



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 12:31 AM UTC

PDB ID : 2FN1 / pdb_00002fn1
Title : Crystal structures of Yersinia enterocolitica salicylate synthase (Irp9) in complex with the reaction products salicylate and pyruvate
Authors : Kerbarh, O.; Chirgadze, D.Y.; Blundell, T.L.; Abell, C.
Deposited on : 2006-01-10
Resolution : 2.10 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

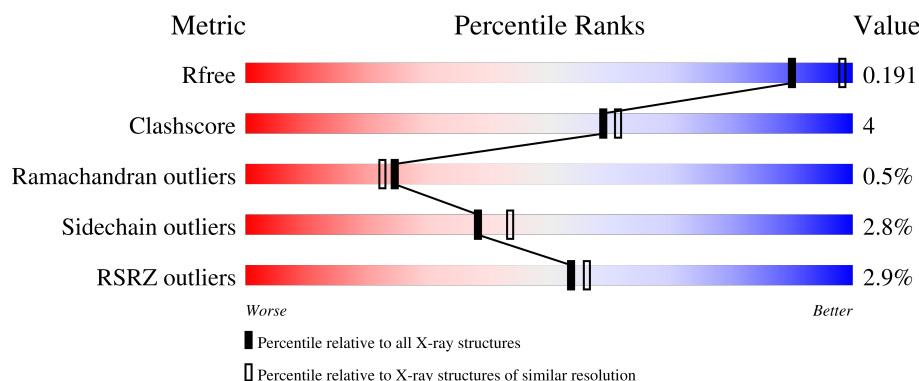
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	437	3% 82% 11% 7%
1	B	437	2% 79% 13% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6575 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 salicylate synthetase, Irp9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3100	1953	552	581	14			
1	B	411	Total	C	N	O	S	0	0	0
			3141	1987	560	580	14			

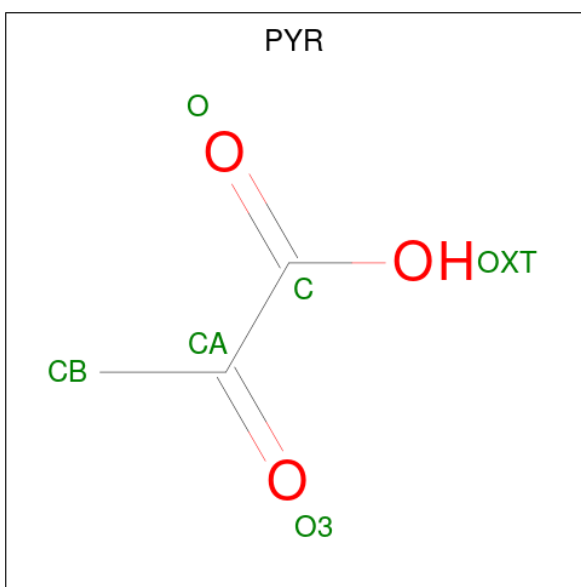
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	cloning artifact	GB 5420055
A	-1	SER	-	cloning artifact	GB 5420055
A	0	HIS	-	cloning artifact	GB 5420055
B	-2	GLY	-	cloning artifact	GB 5420055
B	-1	SER	-	cloning artifact	GB 5420055
B	0	HIS	-	cloning artifact	GB 5420055

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

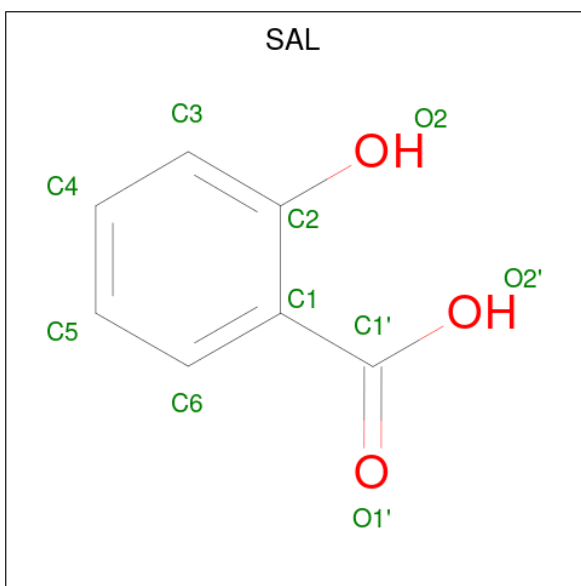
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PYRUVIC ACID (CCD ID: PYR) (formula: C₃H₄O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is 2-HYDROXYBENZOIC ACID (CCD ID: SAL) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	7	3		
4	B	1	Total	C	O	0	0
			10	7	3		

