%)	30 (3%)	2 (0%)	43	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	241	VAL
2	B	420	PRO

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	445/495 (90%)	423 (95%)	22 (5%)	22	54
2	B	348/390 (89%)	328 (94%)	20 (6%)	18	49
All	All	793/885 (90%)	751 (95%)	42 (5%)	20	52

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	THR
1	A	74	LEU
1	A	142	ILE
1	A	195	ILE
1	A	224	GLU
1	A	248	GLU
1	A	276	VAL
1	A	322	SER
1	A	338	THR
1	A	353	LYS
1	A	366	LYS
1	A	385	LYS
1	A	402	TRP
1	A	403	THR
1	A	452	LEU
1	A	459	THR
1	A	463	ARG
1	A	471	ASN
1	A	484	LEU
1	A	507	GLN
1	A	515	SER
1	A	551	LEU
2	B	39	THR
2	B	64	LYS
2	B	73	LYS
2	B	85	GLN
2	B	132	ILE

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Mol	Chain	Res	Type
2	B	139	THR
2	B	163	SER
2	B	187	LEU
2	B	189	VAL
2	B	200	THR
2	B	214	LEU
2	B	261	VAL
2	B	282	LEU
2	B	283	LEU
2	B	293	ILE
2	B	310	LEU
2	B	317	VAL
2	B	362	THR
2	B	422	LEU
2	B	423	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	147	ASN
1	A	161	GLN
1	A	182	GLN
1	A	340	GLN
1	A	367	GLN
1	A	494	ASN
2	B	85	GLN
2	B	91	GLN
2	B	269	GLN
2	B	336	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 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	$\# Z > 2$
3	M9A	A	601	-	34,34,34	0.20	0	47,47,47	0.44	0
5	SO4	A	603	-	4,4,4	0.24	0	6,6,6	0.08	0

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	M9A	A	601	-	-	0/12/12/12	0/4/4/4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 ⓘ

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	546/557 (98%)	0.48	32 (5%)	28 22	59, 89, 137, 167	0
2	B	409/428 (95%)	0.48	24 (5%)	28 22	54, 86, 143, 210	0
All	All	955/985 (96%)	0.48	56 (5%)	28 22	54, 88, 141, 210	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	SER	6.2
2	B	232	TYR	4.0
2	B	237	ASP	3.7
2	B	425	LEU	3.6
2	B	420	PRO	3.4
2	B	423	VAL	3.3
2	B	297	GLU	3.3
1	A	61	PHE	3.3
1	A	92	LEU	3.3
1	A	359	GLY	3.3
1	A	356	ARG	3.2
1	A	218	ASP	3.1
1	A	60	VAL	3.0
2	B	281	LYS	3.0
2	B	87	PHE	3.0
1	A	355	ALA	2.9
1	A	24	TRP	2.9
2	B	5	ILE	2.9
1	A	410	TRP	2.8
1	A	444	GLY	2.7
1	A	357	MET	2.7
1	A	90	VAL	2.6
2	B	11	LYS	2.5
1	A	25	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	409	THR	2.5
1	A	64	LYS	2.5
1	A	402	TRP	2.5
1	A	404	GLU	2.5
2	B	284	ARG	2.5
2	B	360	ALA	2.5
2	B	285	GLY	2.4
2	B	24	TRP	2.4
2	B	357	MET	2.4
2	B	239	TRP	2.4
1	A	411	ILE	2.4
1	A	52	PRO	2.4
2	B	116	PHE	2.3
1	A	398	TRP	2.3
2	B	212	TRP	2.3
1	A	250	ASP	2.3
1	A	137	ASN	2.3
1	A	28	GLU	2.3
1	A	334	GLN	2.2
1	A	358	ARG	2.2
2	B	421	PRO	2.2
2	B	113	ASP	2.1
1	A	362	THR	2.1
1	A	136	ASN	2.1
2	B	238	LYS	2.1
1	A	548	VAL	2.1
2	B	417	VAL	2.1
1	A	543	GLY	2.1
1	A	91	GLN	2.0
1	A	551	LEU	2.0
2	B	422	LEU	2.0
2	B	94	ILE	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
5	SO4	A	603	5/5	0.60	0.10	137,138,138,140	0
3	M9A	A	601	31/31	0.93	0.10	61,65,78,90	0
4	MG	A	602	1/1	0.97	0.15	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.