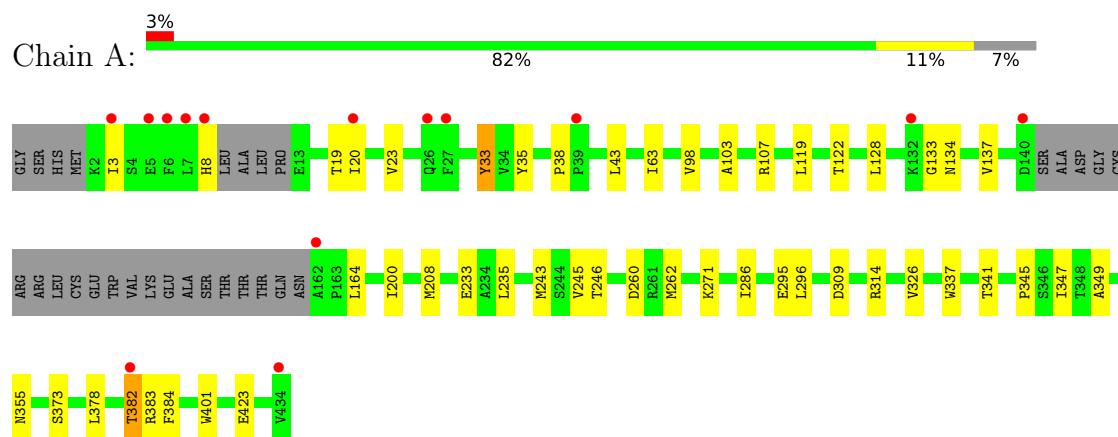
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	176	Total 176	O 176	0	0
5	B	124	Total 124	O 124	0	0

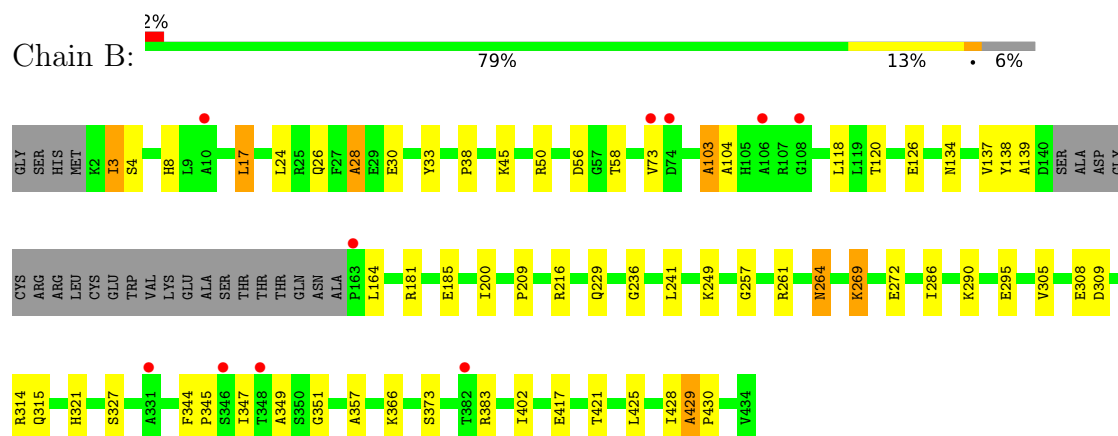
3 Residue-property plots [i](#)

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: salicylate synthetase, Irp9



- Molecule 1: salicylate synthetase, Irp9



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.57Å 145.30Å 58.86Å 90.00° 108.39° 90.00°	Depositor
Resolution (Å)	27.37 – 2.10 27.37 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.6 (27.37-2.10) 94.0 (27.37-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.58 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.245 0.190 , 0.191	Depositor DCC
R_{free} test set	2440 reflections (4.62%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6575	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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

5.1 Standard geometry

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

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	0.91	1/3159 (0.0%)	0.96	3/4285 (0.1%)
1	B	0.91	0/3204	1.01	6/4345 (0.1%)
All	All	0.91	1/6363 (0.0%)	0.98	9/8630 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	ILE	CA-CB	5.48	1.59	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	38	PRO	N-CA-CB	8.46	111.29	103.08
1	A	38	PRO	N-CA-CB	7.77	110.62	103.08
1	B	236	GLY	N-CA-C	5.36	118.40	110.42
1	B	249	LYS	N-CA-C	5.34	117.45	108.96
1	B	383	ARG	N-CA-C	5.33	117.92	109.50
1	B	429	ALA	CA-C-N	5.24	125.32	119.87
1	B	429	ALA	C-N-CA	5.24	125.32	119.87
1	A	401	TRP	N-CA-C	5.09	116.57	108.79
1	A	383	ARG	N-CA-C	5.08	116.78	108.76

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	3100	0	3030	24	0
1	B	3141	0	3103	32	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
4	A	10	0	4	0	0
4	B	10	0	4	0	0
5	A	176	0	0	0	0
5	B	124	0	0	2	0
All	All	6575	0	6141	55	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 4.

All (55) 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:103:ALA:HB2	1:B:345:PRO:HD3	1.36	1.04
1:A:337:TRP:O	1:A:341:THR:HG23	1.82	0.78
1:A:8:HIS:HA	1:A:134:ASN:HD22	1.52	0.74
1:B:103:ALA:CB	1:B:345:PRO:HD3	2.20	0.68
1:B:8:HIS:CD2	1:B:134:ASN:OD1	2.49	0.66
1:A:260:ASP:HB2	1:A:262:MET:HE2	1.81	0.62
1:B:344:PHE:CD1	1:B:345:PRO:HA	2.38	0.59
1:A:8:HIS:HA	1:A:134:ASN:ND2	2.18	0.57
1:B:261:ARG:HD2	1:B:315:GLN:OE1	2.05	0.56
1:A:260:ASP:CB	1:A:262:MET:HE2	2.37	0.55
1:B:181:ARG:O	1:B:185:GLU:HG3	2.07	0.54
1:B:402:ILE:HD12	1:B:425:LEU:HD22	1.90	0.54
1:B:126:GLU:HG2	1:B:139:ALA:HA	1.90	0.54
1:B:349:ALA:HB1	1:B:373:SER:HB2	1.90	0.53
1:B:120:THR:HG21	1:B:229:GLN:HE22	1.74	0.52
1:A:208:MET:HE2	1:A:233:GLU:HB3	1.92	0.52
1:A:295:GLU:CD	1:A:347:ILE:HD11	2.36	0.51
1:A:19:THR:O	1:A:23:VAL:HG23	2.11	0.50
1:A:128:LEU:CD2	1:A:137:VAL:HG22	2.42	0.50
1:A:243:MET:HE3	1:A:245:VAL:HG23	1.95	0.49
1:B:417:GLU:O	1:B:421:THR:HG23	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:GLU:OE1	1:B:45:LYS:HE2	2.13	0.48
1:A:246:THR:HG23	1:A:382:THR:O	2.13	0.48
1:B:33:TYR:OH	1:B:50:ARG:NH2	2.47	0.47
1:A:20:ILE:HG23	1:A:43:LEU:HD12	1.96	0.47
1:A:286:ILE:HG13	1:B:286:ILE:HG13	1.96	0.47
1:A:107:ARG:HD3	1:A:355:ASN:OD1	2.14	0.47
1:B:305:VAL:HA	1:B:327:SER:O	2.15	0.46
1:B:17:LEU:HD11	1:B:216:ARG:HB3	1.98	0.45
1:B:257:GLY:O	1:B:321:HIS:HA	2.16	0.45
1:A:309:ASP:OD2	1:A:314:ARG:NH2	2.50	0.45
1:B:103:ALA:O	1:B:104:ALA:C	2.60	0.45
1:B:264:ASN:OD1	1:B:264:ASN:N	2.48	0.44
1:A:98:VAL:HG22	1:A:119:LEU:HD12	1.99	0.44
1:B:309:ASP:OD2	1:B:314:ARG:NH2	2.48	0.44
1:A:349:ALA:HB1	1:A:373:SER:HB2	2.00	0.44
1:A:35:TYR:CD2	1:A:378:LEU:HD22	2.53	0.43
1:B:295:GLU:CD	1:B:347:ILE:HD11	2.44	0.43
1:A:103:ALA:HB2	1:A:345:PRO:HD3	2.00	0.43
1:B:24:LEU:HG	1:B:209:PRO:HG3	2.01	0.43
1:A:128:LEU:HD22	1:A:137:VAL:HG22	2.01	0.42
1:B:308:GLU:OE2	1:B:327:SER:OG	2.27	0.42
1:B:429:ALA:HB3	1:B:430:PRO:HD3	2.01	0.42
1:B:4:SER:HA	1:B:137:VAL:O	2.19	0.42
1:A:262:MET:HE1	1:A:423:GLU:HG2	2.01	0.42
1:A:271:LYS:HA	1:A:271:LYS:HD3	1.91	0.42
1:A:33:TYR:OH	1:A:122:THR:HG21	2.20	0.41
1:B:4:SER:HB3	1:B:138:TYR:CD1	2.56	0.41
1:B:56:ASP:OD1	1:B:58:THR:OG1	2.26	0.41
1:B:269:LYS:HD3	1:B:272:GLU:OE1	2.21	0.41
1:A:296:LEU:HD12	1:A:326:VAL:HG12	2.03	0.40
1:B:3:ILE:HA	5:B:554:HOH:O	2.21	0.40
1:B:26:GLN:C	1:B:28:ALA:H	2.28	0.40
1:B:30:GLU:HG3	5:B:581:HOH:O	2.20	0.40
1:B:351:GLY:HA3	1:B:357:ALA:CB	2.51	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	402/437 (92%)	387 (96%)	14 (4%)	1 (0%)	43	44
1	B	407/437 (93%)	387 (95%)	17 (4%)	3 (1%)	18	15
All	All	809/874 (93%)	774 (96%)	31 (4%)	4 (0%)	24	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	103	ALA
1	B	28	ALA
1	A	133	GLY
1	B	73	VAL

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	314/357 (88%)	307 (98%)	7 (2%)	45	53
1	B	321/357 (90%)	310 (97%)	11 (3%)	32	35
All	All	635/714 (89%)	617 (97%)	18 (3%)	38	43

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	33	TYR

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Mol	Chain	Res	Type
1	A	63	ILE
1	A	164	LEU
1	A	235	LEU
1	A	382	THR
1	A	384	PHE
1	B	3	ILE
1	B	17	LEU
1	B	118	LEU
1	B	164	LEU
1	B	200	ILE
1	B	241	LEU
1	B	264	ASN
1	B	269	LYS
1	B	290	LYS
1	B	366	LYS
1	B	428	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	134	ASN
1	A	229	GLN
1	B	8	HIS
1	B	134	ASN
1	B	171	ASN
1	B	229	GLN
1	B	359	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
4	SAL	B	503	2	10,10,10	1.66	2 (20%)	13,13,13	1.25	2 (15%)
4	SAL	A	506	2	10,10,10	2.15	1 (10%)	13,13,13	1.34	2 (15%)
3	PYR	A	505	-	5,5,5	3.01	3 (60%)	3,6,6	1.59	1 (33%)
3	PYR	B	502	-	5,5,5	2.75	3 (60%)	3,6,6	1.96	1 (33%)

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
4	SAL	B	503	2	-	0/4/4/4	0/1/1/1
4	SAL	A	506	2	-	2/4/4/4	0/1/1/1
3	PYR	A	505	-	-	0/4/4/4	-
3	PYR	B	502	-	-	0/4/4/4	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	506	SAL	C1-C2	5.95	1.50	1.40
3	A	505	PYR	CA-C	-4.51	1.39	1.54
3	B	502	PYR	CA-C	-4.45	1.39	1.54
4	B	503	SAL	C1-C2	4.18	1.47	1.40
3	A	505	PYR	O-C	3.99	1.32	1.22
3	B	502	PYR	O-C	3.26	1.30	1.22
3	A	505	PYR	O3-CA	2.99	1.30	1.23
3	B	502	PYR	O3-CA	2.67	1.29	1.23
4	B	503	SAL	O1'-C1'	2.32	1.29	1.22

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	502	PYR	OXT-C-CA	3.00	121.90	113.59
4	B	503	SAL	O2-C2-C1	-2.50	117.08	121.71
4	A	506	SAL	O2-C2-C1	-2.44	117.19	121.71
3	A	505	PYR	OXT-C-O	-2.13	118.84	123.90
4	B	503	SAL	C4-C5-C6	2.09	122.82	120.24
4	A	506	SAL	C6-C1-C1'	2.09	123.44	118.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	506	SAL	C2-C1-C1'-O1'
4	A	506	SAL	C2-C1-C1'-O2'

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 [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	408/437 (93%)	-0.19	14 (3%)	48 50	17, 29, 61, 74	0
1	B	411/437 (94%)	-0.02	10 (2%)	59 62	19, 32, 56, 71	0
All	All	819/874 (93%)	-0.11	24 (2%)	53 56	17, 31, 58, 74	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	73	VAL	3.7
1	A	3	ILE	3.6
1	A	27	PHE	3.4
1	A	7	LEU	3.2
1	B	106	ALA	3.1
1	A	140	ASP	2.9
1	B	74	ASP	2.9
1	B	163	PRO	2.9
1	A	132	LYS	2.8
1	B	10	ALA	2.6
1	B	382	THR	2.6
1	A	162	ALA	2.6
1	A	382	THR	2.5
1	B	348	THR	2.4
1	B	331	ALA	2.4
1	A	434	VAL	2.4
1	B	346	SER	2.4
1	A	26	GLN	2.4
1	A	8	HIS	2.3
1	A	6	PHE	2.2
1	A	20	ILE	2.2
1	A	5	GLU	2.1
1	B	108	GLY	2.1
1	A	39	PRO	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
4	SAL	A	506	10/10	0.91	0.09	26,29,34,35	0
4	SAL	B	503	10/10	0.91	0.10	19,26,27,37	0
3	PYR	A	505	6/6	0.97	0.07	24,25,25,30	0
3	PYR	B	502	6/6	0.97	0.05	18,19,23,28	0
2	MG	A	504	1/1	0.99	0.02	29,29,29,29	0
2	MG	B	501	1/1	0.99	0.02	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.